### CORRECTED VERSION

# (19) World Intellectual Property Organization International Bureau



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09/598,042	9 July 2000 (09.07.2000)	US
09/620,312	19 July 2000 (19.07.2000)	US
09/653,450	3 August 2000 (03.08.2000)	US
09/662,191	14 September 2000 (14.09.2000)	US
09/693,036	19 October 2000 (19.10.2000)	US
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(63) Related by continuation (CON) or continuation-in-part (CIP) to earlier applications:

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- (71) Applicant (for all designated States except US): HYSEQ, INC. [US/US]; 670 Almanor Avenue, Sunnyvale, CA 94086 (US).
- (72) Inventors; and
- (75) Inventors/Applicants (for US only): TANG, Y., Tom [US/US]; 4230 Ranwick Court, San Jose, CA 95118 (US).

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- (74) Agent: ELRIFI, Ivor, R.; Mintz, Levin, Cohn, Ferris, Glovsky, and Popeo, P.C., One Financial Center, Boston, MA 02111 (US).
- (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

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[Continued on next page]

(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.





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1 November 2001

(15) Information about Correction: see PCT Gazette No. 44/2001 of 1 November 2001, Section II For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

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(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.





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### REVISED VERSION

### INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/34263

GT 4.00	CHEICATION OF SUBJECT MATTER		
A. CLASSIFICATION OF SUBJECT MATTER  IPC(7) : C07H 21/04; C12N 15/11, 15/63, 15/70, 15/82, 15/85; C07K 14/00			
TIC CI	TIS CT . 536/23 1: 435/320 1 455, 468, 530/300, 350		
According to l	International Patent Classification (IPC) or to both natio	nal classification and IPC	
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Minimum doc U.S.: 53	Minimum documentation searched (classification system followed by classification symbols) U.S.: 536/23.1; 435/320.1, 455, 468, 530/300, 350		
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched			n the fields searched
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) MEDLINE, EAST			
C. DOC	UMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where app	propriate, of the relevant passages	Relevant to claim No.
A	WAJIMA et al. The cDNA cloning and transient expr hydroxysteroid dehydrogenase of chickens. Gene. 199	9, Vol.233, pages 75-82	1-11, 13-16, and 19-26
A	US 5,175,095 A (MARTINEAU et al) 29 December 1 columns 3-18.	1992 (29.12.1992), see especially	1-11, 13-16, and 19-26
A	Database PubMed, ID No. 2393392, FREUDENSTEI inhibitor of metalloproteinase: sequence and expression Biophys. Res. Commun. August 1990. Vol.171. No.	on in bovine ovarian tissue. Biochem.	1-11, 13-16, and 19-26
A,P	Database PubMed, ID No. 10919256, HENNEBOLE generation and characterization of an ovary-selective clibrary. Endocrinology. August 2000. Vol.141. No.8.	complementary deoxyribonucleic acid	1-11, 13-16, and 19-26
A	Database PubMed, ID No. 2760883, BEIL et al. Synthe baboon (Papio anubis). J. Reprod. Fertil. July 198 Abstract.	thesis of polypeptides by the cervix of 39. Vol.86. No.2. pages 535-544, see	1-11, 13-16, and 19-26
A,P	Database PubMed, ID No. 10830289, HINSHELWO upstream of the human CYP19 (aromatase) gene med transgenic mice. Endocrinology. June 2000. Vol.141	iates ovary-specific expression in	1-11, 13-16, and 19-26
Furthe	er documents are listed in the continuation of Box C.	See patent family annex.	
•	Special categories of cited documents:	"T" later document published after the in date and not in conflict with the appl	lication but cited to understand the
"A" docume of partic	nt defining the general state of the art which is not considered to be cular relevance	principle or theory underlying the in "X" document of particular relevance; th	vention
1	application or patent published on or after the international filing date	considered novel or cannot be considered when the document is taken alone	dered to involve an inventive step
establisi specifie		"Y" document of particular relevance; the considered to involve an inventive strombined with one or more other su	tep when the document is such documents, such combination
"O" docume	ent referring to an oral disclosure, use, exhibition or other means	being obvious to a person skilled in	
"P" docume	ent published prior to the international filing date but later than the date claimed	"&" document member of the same pater	
Date of the actual completion of the international search Date of mailing of the internation		Date of mailing of the international se	arch report
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В	ommissioner of Patents and Trademarks ox PCT	Michael Woodward //	K
W	/ashington, D.C. 20231 No. (703)305-3230	Telephone No. (703)/308-0196	

Form PCT/ISA/210 (second sheet) (July 1998)

# INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/34263

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)
Box I Observations where certain claims were reasons:  This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:
This international report has not been established in responsible in the stabilished in responsible in the stabilished in the s
1. Claim Nos.: because they relate to subject matter not required to be searched by this Authority, namely:
2. Claim Nos.: because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. Claim Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).
Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)
This International Searching Authority found multiple inventions in this international application, as follows: This includes 4 invention Groups and 3572 sequence species
<ol> <li>As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.</li> <li>As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.</li> <li>As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:</li> </ol>
A. No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-11, 13-16; and 14-26  Remark on Protest  The additional search fees were accompanied by the applicant's protest.  No protest accompanied the payment of additional search fees.

Form PCT/ISA/210 (continuation of first sheet(1)) (July 1998)

#### INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/34263

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional serch fees must be paid. Group I, claims 1-11, 13-16, and 19-26, drawn to nucleic acid molecules, vector molecules and host cells containing said nucleic acids, polypeptides, methods of making said polypeptides and method of detection using said nucleic acids and polypeptides. Group II, claim 12 and 28, drawn to antibodies and method of treatment using composition comprising said antibodies. Group III, claims 17-18, drawn to methods of indentifying a binding partner to a polypeptides. Group IV, claim 27, drawn to method of treatment using composition comprising polypeptides.

The inventions listed as Groups I-IV do not relate to a single inventive concept under PCT Rule 13.1 because, udner PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Group I encompasses nucleic acids, polypeptides expressed thereby, vectors and host cells containg same, respectively, and methods of making as well as the first method of use of this jubject matter. Groups II-V all are directed to different special technical features as summarized as follows: Group II is directed to an antibody and method of treatment using same, which antibody undergoes recognition and binding reactions wherein what is bound is different from what is bound by the compositions of Group I. For example, the polypeptides of Group I do not bind the polypeptides of Group I as the antibody of Group II does. Identification of binding partner and treatment are clearly different special technical features from detection. Group III is directed to the identification of a binding partner of a polypeptide, which is not identified in any of the other Groups and thus clearly contains its own special technical feature. Group IV is directed to treatment, which is a clearly different methods than the methods in the other Groups. Thus, in summary, each of Groups I-IV are directed to different special technical features and thus support this lack of unity.

Additionally, each of the claims is directed to more than one species of the generic invention. These species are deemed to lack unity of invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be searched, the appropriate additional search fees must be paid. The species are as follows: The claims include a series of polynucleotides and the polypeptides encoded thereby as represented by the sequences of SEQ ID Nos: 1-1786, and 3573-5358. Each of these polynucleotide sequences encodes a separate polypeptide and thus represent a separate gene. Therefore, each of these genes defines its own special technical feature. In summary, one species is a gene represented by one polynucleotide sequence and one polypeptide sequence encoded thereby.

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- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

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- before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments

[Continued on next page]

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### NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

#### 1. TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

#### 2. BACKGROUND

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Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs, chemokines, and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, ferrexample, diagnostics, forensics, gene mapping; identification of mutations responsible for genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

#### 3. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1-1786 and 3573-5358. The polypeptides sequences are designated SEQ ID NO: 2n (wherein n = 1 to 20). The nucleic acids and polypeptides are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, \* corresponds to the stop codon.

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The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO:1-1786 and 3573-5358 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO:1-1786 and 3573-5358. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO:1-1786 and 3573-5358 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO:1-1786 and 3573-5358. The sequence information can be a segment of any one of SEQ ID NO:1-1786 and 3573-5358 that uniquely identifies or represents the sequence information of SEQ ID NO:1-1786 and 3573-5358.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing

full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-1786 and 3573-5358 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-1786 and 3573-5358 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

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The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO:1-1786 and 3573-5358; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO:1-1786 and 3573-5358; and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO:1-1786 and 3573-5358. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO:1-1786 and 3573-5358; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO:1-1786 and 3573-5358; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

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Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, e.g., in situ hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

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The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (i.e., increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (e.g., bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound the binds to a polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products. Compounds and other substances can

effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in Table 2); for which they have a signature region (as set forth in Table 3); or for which they have homology to a gene family (as set forth in Table 4). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

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### 4. DETAILED DESCRIPTION OF THE INVENTION

appropriate animals or cells and to bind with specific antibodies.

#### 4.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady

and continuous source of germ cells for the production of gametes. The term "primordial germ cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived. The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

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The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonculeotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100 nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30

nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NOs:1-20.

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Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO:1-1786 and 3573-5358. The sequence information can be a segment of any one of SEQ ID NO:1-1786 and 3573-5358 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NO:1-1786 and 3573-5358. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4<sup>20</sup> possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match  $(1 \div 4^{25})$  times the increased probability for mismatch at each nucleotide position  $(3 \times 25)$ . The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements e.g. repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

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The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include the initial methionine residue. The methionine residue may be removed from the protein during processing in the cell. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (e.g., with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

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The term "variant" (or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, e g., recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations

can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

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The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, e.g., polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (e.g., nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (e.g., microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (e.g., yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, e.g., E. coli, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use

in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

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The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (e.g. Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134-143) and factors released from damaged cells (e.g. Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (i.e., hybridization to filter-bound DNA in 0.5 M NaHPO<sub>4</sub>, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (i.e., washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

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As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (i.e., the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, e.g., mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more that 5% (95% sequence identity). Substantially equivalent, e.g., mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 90% sequence identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, and most preferably at least about 95% identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (e.g., via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, e.g., using the Jotun Hein method (Hein, J. (1990) Methods Enzymol. 183:626-645). Identity between sequences can also be determined by other methods known in the art, e.g. by varying hybridization conditions.

The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The

term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

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Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

### 4.2 NUCLEIC ACIDS OF THE INVENTION

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Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358; a polynucleotide encoding any one of the peptide sequences of SEQ ID NO:1787-3572 and 5359-7144; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of any one of SEQ ID NO:1787-3572 and 5359-7144. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO:1-1786 and 3573-5358; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO:1787-3572 and 5359-7144. Domains of interest may depend on the nature of the encoded polypeptide; e.g., domains in receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, e.g., cDNA and genomic DNA, and RNA, e.g., mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

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The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO:1-1786 and 3573-5358 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO:1-1786 and 3573-5358 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpri, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, e.g., at least about 65%, at least about 70%, at least about 75%, at least about 80%, more typically at least about 90%, and even more typically at least about 95%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, e.g. 15, 17, or 20 nucleotides or more that are selective for (i.e. specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in

the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided SEQ ID NO:1-1786 and 3573-5358, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NO:1-1786 and 3573-5358 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

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The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NO:1-1786 and 3573-5358, can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altshul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, e.g., by substituting first with conservative choices (e.g.,

hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (e.g., hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., *DNA* 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, *Nucleic Acids Res.* 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., supra, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

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In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO:1-1786 and 3573-5358, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, e.g., plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following

vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

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The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., Nucleic Acids Res. 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, Methods in Enzymology 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of E. coli and S. cerevisiae TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for

transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

#### 4.3 ANTISENSE

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Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1-1786 and 3573-5358, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEQ ID NO:1787-3572 and 5359-7144 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO:1-1786 and 3573-5358 are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (i.e., also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding a nucleic acid disclosed herein (e.g., SEQ ID NO:1-1786 and 3573-5358, antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of a mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of a mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used.

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Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-

- 25 2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil,
- 30 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a 35

nucleic acid has been subcloned in an antisense orientation (i.e., RNA transcribed from the

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inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

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The antisense nucleic acid molecules of the invention are typically administered to a subject or generated in situ such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, e.g., by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, e.g., by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α-anomeric nucleic acid molecule. An α-anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β-units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA -DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

### 4.4 RIBOZYMES AND PNA MOIETIES

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as a mRNA, to which they have a complementary region. Thus, ribozymes (e.g., hammerhead ribozymes (described in Haselhoff and Gerlach (1988) Nature 334:585-591)) can be used to catalytically cleave a mRNA transcripts to thereby inhibit translation of a mRNA. A ribozyme having specificity for a nucleic acid of the invention can be designed based upon the nucleotide sequence of a DNA disclosed herein (i.e., SEQ ID NO:1-1786 and 3573-5358). For example, a derivative of a Tetrahymena L-19 IVS RNA can be

constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a SECX-encoding mRNA. See, e.g., Cech et al. U.S. Pat. No. 4,987,071; and Cech et al. U.S. Pat. No. 5,116,742. Alternatively, SECX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, e.g., Bartel et al., (1993) Science 261:1411-1418.

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Alternatively, gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region (e.g., promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells. See generally, Helene. (1991) Anticancer Drug Des. 6: 569-84; Helene. et al. (1992) Ann. N.Y. Acad. Sci. 660:27-36; and Maher (1992) Bioassays 14: 807-15.

In various embodiments, the nucleic acids of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, e.g., the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup et al. (1996) Bioorg Med Chem 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, e.g., DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup et al. (1996) above; Perry-O'Keefe et al. (1996) PNAS 93: 14670-675.

PNAs of the invention can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, e.g., inducing transcription or translation arrest or inhibiting replication. PNAs of the invention can also be used, e.g., in the analysis of single base pair mutations in a gene by, e.g., PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, e.g., S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup et al. (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of the invention can be modified, e.g., to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, e.g., RNase H and DNA polymerases, to interact with the DNA portion while the PNA

portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors in vivo), or agents facilitating transport across the cell membrane (see, e.g., Letsinger et al., 1989, Proc. Natl. Acad. Sci. U.S.A. 86:6553-6556; Lemaitre et al., 1987, Proc. Natl. Acad. Sci. 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, e.g., PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, e.g., Krol et al., 1988, BioTechniques 6:958-976) or intercalating agents. (See, e.g., Zon, 1988, Pharm. Res. 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, e.g., a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

### **4.5 HOSTS**

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The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express

the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in coamplification of the desired protein coding sequences in the cells.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., Basic Methods in Molecular Biology (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

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Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, ct al., in Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, Cell 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK,

HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include Saccharomyces cerevisiae, Schizosaccharomyces pombe, Kluyveromyces strains, Candida, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include Escherichia coli, Bacillus subtilis, Salmonella typhimurium, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the

protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, e.g., inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference

PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

### 4.6 POLYPEPTIDES OF THE INVENTION

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The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO:1787-3572 and 5359-7144 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO:1-1786 and 3573-5358 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NO:1-1786 and 3573-5358 or (b) polynucleotides encoding any one of the amino acid sequences

set forth as SEQ ID NO:1787-3572 and 5359-7144 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO:1787-3572 and 5359-7144 or the corresponding full length or mature protein; and "substantial equivalents" thereof (e.g., with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, typically at least about 95%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO:1787-3572 and 5359-7144.

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Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., Bio/Technology 10, 773-778 (1992) and in R. S. McDowell, et al., J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (e.g., an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, e.g., Scopes, Protein Purification: Principles and Practice, Springer-Verlag (1994); Sambrook, et al., in Molecular Cloning: A Laboratory Manual; Ausubel et al., Current Protocols in Molecular Biology. Polypeptide fragments that

retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

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The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for e.g., small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO:1787-3572 and 5359-7144.

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological

methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, Calif., U.S.A. (the MaxBat<sup>TM</sup> kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

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The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl<sup>TM</sup> or Cibacrom blue 3GA Sepharose<sup>TM</sup>; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, e.g., targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, e.g., antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

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# 4.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., Nucleic Acids Research 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., J. Molec. Biol. 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., Nucleic Acids Res. vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., J. Comp. Biol., Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, ISMB-97, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference) and the Kyte-Doolittle hydrophobocity prediction algorithm (J. Mol Biol, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al., NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., J. Mol. Biol. 215:403-410 (1990).

### 4.7 CHIMERIC AND FUSION PROTEINS

The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to

another polypeptide. Within a fusion protein the polypeptide according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate that the polypeptide according to the invention and the other polypeptide are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus.

For example, in one embodiment a fusion protein comprises a polypeptide according to the invention operably linked to the extracellular domain of a second protein.

In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences.

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which the polypeptide sequences according to the invention comprises one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand and a protein of the invention on the surface of a cell, to thereby suppress signal transduction *in vivo*. The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand. Inhibition of the ligand/protein interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, *e,g.*, cancer as well as modulating (*e.g.*, promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays to identify molecules that inhibit the interaction of a polypeptide of the invention with a ligand.

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, e.g., by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for

example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the protein of the invention.

#### 4.8 GENE THERAPY

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Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected ex vivo, in situ, or in vivo by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or ex vivo by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or artificial chromosomes (stable expression). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered in vivo to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in

the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

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In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, e.g., inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are

added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

#### 4.9 TRANSGENIC ANIMALS

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In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous

promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

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The polynucleotides of the present invention also make possible the development, through, e.g., homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

# 4.10 USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the

polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, e.g., via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

#### 4.10.1 RESEARCH USES AND UTILITIES

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The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

#### 4.10.2 NUTRITIONAL USES

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Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

# 4.10.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient

confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK,

HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

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Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin-γ, Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 20 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse 25 and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Aced. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 30 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober,

Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

### 4.10.4 STEM CELL GROWTH FACTOR ACTIVITY

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A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells in vivo or ex vivo is expected to maintain and expand cell populations in a totipotential or pluripotential state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder

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layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotential/pluripotential stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotential/pluripotential mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., Differentiation, 48: 173-182, (1991); Klug et al., J. Clin. Invest., 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering eds*. Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell

sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support e.g. as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

#### 4.10.5 HEMATOPOIESIS REGULATING ACTIVITY

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A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

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#### 4.10.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

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The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular

endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

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A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

## 4.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes viruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus,

rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof, including antibodies) of the present invention may also to be useful in the treatment of allergic reactions and conditions (e.g., anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by in vivo animals models such as the cumulative contact enhancement test (Lastbom et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxocol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

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Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic

composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

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Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

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Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

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A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β2 microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and 30 Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., I. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bowman et al., J. Virology 61:1992-1998; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

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Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

#### 4.10.8 ACTIVIN/INHIBIN ACTIVITY

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A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

# 4.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population.

Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

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#### 4.10.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

A polypeptide of the invention may also be involved in hemostatis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

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Therapeutic compositions of the invention can be used in the following:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

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#### 4.10.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention

may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

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Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Karposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine. Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide,

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Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog), 5 Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

In vitro models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These in vitro models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wily-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available, e.g. from American Type Tissue Culture Collection catalogs.

#### 4.10.12 RECEPTOR/LIGAND ACTIVITY

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A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen

recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or a toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14. Examples of colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

#### 4.10.13 DRUG SCREENING

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This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such

transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (i.e., increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

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Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science 282*:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, Curr. Opin. Biotechnol. 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., Mol. Biotechnol, 9(3):205-23 (1998); Hruby et al., Curr Opin Chem Biol, 1(1):114-19 (1997); Dorner et al., Bioorg Med Chem, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding

molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

#### 4.10.14 ASSAY FOR RECEPTOR ACTIVITY

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The invention also provides methods to detect specific binding of a polypeptide e.g. a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (i.e., increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The response of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then be assayed for expected modifications i.e. phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

### 4.10.15 ANTI-INFLAMMATORY ACTIVITY

Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflamation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic mylegenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

# 4.10.16 LEUKEMIAS

Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

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# 4.10.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of therapeutic utility, include but are not limited to nervous system injuries, and diseases or

disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

 (i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;

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- (ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;
- (iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;
- (iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;
- (v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;
- (vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis:
- (vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and
- (viii) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple sclerosis, human immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or

differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

(i) increased survival time of neurons in culture;

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- (ii) increased sprouting of neurons in culture or in vivo;
- (iii) increased production of a neuron-associated molecule in culture or in vivo, e.g., choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
  - (iv) decreased symptoms of neuron dysfunction in vivo.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, etc., depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, e.g., weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

# 4.10.18 OTHER ACTIVITIES

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or

elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

#### 4.10.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis and treatment. Such polymorphisms may be associated with, e.g., differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified

nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, e.g., by an antibody specific to the variant sequence.

#### 4.10.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis is determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et at., 1983, Science, 219:56, or by B. Waksman et al., 1963, Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

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#### 4.11 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

#### 4.11.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of

administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about  $0.01\mu g/kg$  to 100 mg/kg of body weight, with the preferred dose being about  $0.1\mu g/kg$  to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

# 15 4.12 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

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A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet-derived growth factor (PDGF), transforming growth factors (TGF-α and TGF-β), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

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As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (e.g., at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, e.g., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co- administered with one or more cytokines, lymphokines or other hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic

factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

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# 4.12.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

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### 4.12.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be

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manufactured in a manner that is itself known, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers

enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

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Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, e.g., dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, e.g., gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral administration by injection, e.g., by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, e.g., in ampules or in multi-dose containers, with

an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, e.g., sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, e.g., containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, e.g. polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well

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known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent.

Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable

lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

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The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 µg to about 100 mg (preferably about 0.1 µg to about 10 mg, more preferably about 0.1 µg to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic. composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions

may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

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A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF-α and TGF-β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which

modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either in vivo or ex vivo into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes.

# 4.12.3 EFFECTIVE DOSAGE

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Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate in vitro assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC<sub>50</sub> as determined in cell culture (i.e., the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD<sub>50</sub> (the dose lethal to 50% of the

population) and the ED<sub>50</sub> (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD<sub>50</sub> and ED<sub>50</sub>. Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED<sub>50</sub> with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, e.g., Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from in vitro data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen which maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about  $0.01~\mu g/kg$  to 100~mg/kg of body weight daily, with the preferred dose being about  $0.1~\mu g/kg$  to 25~mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

# **4.12.4 PACKAGING**

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The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the

invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

### 4.13 ANTIBODIES

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Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain,  $F_{ab}$ ,  $F_{ab}$  and  $F_{(ab)}$  fragments, and an  $F_{ab}$  expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as  $IgG_1$ ,  $IgG_2$ , and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, such as an amino acid sequence shown in SEQ ID NO: 1787, and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of -related protein that is located on the surface of the protein, e.g., a hydrophilic region. A hydrophobicity analysis of the human related protein sequence will indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte

Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, e.g., Hopp and Woods, 1981, Proc. Nat. Acad. Sci. USA 78: 3824-3828; Kyte and Doolittle 1982, J. Mol. Biol. 157: 105-142, each of which is incorporated herein by reference in its entirety. Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, Antibodies: A Laboratory Manual, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

### 5.13.1 Polyclonal Antibodies

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For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and Corynebacterium parvum, or similar immunostimulatory agents. Additional examples of adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the

target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

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### 5.13.2 Monoclonal Antibodies

The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro. The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego,

California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, <u>J. Immunol., 133</u>:3001 (1984); Brodeur et al., <u>Monoclonal Antibody Production Techniques and Applications</u>, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, <u>Anal. Biochem.</u>, <u>107</u>:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal. The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin

polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

### 5 5.13.2 Humanized Antibodies

The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, 10 immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')2 or other antigenbinding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., 15 Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the 20 humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human 25 immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., <u>2</u>:593-596 (1992)).

#### 5.13.3 Human Antibodies

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Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein. Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 Immunol Today 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal

antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

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In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (Bio/Technology 10, 779-783 (1992)); Lonberg et al. (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al. (Nature Biotechnology 14, 826 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the Xenomouse<sup>TM</sup> as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

## 5.13.4 Fab Fragments and Single Chain Antibodies

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According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see e.g., U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of  $F_{ab}$  expression libraries (see e.g., Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal  $F_{ab}$  fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an  $F_{(ab)/2}$  fragment produced by pepsin digestion of an antibody molecule; (ii) an  $F_{ab}$  fragment generated by reducing the disulfide bridges of an  $F_{(ab)/2}$  fragment; (iii) an  $F_{ab}$  fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv)  $F_v$  fragments.

# 5.13.5 Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the

binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, Nature, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker et al., 1991 EMBO J., 10:3655-3659.

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Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g.  $F(ab')_2$  bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate  $F(ab')_2$  fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to

stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from E. coli and chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody F(ab')<sub>2</sub> molecule. Each Fab' fragment was separately secreted from E. coli and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

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Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V<sub>H</sub>) connected to a light-chain variable domain (V<sub>L</sub>) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V<sub>H</sub> and V<sub>L</sub> domains of one fragment are forced to pair with the complementary V<sub>L</sub> and V<sub>H</sub> domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., <u>J. Immunol.</u> 147:60 (1991). Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcyR), such as FcyRI (CD64), FcyRII (CD32) and FcyRII (CD16) so as to focus cellular

defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

### 5.13.6 Heteroconjugate Antibodies

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Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

# 5.13.7 Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced antitumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., Anti-Cancer Drug Design, 3: 219-230 (1989).

5.13.8 Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from Pseudomonas aeruginosa), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include <sup>212</sup>Bi, <sup>131</sup>In, <sup>90</sup>Y, and <sup>186</sup>Re.

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutareldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science, 238: 1098 (1987). Carbon-14-labeled I-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is in turn conjugated to a cytotoxic agent.

# 4.14 COMPUTER READABLE SEQUENCES

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In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon

a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (e.g. text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NO:1-1786 and 3573-5358 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and

software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to. Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments. such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

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### 4.15 TRIPLE HELIX FORMATION

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA.

Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are

designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

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### 4.16 DIAGNOSTIC ASSAYS AND KITS

The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary.

Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification or immunological assay formats can readily be adapted to employ the nucleic acid

probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., An Introduction to Radioimmunoassay and Related Techniques, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., Techniques in Immunocytochemistry, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

# 4.17 MEDICAL IMAGING

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The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (e.g., where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, e.g., Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

# 4.18 SCREENING ASSAYS

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Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NO:1-1786 and 3573-5358, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

- (a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and
  - (b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to

activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

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For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription

from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents which bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

# 10 4.19 USE OF NUCLEIC ACIDS AS PROBES

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Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NO:1-1786 and 3573-5358. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from of any of the nucleotide sequences SEQ ID NO:1-1786 and 3573-5358 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes in vitro by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of

chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent in situ hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

# 4.20 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

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Oligonucleotides, i.e., small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata et al., 1985; Dahlen et al., 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller et al., 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, e.g., Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed Covalink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen et al., (1991) Anal. Biochem. 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen et al., (1991). In this technology, a phosphoramidate bond is employed (Chu et al., (1983) Nucleic Acids Res. 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm<sub>7</sub>), is then added to a final concentration of 10 mM 1-MeIm<sub>7</sub>. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

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Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm<sub>7</sub>, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphorate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) Science 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) Anal. Biochem. 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

# 4.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

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The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook et al. (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer et al. (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, *Cvi*II, described by Fitzgerald *et al.* (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation

of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease CviJI normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (CviJI\*\*), yield a quasi-random distribution of DNA fragments form the small molecule pUC19 (2688 base pairs). Fitzgerald et al. (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a CviJI\*\* digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that CviJI\*\* restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

## 4.22 PREPARATION OF DNA ARRAYS

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Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm², depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane.

Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm<sup>2</sup> and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers e.g. a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

# 20 5.0 EXAMPLES

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### 5.1.1 EXAMPLE 1

# Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

#### 5.1.2 EXAMPLE 2

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### Assemblage of Novel Nucleic Acids

The contigs or nucleic acids of the present invention, designated as SEQ ID NO: 3573-5358 were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UniGene version 101) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

A polypeptide was predicted to be encoded by each of SEQ ID NO:3573-5358 as set forth below. The polypeptides was predicted using a software program called FASTY (available from <a href="http://fasta.bioch.virginia.edu">http://fasta.bioch.virginia.edu</a>) which selects a polypeptides based on a comparison of translated novel polynucleotide to known polynucleotides (W.R. Pearson, Methods in Enzymology, 183:63-98 (1990), herein incorporated by reference. The predicted polypeptides are shown in Table 7.

### **5.2.2 EXAMPLE 3**

#### **Novel Nucleic Acids**

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genebank. Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, ed-ext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS:1-327.

Table 1 shows the various tissue sources of SEQ ID NO: 1-327.

The nearest neighbor results for SEQ ID NO: 1-327 were obtained by a FASTA version 3 search against Genpept release 117, using FASTXY algorithm. FASTXY is an improved version of FASTA alignment which allows in-codon frame shifts. The nearest neighbor result showed the closest homologue for SEQ ID NO: 1-327 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The nearest neighbor results for SEQ ID NO: 1-327 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the

signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

### **5.3.2 EXAMPLE 4**

### Novel Nucleic Acids

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Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 117, gb pri 117, UniGene version 117, Genpept release 117). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, edext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 328-1413.

Table 1 shows the various tissue sources of SEQ ID NO: 328-1413.

The nearest neighbor results for SEQ ID NO: 328-1413 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 118, using BLAST algorithm. The nearest neighbor result showed the closest homologue for SEQ ID NO: 328-1413 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in

the Sequence Listing. The nearest neighbor results for SEQ ID NO: 328-1413 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were

10 examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

### 5.3.2 EXAMPLE 5

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### **Novel Nucleic Acids**

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 117, gb pri 117, UniGene version 117, Genpept release 117). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, edext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide sequences, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 1414-1652.

Table 1 shows the various tissue sources of SEQ ID NO: 1414-1652.

The nearest neighbor results for SEQ ID NO: 1414-1652 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 118, using BLAST algorithm. The nearest neighbor result showed the closest homologue for SEQ ID NO: 1414-1652 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The nearest neighbor results for SEQ ID NO: 1414-1652 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

## **5.4.2 EXAMPLE 6**

## Novel Nucleic Acids

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Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 118, gb pri 118,

UniGene version 118, Genpept release 118). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, edext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide sequences, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 1653-1745.

Table 1 shows the various tissue sources of SEQ ID NO: 1653-1745.

The homology for SEQ ID NO: 1653-1745 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 118, using BLAST algorithm. The results showed homologues for SEQ ID NO: 1653-1745 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The homologues with identifiable functions for SEQ ID NO: 1653-1745 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

5.5.2 EXAMPLE 7
Novel Nucleic Acids

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Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 119, gb pri 119, UniGene version 119, Genpept release 119). Other computer programs which may have been used

UniGene version 119, Genpept release 119). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, edext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 1746-1768.

Table 1 shows the various tissue sources of SEQ ID NO: 1746-1768.

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The homology for SEQ ID NO: 1746-1768 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 119, using BLAST algorithm. The results showed homologues for SEQ ID NO: 1746-1768 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The homologues with identifiable functions for SEQ ID NO: 1746-1768 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the PFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the PFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

WO 01/53312

## 5.6.2 EXAMPLE 8

## Novel Nucleic Acids

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Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 120, gb pri 120, UniGene version 120, Genpept release 120). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, edext and gc-zip-2 (Hyseq, Inc.). The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The full-length nucleotide, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 1769-1786.

PCT/US00/34263

Table 1 shows the various tissue sources of SEQ ID NO: 1769-1786.

The homology for SEQ ID NO: 1769-1786 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 120 and the amino acid version of Geneseq released on October 26, 2000, using BLAST algorithm. The results showed homologues for SEQ ID NO: 1769-1786 from Genpept. The homologues with identifiable functions for SEQ ID NO: 1769-1786 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by

reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

Table 6 is a correlation table of all of the sequences and the SEQ ID NOS.

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TABLE 1

	TABLE			
	Tissue Origin	RNA Source	Hyseq Library Name	. SEQ ID NOS:
	adult brain	GIBCO	AB3001	
		9.500	WP2007	9 19-21 50-51 65-66 72 78 80 82
H				85 87 107-108 113 116 123 138
		ĺ		140 150-152 159 169 177 192-193
				202-203 212-214 225-226 235-236
				251 258 268-269 272 280-281 295
				298 301 321 326 331-332 334 356-
- 1		•	}	357 362 369 379 382-383 416 423
- 1				443 450 460 473 475 475
ł	!			443 459-460 473 475 477 488 496
- 1			1	500 503 519 526 547 574 582 587
- 1			j	608-609 613 618 633-634 645-646
- 1				652 657-658 660 669-671 678 687
- 1			}	695 697 710 715 724 731 775-777
- 1				796 804 811 857-859 862 869 899-
ĺ			ı	900 912 919 922 924-929 933 936
- 1			J	062 072 000 000 000 000
	ì		l	962 979 988-989 996 1001 1004-
- 1	1		ł	1008 1018 1039 1047 1059 1064
1	l			1067 1070 1078 1082 1107 1113
1			1	1116-1117 1131 1134-1137 1140
İ			1	1149 1151 1157 1180 1206 1229
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ı	j.		i	1279 1288-1290 1294 1307-1308
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1	1		1	1312 1320 1323 1330 1356 1360-
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1	}			1623 1625 1627 1639 1643 1648-
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r	adult brain	GIBCO	ABD003	
1	}		ADD003	3 12-14 18-19 25 30-31 34-36 43-
1	ì	1		45 50-51 56 58 60 65-66 68-69 80
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1	f	1		139 142 146 148-149 152 154 157
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1	ŀ	į		193 196-197 199 203 208 210 212-
1	1	1		214 223 233 235-237 247 257 259
1	ŀ	1		261 268-269 272 276 280-281 284-
L				288 291-292 295 297 300-301 304
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		ŀ		333-334 345-349 356-357 379-381
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l	j			393 401 408 414 419 424 426-428
	ì			430 433-436 438-439 443 445 449
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				478 483 491 494 496 500 503 507-
			. 1	508 516 519-520 525-527 534 536-
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	[	i		570 574-576 586-588 593 595 597
	1	1		601 606-609 616-620 622-623 625
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		l	ì	628-633 635-636 643 645-649 653
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		1	l	802-803 810-811 815 817 820-821
				832 834-836 840 845-847 851 858-
			í	861 864 869 874 878 883 897 901-
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	ļ	1	į	977 979-980 985-986 990 992-993
	1	1	]	997-1001 1005-1007 1012 1017-
		ļ		1020 1023-1024 1029-1031 1034
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			<del></del>	

Tissue Origin	RNA Source	Viscour	
	NW Source	Hyseq Library Name	SEQ ID NOS:
			1097 1103 1107 1109 1112 1116-
	}		1117 1119 1121 1124 1127 1130 1134 1144-1145 1149 1151 1157-
1	1		1158 1167 1170 1178 1184 1188
			1190 1193-1194 1200 1202 1215~
		]	1217 1220 1226-1227 1229 1231
1	}		1241 1243 1247 1252 1258 1263
			1267 1269 1279 1281 1284 1286- 1289 1293-1294 1306-1307 1312
1	ì	1	1316-1320 1326 1333 1338 1341
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			1374 1377 1380 1386 1389-1390
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1			1630-1632 1636 1640-1641 1644-
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			1664 1667 1669 1673 1678-1681
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			1747 1749 1753 1757-1758 1760-
	i		1761 1765 1771 1785
adult brain	Clontech	ABR001	9 29 68-69 113 115 146 152 206
	]		223 245 277 307 320 324 330-331
	]		344 348 352 362 379 384 393 404 408 414 441-442 454 469 481 490
			506 517 586 597 631 641 659 691
	1		715 799 803 833 865 871 875 880
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	ì	•	1027 1036 1041 1043 1075 1107 1112 1121 1127 1136-1137 1144-
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adult brain	Clontech	ABR006	5-8 15-16 168 212-213 271 278
	]	•	280-281 291-292 300-301 310 314
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			360 362 369 374 379 384 393 396- 397 414 419-420 426-428 430 441-
			442 453 506 616-617 661 689 785
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adult brain	Clontech	ABR008	1760-1761 5-10 13-19 22-23 25 29 33 37-39
			43-45 50-51 54-55 57-58 60-66
		f	68-70 72 75 77-80 83 85 89-92 94
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Í	j	[	123 128 133 135-137 139 143 145-
	1		146 148 152 154-155 157 166 168- 172 174-175 181-184 188-190 193-
			194 196 198-200 202 204-205 207-

Tissue Origin	RNA Source	Hyseq	SEO ID MOG.
		Library Name	SEQ ID NOS:
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			231-232 234-241 245-247 251-253
			255 257-259 268-269 271 276-281 285-286 288 290-292 300-302 304
			307 309-311 313 315 317-318 320-
			322 325-326 328 330-331 333-338
			341 344-347 349 352 354 356-357
			362 369-373 376 379-380 382 384
			387 390-391 393-394 397 399-403 405-411 414-415 417-420 426-428
			437-438 440-444 453-455 462 464
į	j		467 469-471 476 478 492-484 488-
			491 497 503 506-513 516-517 520
			524-526 528-530 532-534 537-540
			.542 544 547-551 553 561 565-567 572-574 577 581 585 587-588 590-
			591 597 599 601-602 606-610 612
			615-617 619-620 622-623 628-629
	•		631 633-634 636-641 643 645-647
,	l		651-653 655-664 669-671 673 679
			682 687 689 691-700 702 706 710
		-	715-717 720-721 725-734 736-739 742-743 746 750-752 756 758-759
			762-764 766 768 773-778 780-782
1	. 1		784-785 787-789 794 796 799 802-
	i		803 805 811 814-815 818 825-826
			834-837 839-840 842-843 856-859 861-862 865 867-872 874-875 881
]			883-884 887 889-892 894-895 897-
	1		898 901 904 908 910 912 914 917
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	ĺ		941 943 945 949 953-954 958 961-
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			1085-1093 1095-1096 1108-1112 1114-1125 1127 1131-1133 1135-
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		ļ	1319 1322 1324-1327 1330 1332 1334-1335 1339 1344-1346 1351
}		į	1354-1355 1357-1358 1365-1367
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			1464 1466 1468 1471 1477 1480
	1		1482-1483 1496 1502-1504 1507-
	1		1509 1513 1519-1520 1524-1526
	ĺ		1536 1547 1549-1552 1567 1573- 1574 1578 1586-1589 1597-1598
	1		1601-1602 1605 1607-1609 1611-
			1617 1619-1621 1623 1625-1626
Ì	1		1635-1641 1643-1645 1649 1651
1	1		1653 1656-1658 1664 1669 1671-
			1674 1676-1684 1686 1689-1690
			1694-1696 1704-1705 1708-1709

Library Name    1720-1724   1736-1728   1736-1733   1737-1740   1745-1745   175	Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
1737-1740 1742-1745 1753 1756-1761 1765 1767 1771-   1772 1776-1777 1779-1780 1786     24 75 103 186 210 310-311 364-365 508 623 710 937 1002-1003 1059 1204 1609 1731-1732     adult brain	3			
ABRO11	İ			
adult brain				
adult brain				
1059 1204 1609 1731-1732   adult brain   BioChain   ABR012   46 182-184 204-205 300 739 767   1371 1549 1620 1684   adult brain   Invitrogen   ABR013   188 204-205 364-365 393 497 595 687 692-694 830 845 1068 1320   1413 1640   adult brain   Invitrogen   ABR014   187 301 357 364-365 375 454 463   731 899 939 983 1073 1262 1270   1320 1403 1640 1651 1657 1696   1722 1738   adult brain   Invitrogen   ABR015   619 434-435 441-442 763 789 983   adult brain   Invitrogen   ABR016   312 364-365 379 31320 1334-1335   1674 1722 1788   adult brain   Invitrogen   ABR016   312 364-365 379 31320 1334-1335   1674 1722 1788   adult brain   Invitrogen   ABR016   312 364-365 379 31320 1334-1335   1674 1722 1788   adult brain   Invitrogen   ABR016   312 364-365 379 31320 1334-1335   1674 1722 1785   344-365 379 31320 1334-1335   1674 1722 1785   344-365 379 31320 1334-1335   1674 1722 1785   344-365 379 31320 1334-1335   1674 1722 1785   344-365 379 31320 1334-1335   1674 1722 1785   344-365 379 31320 1334-1335   134-343 146-152 161 173 182-184   149-184 182 161 173 182-184   149-184 182 161 173 182-184   149-184 182 161 173 182-184   149-184 182 161 173 182-184   149-184 182 161 173 182-184   149-184 182 161 173 182-184   149-184 182 161 173 182-184   149-184 182 161 173 182-184   149-184 182 161 173 182-184   149-184 182 161 173 182-184 183 183 183 183 183 183 183 183 183 183	adult brain	Clontech	ABR011	
adult brain				
adult brain	adult brain	PioChain	200020	
adult brain	addit brain	BIOCHAIN	ABKU12	
Se7 692-694 830 845 1068 1320   1413 1640   1413 1640   1413 1640   1413 1640   187 301 357 364-365 375 454 465   172 1738   1389 939 939 31 073 1262 1270   1320 1403 1640 1651 1657 1696   1722 1738   1320   1403 1640 1651 1657 1696   1722 1738   1320   1403 1640 1651 1657 1696   1722 1738   1320   1320   1403 1640 1651 1657 1696   1320   1320   1320   1320   1320   1334 1335   1674 1722 1785   1320   1334 1335   1674 1722 1785   1320   1334 1335   1674 1722 1785   1320   1334 1335   1674 1722 1785   1320   1334 1335   1674 1722 1785   1320	adult brain	Invitrogen	ABR013	
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adult spleen	GIBCO	ASP001	423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776
adult spleen	GIBCO	ASP001	423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99
adult spleen	GIBCO	ASP001	423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141
adult spleen	GIBCO	ASP001	423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174
adult spleen	GIBCO	ASP001	423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776  3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211
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adult spleen	GIBCO	ASP001	423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211 215 219 234 253-254 256 258 264 272 280-281 290 295 302 309 312 325 333 341 349 358 372 382 386- 387 394 406 414 431 434-436 446 448 451 473 481 490-493 500 503
adult spleen	GIBCO	ASPOO1	423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776  3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211 215 219 234 253-254 256 258 264 272 280-281 290 295 302 309 312 325 333 341 349 358 372 382 386- 387 394 406 414 431 434-436 446 448 451 473 481 490-493 500 503 505 517 519 530 534 536-540 547
adult spleen	GIBCO	ASPOO1	423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776  3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211 215 219 234 253-254 256 258 264 272 280-281 290 295 302 309 312 325 333 341 349 358 372 382 386- 387 394 406 414 431 434-436 446 448 451 473 481 490-493 500 503 505 517 519 530 534 536-540 547 554 557 574-576 582 592 595 604
adult spleen	GIBCO	ASPOO1	423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211 215 219 234 253-254 256 258 264 272 280-281 290 295 302 309 312 325 333 341 349 358 372 382 386- 387 394 406 414 431 434-436 446 448 451 473 481 490-493 500 503 505 517 519 530 534 536-540 547 554 557 574-576 582 592 595 604 611-612 620-621 623 631-632 642
adult spleen	GIBCO	ASP001	423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211 215 219 234 253-254 256 258 264 272 280-281 290 295 302 309 312 325 333 341 349 358 372 382 386- 387 394 406 414 431 434-436 446 448 451 473 481 490-493 500 503 505 517 519 530 534 536-540 547 554 557 574-576 582 592 595 604 611-612 620-621 623 631-632 642 652 659 661 667 671 673-675 684
adult spleen	GIBCO	ASP001	423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211 215 219 234 253-254 256 258 264 272 280-281 290 295 302 309 312 325 333 341 349 358 372 382 386- 387 394 406 414 431 434-436 446 448 451 473 481 490-493 500 503 505 517 519 530 534 536-540 547 554 557 574-576 582 592 595 604 611-612 620-621 623 631-632 642 652 659 661 667 671 673-675 684 700 721 728 730 732 738 742-744
adult spleen	GIBCO	ASP001	423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776  3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211 215 219 234 253-254 256 258 264 272 280-281 290 295 302 309 312 325 333 341 349 358 372 382 386- 387 394 406 414 431 434-436 446 448 451 473 481 490-493 500 503 505 517 519 530 534 536-540 547 554 557 574-576 582 592 595 604 611-612 620-621 623 631-632 642 652 659 661 667 671 673-675 684 700 721 728 730 732 738 742-744 746 762 765 774 780 788-789 794
adult spleen	GIBCO	ASPOO1	423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211 215 219 234 253-254 256 258 264 272 280-281 290 295 302 309 312 325 333 341 349 358 372 382 386- 387 394 406 414 431 434-436 446 448 451 473 481 490-493 500 503 505 517 519 530 534 536-540 547 554 557 574-576 582 592 595 604 611-612 620-621 623 631-632 642 652 659 661 667 671 673-675 684 700 721 728 730 732 738 742-744

	7378 G-1100	Wilson	SEO ID NOS:
Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS.
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testis	GIBCO	ATS001	5-8 10 26 30-31 47 50-51 57 68-69 82 84-85 97 102 113 119 137 139 150 152 154 156 163 169 174 176-177 192 194 196-197 212-215 227-228 247 255 258 261 282 285 288-289 301 307 311 316 330 334 349 370-372 392 398 410 415 426-427 430-431 433 437 446 454 461 469 473 477 481-482 493 499 502-503 513 522 526 547 552-553 563-564 572-573 575-576 581-582 585 599-602 605 612 615-617 620 631 637 647 649-650 656 660 665 670 674-675 712 719-721 723 728 731 738 744 746 773 780 784 788-789 802 804 809 811 814 826 831 837 843 845 848 859 866 859 877 905 913 916 919 921 926 929 937 950 960 963 971 975 977 981 990 992-993 1007 1016 1029-1030 1034-1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208-1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287-1289 1291-1293 1307 1311 1317-1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1777 1724 1730 1737-1738 1752
Genomic DNA from BAC 63I18	Research Genetics (CITB BAC Library)	BAC001	686 1352 1412
Genomic DNA from BAC 39316	Research Genetics (CITB BAC Library)	BAC002	1411-1412

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
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adult bladder	Invitrogen	BLD001	5-8 17-18 22-23 33 37-39 56-57 80 93 100 120-121 169 201 237 251-252 272 278 311 348 363 382 413 415 424 430 443 483 502 542- 543 562 564 607 616-617 626 635 652 667 671 710 727 755-756 762 773 786 788 837 840 866 893 898 909 918 929 966 977 983 1016 1025 1055 1073 1082 1140 1167 1185 1189 1199 1270 1369 1481 1536 1560 1573 1596 1614 1636- 1637 1649-1650 1654-1655 1658 1669 1671 1690 1719 1727 1731- 1732 1739 1741 1760-1761 1779
bone marrow	Clontech		3-8 11 13 18 29-31 33 35-36 40 43-45 47-48 50-51 57 60 65-66 75 80 82 85 88-89 94 100 103 107 110 115 118-119 124-125 133-134 136-137 139-141 146 150 152-153 155 161 163 168-170 172 178-180 187 192-193 197-198 203-205 210- 213 215 217 219 222 224-226 233 235-237 242-244 255 258 260 263- 264 266 273 276 278 283 286 290 295 301-302 307 312-313 321 330 333 339 343 352 357-358 370-371 382 384-385 387 389 394 408 410 412 416 421 424-427 429-431 436- 437 439 441-442 445 447 454-456 461-462 471-472 475 477-479 481- 482 485 488 493 498 500 503-506 513 516 519 523-524 526 530 535- 540 542 544-545 549 555 565 567 569-577 581 583-586 588 593 601 603-604 608-609 613-619 621-622 632-633 636-637 642 649-650 656- 660 666 670 672 674-675 679 683 701 708 716 718-720 731 735-736 740-742 744-745 752 761 765 772- 773 775-778 780 785-786 789-791 796 798 802 810-812 823-824 826 830 832-833 837-838 843-844 848- 855 888-859 866-867 869 878-880 883 890-892 896 903 905 908 912- 914 922-924 927 930-931 937 939- 941 952-953 955-958 963 969 973 976 981 985 987 990 992 995 1000 1002 1005-1007 1013 1016 1025 1028-1031 1033 1035 1037 1039 1042 1044 1047 1050 1053-1054 1059 1061 1063 1066 1070-1071 1079 1106 1110-1113 1115-1117 1124 1126 1134-1135 1142 1144- 1145 1163 1172 1178 1197 1199- 1200 1202 1216-1217 1224 1227- 1228 1240 1246 1254 1261 1266 1270 1278 1281 1285 1287 1290- 1291 1293 1299-1301 1308 1314 1317-1320 1327 1331 1339 1343 1346 1349 1353 1356 1361 1367 1369 1372-1374 1379-1380 1394 1400 1403 1406 1408 1413 1417 1419 1423 1425-1427 1430-1431 1433 1439 1443 1446-1449 1459 1463-1464 1482 1486 1493-1494

Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
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	]		1772 1781-1782 1785-1786
bone marrow	Clontech	BMD002	11 15-16 19 30-31 35-36 68-69 75
			83-84 93 99 103 108-109 118 137
			139 169-170 174 177 180 190 193
			212-213 219 222 225-226 232 237
			255 259 264 273-274 284 286 290-
<b>)</b>			292 295 301 303-304 307 312-313
	1		316 324 326 330 334-335 348 352-
	!		353 357 360 370-373 384 386-387
	]		397 403-404 414-416 421 425-427
	ļ		429-430 433-436 440 444 451 454
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	[		990 992 998 1001 1004 1016 1036
}			1042 1048 1051 1054-1055 1058
		•	1088-1089 1106 1112-1114 1155
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			1236-1237 1260-1261 1282-1283
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į l			1324-1327 1330 1333 1341 1343   1347 1350 1353 1355-1357 1367
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1	1		1383-1384 1394 1397 1400 1406
1			1413 1417 1425-1427 1438 1442
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]	ļ		1786
bone marrow	Clontech	BMD004	73-74 503 922 1036 1711
bone marrow	Clontech	EMD007	95-96 866 1320 1475
adult colon	Invitrogen	CLNOO1	17 56-58 103 110 117 144 150 171
			179 185 188-189 201 204-206 210
	1	l	218-221 225-226 231 237 251 277
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		1	394 408 420 455 481 485 503 510-
	Į	1	512 590-591 615 635 647-648 665
		1	672 684 697 710 725-726 743 780
	ļ	1	786 788 826-827 848-850 854-855
1		1	858 866 872 898 918 921-923 953
			976 983 993 1005-1006 1017 1020
		ŀ	1025 1027 1054-1055 1063 1068-
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Tissue Origin	RNA Source	Hyseq	GEO ID VOG
		Library Name	SEQ ID NOS:
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Mixture of 16	Various	CTL016	1765
tissues -	Vendors	C17010	401 1490 1686
mRNAs			
Mixture of 16	Various	CTL021	312 782 1132-1133 1403 1712 1715
tissues -	Vendors		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
mRNAs			j
adult cervix	BioChain	CVX001	1 4-8 11 13 18-21 25-26 30-31 33
			37-39 43 46-47 58 61 64-66 71
	l		73-74 82 85 94 100 103-104 113
J			118 122 126 130 134 140 147 153-
	1		156 163 170 179 181 186 192 195-
	1		196 198 201-202 218-219 222 229-
	}		231 257 266 276-277 285-286 288
1			298 301-302 304 307 312-314 324
ľ	i		326 329-330 332 335 342 352 358
			362 371-372 376 379 381-382 384 388 398 400 410 414 416 419-420
	1		426-427 430-431 433-436 439 446
	Ì		448 461-462 464 471-477 479 482-
			483 491 493 496 503 506 510-513
			516-517 526 530 535 542-544 546-
	1	ĺ	547 557 561 572-573 575-577 581-
•	`		S82 585-586 588-589 593-594 600
	j		602 604-605 607-609 612 615-619
1			623 644 650 654 657-658 662-665
	ł		670 672 680 683 691-694 698 706
)	j		708-709 711 713 720-721 727 729
•			731-732 737 745-747 753-754 760 765 771 774-777 780 790 793 796
	į	ł	798 800 803 805 818 826 828 831-
}		1	832 834-836 843 847-848 851-855
	į		B57-860 864-866 869 871 876 878-
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1		1	905-908 912-913 916 918-919 922
	}	Ţ	927 932 934-938 944 948 955-956
		Í	958 963-964 967 969-970 972 976
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	j		1005-1007 1016-1017 1024 1027
	į	{	1033 1036 1038 1045 1047 1053- 1056 1066-1067 1071 1073 1075
,			1079 1082 1098 1113 1124 1129
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		ĺ	1170 1173 1175 1177 1181 1197
1	1	Ì	1200 1202 1211 1214 1216 1221-
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	]		1241 1243 1258 1264-1265 1268
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		i	1349 1353-1354 1360 1372-1374
			1383-1384 1386 1394 1397 1405-

<sup>\*</sup>The 16 tissue-mRNAs and their vendor source, are as follows: 1) Normal adult brain mRNA (Invitrogen), 2) normal adult kidney mRNA (Invitrogen), 3) normal adult liver mRNA (Invitrogen), 4) normal fetal brain mRNA (Invitrogen), 5) normal fetal kidney mRNA (Invitrogen), 6) normal fetal liver mRNA (Invitrogen), 7) normal fetal skin mRNA (Invitrogen), 8) human adrenal gland mRNA (Clontech), 9) human bone marrow mRNA (Clontech), 10) human leukemia lymphablastic mRNA (Clontech), 11) human thymus mRNA (Clontech), 12) human lymph node mRNA (Clontech), 13) human spinal cord mRNA (Clontech), 14) human thyroid mRNA (Clontech), 15) human esophagus mRNA (BioChain), 16) human conceptional umbilical cord mRNA (BioChain).

Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
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!	[		1674-1675 1683 1685-1688 1699 1702 1709-1710 1715 1717 1722
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			1760-1762 1767 1773 1778 1785-
diaphragm	BioChain	DIA002	137 282 289 730 780 986 1409
			1478 1599 1614
endothelial cells	Strategene	EDT001	3 5-10 13 15-21 24-26 29 34 37-
00115	·		39 42 44-45 50-51 53-55 57-58 60-61 65-66 68-69 73-74 77-78 80
İ	}		82-83 85 87 89 93-96 101-105 108
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	l		192 194 196-201 204-207 210 212-
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. ;	1		240-241 251-252 258 261-262 265
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	1	1	335 340.342 351-355 360 371 375
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1		,	595 597 599 603 607-612 615-617 620 622 626 630 632-634 638-641
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	-		712-713 719 730 732 734 736 738 743-746 751 759 768 771 773 775-
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	j		807 810-811 814 816-818 821-822
			824 826 828-829 832 834-838 842~ 845 848-850 854-860 862 864 869
			871 874 876-879 883 885 887 890-
		1	891 894-895 898-900 903 908 910-
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			959-961 964 969-970 973 975-978
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Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
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<b>!</b>	i		1345~1347 1350 1355-1356 1359
1			1367 1369 1374 1376 1379 1398
Į i			1400 1406 1408 1414 1417 1419
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chromosome 8	Research		
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}	]		379 391 411 481 546 563 607 679   710 867 1012 1031 1055 1251 1262
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			1374 1377-1379 1386 1389-1390
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			1761 1771-1772 1779 1786

Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
thyroid gland	Clontech	Library Name	4 9-10 20-21 37-39 48 50-51 54-
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			647 649-651 660 662-665 668 670
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			727-729 732 734 738 740-741 743
			745 750 759 761 763 765 770 773 780 785 795-796 798 802 804 823-
	ĺ		824 826 828 833 838 841-845 847
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			881 887-888 890-892 894-895 898
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Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
_	_	Library Name	224 1D 102:
			352 372 377 384 414 424 445-446 454 472 474 491 496 560 579 588 593 597 607 612 626 681 702 719 810 859 866 878 894-895 912 916 922 932 935 1046 1075 1080 1099- 1102 1113 1208 1215 1232-1233 1237 1281 1312 1385 1387 1405 1414 1424 1430 1437 1447 1505 1569 1579 1586 1600 1641 1653 1667 1671 1676-1677 1683 1691-
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SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	
ID NO:	NUMBER		223CATF I TON	WATERMAN	IDENTITY
1	Y41736	Homo	Human PRO1114 protein	SCORE 1398	100
2	Y66656	sapiens Homo	sequence.		
3		sapiens	Membrane-bound protein PRO943.	2389	99
	AF113136	Homo sapiens	kinase-M; IRAK-M	3043	100
4	AF017806	Mus musculus	I	6351	77
5	X02761	Homo sapiens		10535	98
6	X02761	Homo sapiens	fibronectin precursor	8990	89
9	X02761	Homo sapiens		12564	99
	AJ011679	Homo sapiens	Rab6 GTPase activating protein, GAPCenA	5251	99
10	W88501	Homo sapiens	Human stomach carcinoma clone HP10415-encoded protein.	2381	100
11	AF117754	Homo sapiens	thyroid hormone receptor- associated protein complex component TRAP240	11336	98
12	297630	Homo sapiens	dJ466N1.4 (novel protein similar to ANK3 (ankyrin 3, node of Ranvier (ankyrin (G)))	896	100
13	Y58620	Homo sapiens	Protein regulating gene expression PRGE-13.	1894	98
14	AF213457	Homo sapiens	triggering receptor expressed	1238	100
16	AF233453	Homo sapiens	on myeloid cells 2 RACK-like protein PRKCBP1	3124	
17	AF201303	Homo sapiens	dhfr oribeta-binding protein	3124	99
18	AF064205	ļ,,	RIP60		1
19	U00059	Homo sapiens	dynactin 1 p150 isoform	6377	100
		s cerevisiae	Yhrl21wp	174	26
20	AB032903	Homo sapiens	guanosine monophosphate reductase isolog	1801	99
21	AB032903	Homo sapiens	guanosine monophosphate reductase isolog	1485	99
22	AF140507	Homo sapiens	Ca2+/calmodulin-dependent protein kinase kinase beta	3083	99
23	AF140507	Homo sapiens	Ca2+/calmodulin-dependent	2300	99
24	AJ289131	Homo sapiens	protein kinase kinase beta chondroitin 4-0-	2211	99
25	U33460	Ното	sulfotransferase DNA-directed RNA polymerase	8777	98
26	11.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1	sapiens	I, largest subunit	] " ]	30
27	Y44488	Homo sapiens	ACRP30R2 variant protein.	1387	100
28	U43701 U02032	Homo sapiens	ribosomal protein L23a	791	100
29	Y41324	Homo sapiens	ribosomal protein L23a	767	97
	141324	Homo sapiens	Human secreted protein encoded by gene 17 clone HNFIY77.	1083	99
30	W71749	Homo sapiens	Human ubiquitin conjugation system protein 2.	715	90
31	W71749	Homo sapiens	Human ubiquitin conjugation system protein 2.	631	82
32	AF231917	Homo sapiens	long-chain 2-hydroxy acid	1811	100
33	Z29481	Homo sapiens	oxidase HAOX2 3-hydroxyanthranilic acid dioxygenase	1507	99
34	AB001451	Homo sapiens	Sck	2869	100
	Y00644	Homo sapiens	precursor polypeptide (AA -34 to 287)		99
36	Y00644	Homo sapiens	precursor polypeptide (AA -34	1104	98
37	¥78795	Homo sapiens	to 287)  Human antizuai-2 (AZ-2) amino	3586	78
38	¥78795	Homo sapiens	acid sequence. Human antizuai-2 (AZ-2) amino	4726	99
			acid sequence.		

SEQ ID NO: 39 40 41 42 43 44 45 46 47 49 51	ACCESSION NUMBER Y78795 U93121 Y42750 AF282626 G02150 U19617 U19617 AF100758 Y87591 X04145 X63547 M94043 L31783 X83973 AF224741	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus Homo sapiens Homo sapiens Homo sapiens Homo sapiens Attus Rattus norvegicus Mus musculus	Human antizuai-2 (AZ-2) amino acid sequence.  M-phase phosphoprotein-1 Human calcium binding protein 1 (CaBP-1). latexin Human secreted protein, SEQ ID NO: 6231. Elf-1 Elf-1 osteoinductive factor OIF Human SPROUTY-1 protein, SEQ ID NO:24. T3 gamma precursor (aa -22 to 160) oncogene rab-related GTP-binding	SMITH-WATERMAN SCORE 3556 3747 795 1189 384 2724 2062 1538 1737 942 5845 1089	1DENTITY 77 100 100 100 94 88 86 100 99
39 40 41 42 43 44 45 46 47	U93121 Y42750 AF282626 G02150 U19617 U19617 V19617 XF100758 Y87591 X04145 X63547 M94043 L31783 X83973	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus Homo sapiens Homo sapiens Homo sapiens Homo sapiens	acid sequence.  M-phase phosphoprotein-1  Human calcium binding protein 1 (CaBP-1).  latexin  Human secreted protein, SEQ ID NO: 6231.  Elf-1  Elf-1  osteoinductive factor OIF  Human SPROUTY-1 protein, SEQ ID NO:24.  T3 gamma precursor (aa -22 to 160)  oncogene rab-related GTP-binding	3556 3747 795 1189 384 2724 2062 1538 1737 942	100 100 100 94 88 86 100 99
40 41 42 43 44 45 46 47	U93121 Y42750 AF282626 G02150 U19617 U19617 V19617 XF100758 Y87591 X04145 X63547 M94043 L31783 X83973	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus Homo sapiens Homo sapiens Homo sapiens Homo sapiens	acid sequence.  M-phase phosphoprotein-1  Human calcium binding protein 1 (CaBP-1).  latexin  Human secreted protein, SEQ ID NO: 6231.  Elf-1  Elf-1  osteoinductive factor OIF  Human SPROUTY-1 protein, SEQ ID NO:24.  T3 gamma precursor (aa -22 to 160)  oncogene rab-related GTP-binding	3747 795 1189 384 2724 2062 1538 1737 942	100 100 100 94 88 86 100 99
41 42 43 44 45 46 47	Y42750  AF282626 G02150  U19617 U19617 AF100758 Y87591  X04145  X63547 M94043  L31783 X83973	Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus Homo sapiens Homo sapiens Homo sapiens Rattus norvegicus	Human calcium binding protein 1 (CaBP-1). 1atexin Human secreted protein, SEQ ID NO: 6231. Elf-1 Elf-1 osteoinductive factor OIF Human SPROUTY-1 protein, SEQ ID NO:24. T3 gamma precursor (aa -22 to 160) oncogene rab-related GTP-binding	795 1189 384 2724 2062 1538 1737 942	100 100 94 88 86 100 99
42 43 44 45 46 47	AF282626 G02150 U19617 U19617 AF100758 Y87591 X04145 X63547 M94043 L31783 X83973	Homo sapiens Homo sapiens Mus musculus Mus musculus Homo sapiens Homo sapiens Homo sapiens Rattus norvegicus	l (CaBP-1). latexin Human secreted protein, SEQ ID NO: 6231. Elf-1 Elf-1 osteoinductive factor OIF Human SPROUTY-1 protein, SEQ ID NO:24. T3 gamma precursor (aa -22 to 160) oncogene rab-related GTP-binding	1189 384 2724 2062 1538 1737 942	100 94 88 86 100 99
43 44 45 46 47	G02150 U19617 U19617 AF100758 Y87591 X04145 X63547 M94043 L31783 X83973	Homo sapiens  Mus musculus  Mus musculus  Homo sapiens  Homo sapiens  Homo sapiens  Homo sapiens  Rattus  norvegicus	Human secreted protein, SEQ ID NO: 6231.  Elf-1 Elf-1 osteoinductive factor OIF Human SPROUTY-1 protein, SEQ ID NO:24. T3 gamma precursor (aa -22 to 160) oncogene rab-related GTP-binding	384 2724 2062 1538 1737 942	94 88 86 100 99
44 45 46 47	U19617 U19617 AF100758 Y87591 X04145 X63547 M94043 L31783 X83973	Mus musculus Mus musculus Homo sapiens Homo sapiens Homo sapiens Rattus norvegicus	ID NO: 6231.  Elf-1  Elf-1  osteoinductive factor OIF  Human SPROUTY-1 protein, SEQ  ID NO:24.  T3 gamma precursor (aa -22 to 160)  oncogene  rab-related GTP-binding	2724 2062 1538 1737 942	88 86 100 99
45 46 47 49	U19617 AF100758 Y87591 X04145 X63547 M94043 L31783 X83973	Mus musculus Homo sapiens Homo sapiens Homo sapiens Rattus norvegicus	Elf-1 Elf-1 osteoinductive factor OIF Human SPROUTY-1 protein, SEQ ID NO:24. T3 gamma precursor (aa -22 to 160) oncogene rab-related GTP-binding	2062 1538 1737 942 5845	86 100 99 99
46 47 49	AF100758 Y87591 X04145 X63547 M94043 L31783 X83973	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Rattus norvegicus	osteoinductive factor OIF Human SPROUTY-1 protein, SEQ ID NO:24. T3 gamma precursor (aa -22 to 160) oncogene rab-related GTP-binding	1538 1737 942 5845	99 99
47	Y87591 X04145 X63547 M94043 L31783 X83973	Homo sapiens Homo sapiens Homo sapiens Rattus norvegicus	Human SPROUTY-1 protein, SEQ ID NO:24. T3 gamma precursor (aa -22 to 160) oncogene rab-related GTP-binding	1737 942 5845	99
49	X04145 X63547 M94043 L31783 X83973	Homo sapiens Homo sapiens Rattus norvegicus	ID NO:24. T3 gamma precursor (aa -22 to 160) oncogene rab-related GTP-binding	942	99
	X63547 M94043 L31783 X83973	Homo sapiens Rattus norvegicus	160)   oncogene   rab-related GTP-binding	5845	99
51	M94043 L31783 X83973	Rattus norvegicus	oncogene rab-related GTP-binding		
	L31783 X83973	norvegicus	rab-related GTP-binding		
52	X83973				96
- 1	X83973	Marg marganilar	protein		1 -0
53		Luna mascatas	uridine kinase	917	71
54	AF774743	Homo sapiens	transcription factor	4486	98
55		Homo sapiens	chloride channel protein 7	4128	99 .
56	W74805	Homo sapiens	Human secreted protein encoded by gene 77 clone HOEAS24.	1491	100
57	250907	Homo sapiens	Human TBC-1 cDNA from second transcript.	4824	100
58	D79994	Homo sapiens	similar to ankyrin of Chromatium vinosum.	6089	99
59	D79994	Homo sapiens	similar to ankyrin of Chromatium vinosum.	4014	91
60	¥59738	Homo sapiens	Human normal ovarian tissue derived protein 15.	601	100
61	AB031069	Homo sapiens	protein containing CXXC domain 1	1390	100
62	Y66660	Homo sapiens	Membrane-bound protein PRO783.	2492	99
63	Y66660	Homo sapiens	Membrane-bound protein PRO783.	1709	99
	S70011	Rattus sp.	tricarboxylate carrier	895	55
65	AF139518	Rattus norvegicus	A-kinase anchor protein	178	24
66	W29666	Homo sapiens	Homo sapiens DH1308 1 clone secreted protein.	157	30
	AJ245738	Homo sapiens	claudin-15	1206	100
68	AF099138	Rattus norvegicus	GLUT4 vesicle protein	4183	87
69	AF099138	Rattus norvegicus	GLUT4 vesicle protein	4906	86
	282059	Caenorhabdit is elegans	Similarity to Drosophila ring canal protein comes from this gene	1285	44
	AF224278	Homo sapiens	PMEPAl protein	1282	100
	AF126426	Homo sapiens	neurotrimin	1809	100
	Y41652	Homo sapiens	Human MEK2 protein sequence.	2065	99
74	Y41652	Homo sapiens	Human MEK2 protein sequence.	1207	100
75	AF188622	Mus musculus	selectively expressed in embryonic epithelia protein-1	1485	74
76	AE000406	Escherichia coli	putative DNA topoisomerase	950	100
77	X99302	Homo sapiens	Pop1	655	100
	AL136538	Schizosaccha romyces	similarity to S. cerevisiae ktil2 protein	210	31
9 1		pombe			
	M. 123/30	Homo sapiens	G4	1554	99

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	7 - 8 -
ID No:	NUMBER			WATERMAN	IDENTITY
80	AL096768	Homo sapiens	dJ858816.2	SCORE 2033	1.00
		)	(phosphatidylserine	2033	100
		ì	decarboxylase (PSSC, EC	1	•
	_l		4.1.1.65))		]
81	AL096768	Homo sapiens	dJ858B16.2	1220	96
	1		(phosphatidylserine	ì	1
	į		decarboxylase (PSSC, EC	1	
82	X57351	<del> </del>	4.1.1.65))	1	
83	AC005594	Homo sapiens	1-8D	677	98
84	X73113	Homo sapiens	R26984_1	2700	98
85	AF097330	Homo sapiens	fast MyBP-C	5959	99
0.3	A£037330	Homo sapiens	H1 chloride channel; p64H1;	1305	99
86	AB018423	Mus musculus	SH2 domain-containing protein	<del> </del>	<u> </u>
87	AF272151	Homo sapiens	adaptor protein CIKS	3084	78
88	AF196329	Homo	triggering receptor expressed	1214	99
	1	sapiens	on monocytes 1	1214	100
89	AB016879	Arabidopsis	contains similarity to pre-	634	36
	1	thaliana	mRNA splicing	1	1 20
		L	factor~gene_id:MRB17.2		i
90	AJ133721	Mus musculus	homeodomain protein	654	57
91	AJ242864	Mus musculus	phtf protein	619	61
92 93	A61971 Y99365	unidentified	MCSP	11676	99
23	199365	Homo sapiens	Human PRO1250 (UNQ633) amino	3890	100
94	Y87231	Homo sapiens	acid sequence SEQ ID NO:85.		
٠.	10/231	nomo sapiens	Human signal peptide containing protein HSPP-8	1031	100
			SEO ID NO:8.		
95	AF227741	Rattus	protein kinase WNK1	2428	95
		norvegicus	Product Hands HAMI	2420	1 33
96	AF227741	Rattus	protein kinase WNK1	1961	94
		norvegicus			
97	¥92513	Homo sapiens	Human OXRE-10.	1626	100
98	AL021366	Homo sapiens	cICK0721Q.3 (Kinesin related	3423	100
99	AC005783	*****	protein)		
100	Y95293	Homo sapiens	R33083_1 Human GEF containing NEK-like	1974	99
		HOWO SUPTEMB	kinase substrate sGNK.	4092	99
101	AL118501	Homo sapiens	dJ1191N16.1 (A novel protein	1509	100
			(translation of the cDNA	1309	100
			DKFZp566A0946, Em:AL050069))		
102	AJ006267	Homo sapiens	ClpX-like protein	3233	100
103	AF100753	Homo sapiens	ancient ubiquitous 46 kDa	.2042	96
			protein AUP1		
104	AB015982	Homo sapiens	serine/threonine kinase	4718	100
105 106	AF151074	Homo sapiens	HSPC240	831	64
700	M35522	Canis familiaris	GTP-binding protein (rab7)	354	50
107	R99800	Homo sapiens	NTII-1 nerve protein,		
	1	Homo sapiens	<b>-</b>	2337	93
Ì	1		nerve cells.		
108	AF125533	Homo sapiens	NADH-cytochrome b5 reductase	1290	-03
ſ			isoform	4270	93
109	AC005614	Homo sapiens	F23269 2	3369	99
110	AF064729	Homo sapiens	RAN binding protein 16	3285	100
111	X52425	Homo sapiens	interleukin 4 receptor	4496	100
112	Y41686	Homo	Human PRO274 protein	2285	100
	74 550 5	sapiens	sequence.	j	
113	W15506	Homo sapiens	Mitogen activating protein	1991	100
114	Y71071		kinase ERK1.		
	1,10,1	Homo sapiens	Human membrane transport	1190	99
1.15	AL049548	Homo sapiens	protein, MTRP-16.		
		sapiens	dJ398G3.1 (ortholog of rat CPG2)	3497	99
116	AF189817	Mus musculus	evectin-2	1124	
117	W30891		Human cytostatin III protein.	715	90
				145	22

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	T 2
ID	NUMBER			WATERMAN	IDENTITY
NO:				SCORE	
		sapiens			
118	AF116618	Homo sapiens		1469	100
119 120	Y08915 AF098070	Homo sapiens	,	1748	100
		Drosophila melanogaster	Lis1 homolog	192	39
121	AF052432	Homo sapiens		181	37
122	Y70743	Homo sapiens	PSEQ-1 protein encoded by NSEQ gene associated with matrix remodelling.	2637	98
123	AF083246	Homo sapiens	HSPC028	2132	100
124	Y27096	Homo sapiens	Human viral receptor protein (ACVRP).	833	99
125	M63109	Leishmania	glycoprotein 96-92	172	27
126	U75467	major Drosophila	Atu	935	36
127	Z68220	melanogaster			
127	268220	Caenorhabdit is elegans	Similarity to Human ADP/ATP carrier protein	438	43
128	AF095927	Rattus	protein phosphatase 2C	1927	94
		norvegicus	<u>'</u>	1	1
129	W92958	Homo sapiens	Human zsig44 protein.	463	100
130	AF115391	Lactobacillu s sakei	ribokinase RbsK	508	37
131	X93498	Homo sapiens	21-Glutamic Acid-Rich Protein	1250	100
132	X93498	Homo sapiens	21-Glutamic Acid-Rich Protein	916	87
133	W52811	Homo sapiens	Human DBI/ACBP -like protein (DBIH).	705	97
134	Y84444	Homo sapiens	Amino acid sequence of a human RNA-associated protein.	3230	100
135	M69181	Homo sapiens	non-muscle myosin B	189	20
136	W74882	Homo sapiens	Human secreted protein	480	100
			encoded by gene 154 clone HE6FL83.	440	100
137	W78200	Homo sapiens	Human secreted protein	855	99
			encoded by gene 75 clone HHGAU81.		
138	AL033520	Homo sapiens	dJ349A12.1 (similar to KIAA0701 protein)	424	39
139	AF020261	Santalum album	proline rich protein	119	30
140	X70394	Homo sapiens	zinc finger protein	1634	100
141	Y06439	Homo sapiens	Human protease HUPM-8.	936	100
142	268493	Caenorhabdit is elegans	predicted using Genefinder	365	42
143	AB018107	Arabidopsis thaliana	ADP-ribosylation factor-like protein	596	65
144	AF161483	Homo sapiens	HSPC134	580	51
145	Y84902	Homo sapiens	A human proliferation and	480	100
146	AB004906	Ipomoea	apoptosis related protein.	146	20
147	AC007357	purpurea Arabidopsis	F3F19.18	647	31
148	W75155	thaliana Homo sapiens	Human secreted protein	1494	98
140	ŕ		encoded by gene 41 clone HNTME13.		
149	AF056490	Homo sapiens	cAMP-specific phosphodiesterase 8A	3710	99
150	Y58171	Homo sapiens	Human hydrolase homologue	785	99
151	U10397	Saccharomyce s cerevisiae	Yhr145wp	515	53
152	X73478	Homo sapiens	phosphotyrosyl phosphatase activator	1719	99
153	AL049697	Homo sapiens	dJ382I10.5.1 (novel protein	2034	99
			The state of the s	~~~	

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	- 8
ID	NUMBER			WATERMAN	IDENTITY
NO:				SCORE	J
			similar to arginyl-tRNA)		
154	AF169802	Homo sapiens	cytochrome b5 reductase b5R.2	1455	99
155	X94703	Homo sapiens	rab28	1126	99
156	Y25716	Homo sapiens	Human secreted protein encoded from gene 6.	1471	100
158	W77404	Homo sapiens	Secreted salivary polypeptide	937	100
159	Y17248	Homo sapiens	zsig32. Human protein kinase	383	100
			inhibitor-2 (PKI-2).		
160	J04970	Homo sapiens	carboxypeptidase M precursor	2395	100
161	W54040	Homo sapiens	Human interferon-inducible protein, HIFI.	484	98
162	AL022724	Homo sapiens	dJ413H6.1.1 (hamster	1357	100
102	ABOZZ/ZI	nono suprems	Androgen-dependent Expressed Protein LIKE PUTATIVE protein) (isoform 1)	1337	100
163	AF125535	Homo sapiens	pp21 homolog	193	45
154	G03632	Homo sapiens	Human secreted protein, SEQ ID NO: 7713.	463	97
165	AJ250839	Homo sapiens	serine/threonine protein	1442	71
166	L09649	Zymomonas	kinase	173	37
		mobilis			
167	¥73337	Homo sapiens	HTRM clone 1944530 protein sequence.	1204	100
168	W88645	Homo sapiens	Secreted protein encoded by gene 112 clone HUKFC71.	1084	100
169	AF214731	Homo sapiens	ATP-dependent RNA helicase	4402	100
170	AE000871	Methanobacte	conserved protein	166	27
		rium thermoautotr ophicum	•		
171	Y27684	Homo sapiens	Human secreted protein encoded by gene No. 118.	821	100
172	AF226044	Homo sapiens	HSNFRK	2904	100
173	AJ245946	Homo sapiens	neuroglobin	779	100
174	D43949	Homo sapiens	This gene is novel.	3202	100
175	¥07923	Homo sapiens	GTP-binding protein	1205	100
176	W90338	Homo sapiens	Human DP1 homologue protein.	966	100
177	Y41675	Homo sapiens	Human channel-related molecule HCRM-3.	1122	100
178	Y41674	Homo sapiens	Human channel-related	936	99
			molecule HCRM-2.		
179	AF220492	Homo sapiens	krueppel-like zinc finger protein HZF2	4100	99
180	X03084	Homo sapiens	Clq B-chain precursor	1240	100
181	U57344	Mus musculus	Meis3	1813	89
183	U57344	Mus musculus	Meis3	1743	86
184	U57344	Mus musculus	Meis3	1070	86
185	AF033120	Homo sapiens	p53 regulated PA26-T2 nuclear protein	1389	58
186	AF200357	Mus musculus	pantothenate kinase 1 beta	1605	82
187	W75058	Homo sapiens	Human secreted protein encoded by gene 2 clone HLDBG33.	1188	99
188	AJ292529	Homo sapiens	suppressor of sterile four 1	2424	100
190	X54134	Homo sapiens	protein-tyrosine phosphatase	3705	100
191	Y22203	Homo sapiens	Human calcium-binding phosphoprotein, CBPP-1, protein sequence.	1083	99
192	W63692	Homo sapiens	Human secreted protein 12.	1975	100
193	W87772	Homo sapiens	Human serum glucocorticoid-	2605	99
		Saprens	regulated kinase (H-SGK2) polypeptide.	2003	J.

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	IDENTITY
194	AF084259	Mus musculus	bromodomain-containing	SCORE 693	54
195	Y00752	Rattus	protein BP75 serine dehydratase (AA 1 -	100	ļ
		norvegicus	327)	994	61
196	W95349	Homo sapiens	Human foetal brain secreted protein fh170_7.	2596	100
197	AB028859	Homo sapiens	hDj9	1890	100
198	W95633	Homo sapiens	Homo sapiens secreted protein gene clone hm236_1.	1614	100
199	Y44277	Homo sapiens	Human nucleic acid methylase- 2.	2096	99
200	AB030039	Homo sapiens	hPACPL1	2258	100
201	X54162	Homo sapiens	64 Kd autoantigen	2918	99
202	G02061	Homo sapiens	Human secreted protein, SEQ ID NO: 6142.	558	99
203	X13885	Nicotiana tabacum	extensin (AA 1-620)	185	33
204	J04204	Bos taurus	32 kd accessory protein	1837	100
205	J04204	Bos taurus	32 kd accessory protein	1101	100
207	Y87283	Homo sapiens	Human signal peptide containing protein HSPP-60 SEQ ID NO:60.	1318	100
208	X02860	Homo sapiens	Fragment of human secreted protein encoded by gene 65.	936	98
209	AL121889	Homo sapiens	dJ1076E17.1 (KIAA0823 protein (continues in AL023803))	694	54
210	AF226732	Homo sapiens	NPD007	1345	76
211	X66295	Mus musculus	Clq C chain	970	73
212	Z29328	Homo sapiens	Ubiquitin-conjugating enzyme UbcH2	966	100
213	229328	Homo sapiens	Ubiquitin-conjugating enzyme UbcH2	542	98
214	AJ002030	Homo sapiens	progresterone binding protein	1163	100
215	X70649	Homo saplens	member of DEAD box protein family	3933	100
216	AF250558	Homo sapiens	claudin-2	1169	99
217	AL021453	Homo sapiens	dJ821D11.1 (PUTATIVE protein)	259	100
218	Y08565	Homo sapiens	UDP-GalNAc:polypeptide N- acetylgalactosaminyltransfera se	3331	99
219	Y94452	Homo sapiens	Human inflammation associated protein	2067	100
220	AL035521	Arabidopsis thaliana	putative protein	315	42
221	AL031786	Schizosaccha romyces pombe	putative proline-trna synthetase	811	41
222	AL109736	Schizosaccha romyces pombe	WD repeat protein	626	40
223	X52493	Glycine max	DNA-directed RNA polymerase	136	23
224	AL035659	Homo sapiens	dJ979N1.1 (dJ979N1.1)	5199	98
225	AB032401	Mus musculus	mmDj4	1761	92
226	AB032401	Mus musculus	mmDj4	1988	92
227	X83502	Saccharomyce s cerevisiae	J1007	112	26
228	X83502	Saccharomyce s cerevisiae	J1007	79	25
229	AF143723	Homo sapiens	heat shock protein HSP60	2557	99
230	Y66677	Homo sapiens	Membrane-bound protein PRO828.	982	100
231	AB027466	Homo sapiens	spondin 2	1756	99
232	W95634	Homo sapiens	Homo sapiens secreted protein.	1391	100
233	W00365	Homo sapiens	Human cyclin B1.	2218	99
234	Y53762	Homo sapiens	A GTP-binding polypeptide	1017	100

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION  designated RAQ.	SMITH- WATERMAN SCORE	IDENTITY
235	250749	Homo sapiens	yeast sds22 homolog	1800	
236	Z50749	Homo sapiens			100
237	AB026491	Homo sapiens	PICK1	1754	98
238	AJ270205	Entodinium		2137	100
220	AD210203	caudatum	putative phosphatidylinositol-4-	114	37
ì	}	Januarcan	phosphate 5-kinase	1	
239	AB030189	Mus musculus			<u> </u>
	1.2030203	Mus musculus	region and ATP binding region	710	93
240	W56538	Homo sapiens	Human hedgehog interacting		<u> </u>
·		suprems	protein (HIP).	3785	99
241	W56538	Homo sapiens			<b>_</b>
		oo bapicits	protein (HIP).	3436	99
242	AF155107	Homo sapiens		1	<u> </u>
243	AF155107	Homo sapiens	NI-REN-3/ antigen	996	99
244	AL031320			1005	100
277	AD031320	Homo sapiens		763	99
	}	1	similar to yeast and	!	
	1	1	bacterial cytosine	1	1
245	U37026	Rattus	deaminase)		
243	03/026		sodium channel beta 2 subunit	162	30
246	AL078599	norvegicus			Ì
490	ALU 76599	Homo sapiens	dJ991C6.1 (novel protein	2391	98
			similar to C. elegans	İ	
247	U32274	C2 - 21	F55A12.9 (Tr:P91086))		
44/	032274	Saccharomyce	Ydr386wp; CAI: 0.12	191	37
248	Y41719	s cerevisiae			
~70	141/19	1	Human PRO864 protein	1879	100
249	AB029434	sapiens	sequence.	<u> </u>	1
250	X97831	Homo sapiens	ghrelin precursor	611	100
230	A9/031	Rattus	carnitine/acylcarnitine	246	38
251	W80993	norvegicus Homo	carrier protein	I	1
231	W80993		Human RIP-interacting factor	1724	100
252	¥94873	sapiens Homo	RIF.	<u></u>	
2,72	1940/3	sapiens	Human protein clone HP02632.	1876	100
253	W59878	Homo sapiens		ļ	
	1133076	HOMO SADIENS	Amino acid sequence of the	765	100
254	AL354533	Leishmania	cDNA clone AIF-2 (HEBGM49).		
	111111111111111111111111111111111111111	major	possible adenylate kinase	265	34
255	AF233322	Mus musculus			
256	Y78113	Homo sapiens	zinc transporter like 2	1916	95
	1,0113	nomo sapiens	Human cytokine signal	2247	99
			regulator CKSR-1 SEQ ID NO:1.	}	
257	AL035539	Arabidopsis			
251	AD035539	thaliana	putative amino acid transport	390	27
258	W74787	Homo sapiens	protein		
200	1 ", 1,0,	nomo sapiens	Human secreted protein	1171	100
	1		encoded by gene 58 clone	ĺ	
259	AL035689	Vomo sandana	HHFHN61.		
200	12033669	Homo sapiens	dJ187J11.1 (novel protein	974	100
			similar to protein kinase C		
260	AE000909	Methanobacte	inhibitors)		
200	AE000909	rium	serine/threonine protein	363	30
	1		kinase related protein	}	}
	l l	thermoautotr	1	}	ĺ
261	AL050131	Ophicum			
262	AF019661	Homo sapiens	hypothetical protein	626	100
263	AL035593	Mus musculus	zeta proteasome chain; PSMA5	1214	100
264	AL035593	Homo sapiens	dJ310J6.1 (novel protein)	821	100
-04	WP0553TR	Homo sapiens	bK150C2.3 (PUTATIVE novel	1072	100
265	ABOUTO	**	protein similar to APOBEC1)	<u>.                                    </u>	
266	AF205940	Homo sapiens	endomucin	1289	100
		Homo sapiens	dJ500L14.1 (novel protein)	789	100
267	AL034548	Homo sapiens	dJ1103G7.3 (novel protein	1888	99
- 1	1	i	kinase domains containing	j	1
ļ	1	Į	protein similar to	[	1
			phosphoprotein C8FW)	ľ	ſ

SEQ	ACCESSION	SPECIES	DESCRIPTION		
ID NO:	NUMBER	0.20120	DESCRIPTION	SMITH- WATERMAN	IDENTITY
268	AF161470	Homo sapiens		SCORE	1
269	AF161470	Homo sapiens		1884	98
270	X90763	Homo sapiens		1232	96
	1	sapiens	HHa5 hair keratin type I intermediate filament	2190	99
271	AF207600	Homo sapiens	ethanolamine kinase	4050	
272	M32334	Homo sapiens		1952	100
1		bapacits	molecule 2	1436	100
273	AF161483	Homo sapiens		663	<u> </u>
274	Y53052	Homo sapiens		587	61
			df202_3 protein sequence SEQ ID NO:110.	587	100
276	¥77576	Homo sapiens	(HCYT) (clone 2195418).	762	100
277	AF077042	Homo sapiens	homolog	1269	100
278	¥94907	Homo sapiens		1619	98
			ca106_19x protein sequence SEQ ID NO:20.		
279	Y68788	Homo sapiens		2801	99
			human phosphorylation effector PHSP-20.	2551	"
280	275134	Canis	rod transducin	1816	100
	<u> </u>	familiaris	1	1010	1 100
281	275134	Canis	rod transducin	1718	96
		familiaris			}
282	AF249873	Homo sapiens	muscle-specific protein	1395	100
283	AL050007	Homo sapiens	hypothetical protein	405	98
284	AF201931	Homo sapiens		1859	99
285	AF156102	Homo sapiens		1318	99
286	¥35897	Homo sapiens	Extended human secreted	1250	99
			protein sequence, SEQ ID NO.		
287	U88964	Homo sapiens	HEM45	923	100
288	AL050143	Homo sapiens	hypothetical protein	598	100
289	AJ011098	Homo sapiens	telethonin	574	100
290	¥66724	Homo	Membrane-bound protein	2321	100
5.5.		sapiens	PRO836.	1	
291	AF034801	Homo sapiens	liprin-alpha4	2565	98
292	AF034801	Homo sapiens	liprin-alpha4	2590	100
293	AL049851	Homo sapiens	dJ889J22B.1 (novel protein	1738	100
294	Y73348		(isoform 1))		
		Homo sapiens	HTRM clone 839651 protein sequence.	1245	99
295	L11672	Homo sapiens	zinc finger protein	1694	44
296	AL035423	Homo sapiens	dJ2013.1 (brain mitochondrial	1024	79
297	35100500		carrier protein-1 (BMCP1))		=
431	AF198532	Homo sapiens	lymphoid enhancer binding	2173	100
298	AF161417	Home and	factor-1		
299	AF159141	Homo sapiens	HSPC299	1147	85
	WET DATAT	Homo sapiens	breast cancer metastasis-	1236	99
300	U26397	Rattus	suppressor 1		
	020391	norvegicus	inositol polyphosphate 4-	160	30
301	AF036145	Homo sapiens	phosphatase		
	020142	women sabreus	meningioma-expressed antigen	3458	100
302	Z82022	Womo so-do-	S CI-V1 P		
303	AF269232	Homo sapiens	GlcNac-1-P transferase	2067	99
		Mus musculus	butyrophilin-like protein BUTR-1	271	50
304	AJ222644	Arabidopsis	asparaginyl-tRNA synthetase	659	50
		thaliana			ł
305	AF054180	Homo	hematopoietic cell derived	351	79
		sapiens	zinc finger protein		1
106		Homo sapiens	APOBEC-1 stimulating protein	3056	100
808	¥44486	Homo	Human GPRW receptor		100
		sapiens	polypeptide.		-
09	AJ131891	Homo sapiens	DNA polymerase mu	2598	100

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	
ID NO:	NUMBER	0.2020		WATERMAN SCORE	IDENTITY
310	AF293335	Homo sapiens	p30 DBC	1248	92
311	AF176525	Mus musculus	F-box protein FBL12	1501	93
312	X57802	Homo sapiens	immunoglobulin lambda light chain	959 .	81
313	236715	Homo sapiens	Net	2048	98
314	AF161532	Homo sapiens	HSPC047	727	100
315	AF208068	Homo sapiens	kelch-like protein KLHL3a	3046	100
316	Y66666	Homo sapiens	Membrane-bound protein PRO1013.	1166	100
317	Y29666	Homo sapiens	Human Ras protein RAPR-1.	1253	98
318	AJ387747	Homo sapiens	sialin	2614	99
319	AF161362	Homo sapiens	HSPC099	224	40
320	Y68773	Homo sapiens	Amino acid sequence of a human phosphorylation effector PHSP-5.	2243	99
321	AJ238379	Homo sapiens	putative TH1 protein	3013	100
322	AB040812	Homo sapiens	protein kinase PAK5	3792	99
323	Y95013	Homo sapiens	Human secreted protein vc48 1, SEQ ID NO:66.	913	100
324	Y13381	Homo sapiens	Amino acid sequence of protein PRO271.	1976	100
325	Y94944	Homo sapiens	Human secreted protein clone bf157_16 protein sequence SEQ ID NO:94.	2305	98
326	Y76884	Homo sapiens	Retinoblastoma binding protein-7sequence.	6728	99
327	AF198532	Homo sapiens	lymphoid enhancer binding factor-1	2173	100
328	Z78013	Caenorhabdit is elegans	Similarity to Drosophila Cadherin-related tumor suppressor	569	33
329	AF212921	Mus musculus	MMTV receptor variant 1	484	94
330	275330	Homo sapiens] >R65207 R65207 02- MAR-1995 27- AUG-1993 Human stromalin-1. [Homo sapiens	nuclear protein SA-1	6492	99
331	AL008583	Homo sapiens	dJ327J16.3 (supported by GENSCAN, FGENES and GENENISE)	2133	99
332	Y36104	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 489.	310	41
333	AJ271669	Homo sapiens	putative sialoglycoprotease	1747	100
334	AF156598	Mus musculus	p53-regulated DDA3	997	64
335	M99058	Eimerla maxima	em100 gene is homologous the Eimeria tenella gene et100	154	26
336	Y85564	Homo sapiens	Human homologue of UNC-53 (Hs-UNC-53/1) sequence.	3386	97
337	Y85564	Homo sapiens	Human homologue of UNC-53 (Hs-UNC-53/1) sequence.	2602	94
338	Y85564	Homo sapiens	Human homologue of UNC-53 (Hs-UNC-53/1) sequence.	3447	98
339	266561	Caenorhabdit is elegans	Similarity to Human rab13 protein (PIR Acc. No. A49647).	716	34
340	AB021643	Homo sapiens	gonadotropin inducible transcription repressor-3	2761	99
341	G01946	Homo sapiens	Human secreted protein, SEQ ID NO: 6027.	465	98
342	AF020591	Homo sapiens	zinc finger protein	1091	48
343	L29154	Homo sapiens	immunoglobulin heavy chain	439 .	84
				1 1	

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	1 - 2
ID	NUMBER			WATERMAN	IDENTITY
NO:				SCORE	
344	U10281		VDJ region		T
345	AK000404	Sus scrofa	gastric mucin	279	24
346	1.22557	Homo sapiens		1177	99
347	L22557	norvegicus	calmodulin-binding protein	1949	84
		Rattus norvegicus	calmodulin-binding protein	2363	91
348	AL049481	Arabidopsis thaliana	AIG1-like protein	316	30
350	AJ251516	Mus musculus	cysteine and histidine-rich protein	1460	99
351	AK024477	Homo sapiens	FLJ00070 protein	1773	100
352	U50133	Homo sapiens	ankyrin	502	33
353 354	AK000625	Homo sapiens	unnamed protein product	721	100
354	AF161420	Homo sapiens	HSPC302	2623	97
355	AJ010014	Homo sapiens	M96A protein	1269	47
357	AF151029	Homo sapiens	HSPC195	941	91
357	AL022327 W78128	Homo sapiens	dJ355C18.1 (KIAA0027)	1911	100
		Homo sapiens	Human secreted protein encoded by gene 3 clone HOSBI96.	1117	100
359	X03414	Drosophila melanogaster	Kr polypeptide	316	45
360	AF151079	Homo sapiens	HSPC245	643	100
361	Y53886	Homo sapiens	A suppressor of cytokine signalling protein designated HSCOP-6.	530	41
362	AF254741	Drosophila melanogaster	Centaurin Gamma IA	681	46
363	AF213465	Homo sapiens	dual oxidase	2016	100
364	AF181562	·Homo sapiens	proSAAS	1319	100
365	AF181562	Homo sapiens	proSAAS	1024	99
366	U73200	Mus musculus	pll6Rip	884	82
367	AF263744	Homo sapiens	erbb2-interacting protein ERBIN	4973	99
368	U37501	Mus musculus	laminin alpha 5 chain	5867	72
369	AF043695	Caenorhabdit is elegans	similar to the protein phosphates 2c family	549	36
370	¥73440	Homo sapiens	Human secreted protein clone yj23_1 protein sequence SEQ ID NO:102.	1484	99
371 372	AF272833 AF198454	Homo sapiens	misato	2869	97
373	Y73345	Homo sapiens	epithelial protein lost in neoplasm beta	3927	100
374	AF169017	Homo sapiens	HTRM clone 438283 protein sequence.	273	80
		Homo sapiens	formiminotransferase cyclodeaminase	2717	98
375	A95106	unidentified	RED ALPHA	1202	99
376	W7482B	Homo sapiens	Human secreted protein encoded by gene 100 clone HLQAB52.	1012	99
377	Y32131	Homo sapiens	Human LYST-2 protein.	3556	99
378	M14912	Homo sapiens	pol	132	86
379	AF090934	Homo sapiens	PR00518	382	100
380	X66363	Homo sapiens	serine/threonine protein kinase	2499	100
381	Y41699	Homo sapiens	Human PRO703 protein sequence.	2362	100
382	AF174498	Homo sapiens	GR AF-1 specific protein phosphatase	7008	98
383	U64608	Caenorhabdit is elegans	coded for by C. elegans cDNA vk173c12.5	246	36
384	U50133	Homo sapiens	ankyrin	502	33
385	AJ238520	Homo sapiens	putative transcription	1 - 1	97
			factor-like nuclear regulator		

SEQ	ACCESSION	SPECIES	DESCRIPTION	- CMTTHE	
ID NO:	NUMBER	1111111	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
387	AF208845	Homo sapiens		1375	99
389	X57821	Homo sapiens	immunoglobulin lambda light chain	797	76
390	AF182404	Homo sapiens	protein 1	1670	99
391	¥85564	Homo sapiens	Human homologue of UNC-53 (Hs-UNC-53/1) sequence.	3386	97
393	AF178432	Homo sapiens	SH3 protein	3700	100
394	AF229928	Drosophila	cytoplasmic protein 89BC	1616	62
395	7.01.01	melanogaster			"
395	AF181721	Homo sapiens		2254	100
	Y69197	Homo sapiens	Amino acid sequence of a human betaIV-spectrin protein.	1626	98
397	U48238	Mus musculus	zinc finger protein neuro-d4	749	60
398	AL390137	Homo sapiens	hypothetical protein	263	51
399	AF217525	Homo sapiens	Down syndrome cell adhesion molecule	5337	60
400	AL022599	Schizosaccha romyces pombe	WD repeat protein	447	27
401	AC004859	Homo sapiens	similar to 2-oxoglutarate dehydrogenase; similar to Q02218 (PID:q1352618)	4176	78
402	AB010266	Mus musculus	tenascin-X	10246	62
403	AL133288	Homo sapiens	dJ671D7.1 (similar to D.melanogaster CG5986 protein)	761	100
404	Z68753	Caenorhabdit is elegans	ZC518.3b	888	48
405	Z78013	Caenorhabdir is elegans	Similarity to Drosophila Cadherin-related tumor	569	33
406	AB031230	Homo sapiens	suppressor protein containing CXXC domain 2	1196	97
407	AF155106	Homo sapiens	NY-REN-36 antigen	1168	100
408	Y57945	Homo sapiens	Human transmembrane protein	1538	99
409	Z18361	Ovis aries	trichohyalin	184	30
410	AF249744	Homo sapiens	RhoGEF	2733	100
411	AF176529	Mus musculus	F-box protein FBX13	2072	94
412	AF210842	Homo sapiens	HARP	4880	100
413	AL031658	Homo sapiens	dJ310013.7 (novel protein similar to H. roretzi HRPET- 3)	776	98
414	X57398	Homo sapiens	pm5 protein	6131	99
415	AB029826	HOmo sapiens	3-methylcrotonyl-CoA carboxylase biotin-containing subunit	2961	99
416	U43503	Saccharomyce s cerevisiae	Lph1p	115	42
417	AL160493	Leishmania major	possible t26f17.21	239	35
418	Y08100	Homo sapiens	Human PRO331 protein.	330	29
419	U15131	Homo sapiens	p126	2228	54
420	AF117946	Homo sapiens	Link guanine nucleotide exchange factor II	2363	100
421	AF190635	Drosophila melanogaster	ankyrin 2	755	30
422	AF302150	Homo sapiens	phosphoinositol 3-phosphate- binding protein-2	1962	100
123		Homo sapiens	hypothetical protein	433	94
424	X63753	Homo sapiens	son-a	7269	100
125	AB027249	Homo sapiens	MAPKK like protein kinase	1693	100
126	AF279144	Homo sapiens	tumor endothelial marker 7 precursor		55

NOMBER   NO.	SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	
Decomposition   Decompositio	ID No:	NUMBER			WATERMAN	IDENTITY
Membrane-bound protein   Membrane-bound   Membrane-b	427	AF279144	Homo sapiens		1259	56
430   APO36837   Drosophila			melanogaster		149	29
Mail					2201	99
AF023674   Homo saplens   Septin 7-like cell division   3783   100			melanogaster		4442	47
ABO06697   AFDOO   Septim 7-like cell division   2284   100					4021	99
Sapiens   Control protein   226						100
Thaliana			sapiens	control protein	2284	100
AB040672   Homo sapiens   UDP-GalNAc: polypeptide N- acetylgalactosaminyltransfera   security   S			thaliana	associated transmembrane protein-like	886	42
AF105228   Bos taurus   Luftelin   285   33		Y94247	Homo sapiens	hCBP.	1704	100
A40   R06463   Homo sapiens   Derived protein of clone   3073   99			Homo sapiens	acetylgalactosaminyltransfera	1075	63
100   100					285	33
A42				ICA13 (ATCC 40553).	3073	99
100   100				alpha-adaptin (A) (AA 1-977)	4897	98
Sapiens   PRO1136.   Sapiens   Sapiens   PRO1136.   Sapiens   Sapiens   PRO1136.   Sapiens	,		norvegicus	938)	3979	81
Thaliana   Thaliana			sapiens		3299	99
AF056035   Rattus   S-nexilin   2662   85	444	AC067754		unknown protein; 20348-23707	114	33
AF056035   Rattus   S-nexilin   2662   85	445	AF229032	Mus musculus	piL	2077	93
W89024	446	AF056035	h .	s-nexilin	2662	
W89024	447	AF132484		unknown	478	51
450   Z68753   Caenorhabdit   is elegans   155   149     451   W39160   Homo sapiens   Human partial complement   155   32     452   W85727   Homo   Sapiens   BM46_10).   Homo sapiens   A bone marrow secreted   2810   100     453   Y53629   Homo sapiens   A bone marrow secreted   2810   100     454   D87438   Homo   Similar to a C.elegans   4069   100     455   AF240468   Homo sapiens   protein in cosmid C14H10   1305   99     456   Z15005   Homo sapiens   CENP-E   13305   99     457   M59216   Homo   gamma-aminobutyric acid   2477   100     458   Y73467   Homo sapiens   Human secreted protein clone   yd61_1 protein sequence SEQ   ID NO:156.   Human secreted protein   535   100     459   W67824   Homo sapiens   Human secreted protein   535   100     460   AF163151   Homo sapiens   dentin sialophosphoprotein   279   19   19     461   D87446   Homo sapiens   F25965   Human secreted protein, SEQ   486   93     462   G04044   Homo sapiens   F25965   10 NO: 8125.   1018   100     463   AC002398   Homo sapiens   F25965   100   1018   100     464   AC002398   Homo sapiens   F25965   1018   100     455   AC002398   Homo sapiens   F25965   1018   100     465   AC002398   Homo sapiens   F25965   100   1018   100     466   AC002398   Homo sapiens   F25965   1018   100     467   AC002398   Homo sapiens   F25965   1018   100     468   AC002398   Homo sapiens   F25965   1018   100     469   ACO02398   Homo sapiens   F25965   1018   100     460   ACO02398   Homo sapiens   F25965   1018   100     460   ACO02398   Homo sapiens   F25965   1018   100     460   ACO02398   Homo sapiens   F25965   1018   100     460   ACO02398   Homo sapiens   F25965   1018   100     460   ACO02398   Homo sapiens   F25965   1018   100     460   ACO02398   Homo sapiens   F25965   1018   100     460   ACO02398   Homo sapiens   F25965   1018   100     460   ACO02398   Homo sapiens   F25965   1018   100     460   ACO02398   Homo Sapiens   F25965   1018   100     460   ACO02398   Homo Sapiens   F25965   1018   100     460   ACO02398   Homo Sapiens   F2	448	W89024	Homo sapiens		528	
is elegans  451 W39160 Homo sapiens Human partial complement factor H protein fragment 3.  452 W85727 Homo sapiens BM46_10).  453 Y53629 Homo sapiens A bone marrow secreted protein designated BMS115.  454 D87438 Homo sapiens protein in cosmid C14H10  455 AF240468 Homo sapiens nicastrin 3687 100  456 Z15005 Homo sapiens CENP-B 13305 99  457 M59216 Homo sapiens receptor beta-1 subunit 2477 100 sapiens receptor beta-1 subunit 458 Y73467 Homo sapiens Human secreted protein clone yd61_1 protein sequence SEQ ID NO:156.  460 AF163151 Homo sapiens dentin sialophosphoprotein encoded by gene 18 clone HSLFM29.  461 D87446 Homo sapiens Similar to a C.elegans protein encoded in cosmid C27F2 (U40419)  462 G04044 Homo sapiens Human secreted protein, SEQ 486 93 ID NO: 8125.  463 AC002398 Homo sapiens F25965 1 1018 100		_	Homo sapiens	HSPC327	1606	100
Section   Factor   Fragment 3.   133   32				ZC518.3b	951	49
Web   Web			-		155	32
Protein designated BMS115.   100			sapiens	Novel protein (Clone	2799	99
D87438			Homo sapiens	protein designated BMS115.	2810	100
456   Z15005   Homo sapiens   CENP-E   13305   99     457   M59216   Homo   gamma-aminobutyric acid   receptor beta-1 subunit   100     458   Y73467   Homo sapiens   Human secreted protein clone   yd61_1 protein sequence SEQ   ID NO:156.   100     459   W67824   Homo sapiens   Human secreted protein   encoded by gene 18 clone   HSLFM29.   100     460   AF163151   Homo sapiens   dentin sialophosphoprotein   279   19   precursor   Similar to a C.elegans   protein encoded in cosmid   C27F2 (U40419)   100			sapiens	Similar to a C.elegans	4069	100
M59216					3687	100
Sapiens   receptor beta-1 subunit   2477   100						
Yd61_1 protein sequence SEQ   ID NO:156.			sapiens	receptor beta-1 subunit	2477	100
encoded by gene 18 clone HSLFM29.  460 AF163151 Homo sapiens dentin sialophosphoprotein precursor  461 D87446 Homo sapiens Similar to a C.elegans protein encoded in cosmid C27F2 (U40419)  462 G04044 Homo sapiens Human secreted protein, SEQ ID NO: 8125.  463 AC002398 Homo sapiens F25965 1 1018 100			_	yd61_1 protein sequence SEQ ID NO:156.	966	100
precursor   1996   99   99   99   99   99   99		_	_	encoded by gene 18 clone HSLFM29.	535	100
D87446   Homo sapiens   Similar to a C.elegans   9196   99			Homo sapiens		279	19
462 GO4044 Homo sapiens Human secreted protein, SEQ 486 93  ID NO: 8125.  463 AC002398 Homo sapiens F25965 1 1018 100		D87446	Homo sapiens	Similar to a C.elegans protein encoded in cosmid	9196	99
				Human secreted protein, SEQ	486	93
ALC INVOCAUES I Dalatina					1018	100
ACE DEPOSITE TO THE PROPERTY OF			Rattus sp.	7acomp protein		84
465 AF223408 Homo sapiens B99 3686 99	465	AF223408	Homo sapiens	B99	3686	99

SEQ	ACCESSION	SPECIES	DESCRIPTION		
ID	NUMBER	Di Della	DESCRIPTION	SMITH-	ę
NO:		l		WATERMAN	IDENTITY
466	AF223408	Homo sapiens	B99	SCORE	
467	AF104415	Mus musculus		2878	87
468	U53450	Rattus	Jun dimerization protein 1	6336	91
		norvegicus	JDP-1	196	49
469	AL031297	Homo sapiens			
470	AF257077	Homo sapiens	eukaryotic translation	3564	99
Ī		Buricus	initiation factor EIF2B	1274	95
1		]	subunit 3		
471	L28125	Podospora	beta transducin-like protein		
		anserina	beed cransducin-like process	284	38
472	Y84903	Homo sapiens	A human proliferation and		
ĺ			apoptosis related protein.	2337	100
473	AF144237	Homo sapiens	LOMP protein	<del> </del>	
474	Y71213	Homo sapiens		252	44
		J Dapacano	related polypeptide IMX39.	838	100 .
475	Y95006	Homo sapiens	Human secreted protein		
	}		vel3_1, SEQ ID NO:52.	3411	100
476	D38549	Homo sapiens	halo25 is new	<del> </del>	<u> </u>
477	AF241230	Homo sapiens	TAK1-binding protein 2	6533	99
478	AL031534	Schizosaccha	putative asparagine synthase	3656	100
	1	romyces	F asparagine synthase	482	40
		pombe			İ
479	L28125	Podospora	beta transducin-like protein	233	
	1	anserina	and the protection	433	26
480	AF161544	Homo sapiens	HSPC059	434	77
481	AJ238248	Homo sapiens	centaurin beta2	3986	99
482	Z38061	Saccharomyce	mal5, stal, len: 1367, CAI:	295	23
	1	s cerevisiae	0.3, AMYH YEAST P08640	233	23
			GLUCOAMYLASE S1 (EC 3.2.1.3)	1	
483	AF161381	Homo sapiens	HSPC263	1404	100
484	AF223468	Homo sapiens	AD021 protein	1314	100
486	X57527	Homo sapiens	alpha 1 (VIII) collagen	4166	99
487 488	Y19062	Homo sapiens	39k3 protein	2475	100
488	Y73373	Homo sapiens	HTRM clone 921803 protein	555	56
489	AL021918		sequence.	1	
403	AD021918	Homo	b3418.1 (Kruppel related Zinc	4184	100
490	X53773	sapiens Rattus	Finger protein 184)	,	ļ
150	1 237/3	-	alpha-c large chain (AA 1-	4675	97
491	U52426	norvegicus Homo sapiens	938)		, v
492	AL359773	Leishmania	GOK	1459	59
	20000777	major	possible threonine synthase	702	45
493	AF226614	Homo sapiens	ferroportinl		_
494	Z93241	Homo sapiens	dJ222E13.1 (novel protein	2929	100
		nome paptens	with some similarity to	513	96
		ľ	Drosophila KHAKEN)		
495	AF036977	Homo sapiens	unknown	1010	
496	U93564	Homo sapiens	p40	1912	100
497	Y91405	Homo sapiens	Human secreted protein		45
. 1	ŀ		sequence encoded by gene 2	357	100
			SEQ ID NO:126.		l
498	AF069781	Drosophila	Bem46-like protein	653	43
		melanogaster	p	533	*2
199	Y16601	Homo sapiens	Human cell-cycle	1658	98
			phosphoprotein CECYP-2.	-050	-0
500	X70944	Homo sapiens	PTB-associated splicing	3883	100
			factor	-003	-30
501		Mus	putative membrane-associated	205	36
		musculus	guanylate kinase 1		
ŀ		mascaras			
02	AF282874		nectin 3; PRR3	2856	99
02 03	AF282874 AJ249732	Homo sapiens		2856 669	99
02 03	AF282874 AJ249732 AF208861	Homo sapiens Homo sapiens Homo sapiens	nectin 3; PRR3 G8 protein BM-019	669	100
602 603 604 605	AF282874 AJ249732 AF208861 L09708	Homo sapiens Homo sapiens Homo sapiens Homo sapiens	nectin 3; PRR3 G8 protein BM-019	669 1629	100
502 503 504 505	AF282874 AJ249732 AF208861 L09708 X66285	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus	nectin 3; PRR3 G8 protein BM-019 complement component C2 HC1 ORF	669 1629 4022	100 100 100
502 503 504 505	AF282874 AJ249732 AF208861 L09708 X66285 D00189	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus	nectin 3; PRR3 G8 protein BM-019 complement component C2	669 1629 4022 115	100

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	identity
509	¥94971	Homo sapiens	Human secreted protein clone fal71_1 protein sequence SEQ ID NO:148.	2176	100
510	AB019038	Homo sapiens		781	
511	AB019038	Homo sapiens	beta-1,4 mannosyltransferase	1347	100
512	AB019038	Homo sapiens		1520	100
513	X84908	Homo sapiens		5729	99
514	X52851	Homo sapiens		650	76
515	AF186084	Homo	epidermal growth factor	3046	99
516	G03602	sapiens Homo sapiens	repeat containing protein	505	99
			ID NO: 7683.	1 303	1 33
517	U04706	Bos taurus	50 kDa protein	1749	77
518	G00653	Homo sapiens	Human secreted protein, SEQ	530	100
519	AF161475	Homo sapiens	HSPC126	1368	100
520	¥99366	Homo sapiens	Human PRO1475 (UNQ746) amino	3394	97
	J	1	acid sequence SEQ ID NO:88.	3334	"
521	AF266852	Homo sapiens	PTPLA	1295	100
522	AE000995	Archaeoglobu	chromosome segregation	153	20
		s fulgidus	protein (smc1)	]	- 4
523	AF062249	Homo sapiens	immunoglobulin heavy chain variable region	605	97
524	AJ223830	Rattus norvegicus	ARE1	2950	98
525	W01535	Homo sapiens	Cellular homologue of the SV40 large T antigen.	1276	83
526	AF145658	Drosophila melanogaster	BcDNA.GH10229	320	33
527	AF112213	Homo sapiens	putative Rab5-interacting	524	79
528	D49387	Homo	protein NADP dependent leukotriene b4	1616	100
529	Y30819	sapiens Homo sapiens	12-hydroxydehydrogenase Human secreted protein	328	
530	AL079335	Homo sapiens	encoded from gene 9.	}	32
	Autijaaa	Homo sapiens	dJ132F21.3 (72.1 KDa protein (DKFZP564A032, SBB188) similar to mouse IFN~gamma induce MG11.)	1059	99
531	Y91506	Homo sapiens	Human secreted protein sequence encoded by gene 56 SEQ ID NO:179.	1159	98
532	X76116	Caenorhabdit	carrier protein (c2)	576	50
533	X76116	is elegans Caenorhabdit	carrier protein (c2)	506	50
534	X12966	is elegans			
		Homo sapiens	3-oxoacyl-CoA thiolase propeptide (424 AA)	1972	100
535	Y09267	Homo sapiens	flavin-containing	2486	100
			monooxygenase 2		
536	Z11773	Homo sapiens	monooxygenase 2 SRE-ZBP	2201	99
536 537	D84224	Homo sapiens		2201 4741	
536 537 538	D84224 D84224	Homo sapiens	SRE-ZBP methionyl tRNA synthetase methionyl tRNA synthetase		99
536 537 538 539	D84224 D84224 D84224	Homo sapiens Homo sapiens Homo sapiens	SRE-ZBP methionyl tRNA synthetase methionyl tRNA synthetase methionyl tRNA synthetase	4741	99
536 537 538 539 540	D84224 D84224 D84224 D84224	Homo sapiens Homo sapiens Homo sapiens Homo sapiens	SRE-ZBP methionyl tRNA synthetase methionyl tRNA synthetase methionyl tRNA synthetase methionyl tRNA synthetase methionyl tRNA synthetase	4741 3887	99 99
536 537 538 539 540 541	D84224 D84224 D84224 D84224 D84224 J03244	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Bos taurus	SRE-ZBP methionyl tRNA synthetase methionyl tRNA synthetase methionyl tRNA synthetase methionyl tRNA synthetase methionyl tRNA synthetase H+ ATPase 31kDa subunit (EC 3.6.1.3)	4741 3887 2933	99 99 99 96
536 537 538 539 540 541	D84224 D84224 D84224 D84224 J03244 Y92514	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Bos taurus Homo sapiens	SRE-ZBP methionyl tRNA synthetase methionyl tRNA synthetase methionyl tRNA synthetase methionyl tRNA synthetase methionyl tRNA synthetase methionyl tRNA synthetase tRH+ ATPase 31kDa subunit (EC 3.6.1.3) Human OXRE-11.	4741 3887 2933 4529 848	99 99 99 96 99
536	D84224 D84224 D84224 D84224 J03244 Y92514 AF221712	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Bos taurus	SRE-ZBP methionyl tRNA synthetase methionyl tRNA synthetase methionyl tRNA synthetase methionyl tRNA synthetase methionyl tRNA synthetase methionyl tRNA synthetase th+ ATPase 31kDa subunit (EC 3.6.1.3) Human OXRE-11. Smad- and Olf-interacting	4741 3887 2933 4529 848	99 99 99 96 99 77
536 537 538 539 540 541	D84224 D84224 D84224 D84224 J03244 J03244 Y92514 AF221712 AE000919	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Bos taurus Homo sapiens	SRE-ZBP methionyl tRNA synthetase methionyl tRNA synthetase methionyl tRNA synthetase methionyl tRNA synthetase methionyl tRNA synthetase methionyl tRNA synthetase tRH+ ATPase 31kDa subunit (EC 3.6.1.3) Human OXRE-11.	4741 3887 2933 4529 848 2301 2151	99 99 99 96 99 77

TABLE 2

SEO	ACCESSION	SPECIES	DECONTRETON		
ID NO:	NUMBER	SFECTES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
546	Y02698	Homo sapiens	encoded by gene 49 clone	854	98
547	AF112205	<del>                                     </del>	HTPCS60.	1	
548	X60271	Homo sapiens Mus musculus		2275	100
549	AC016827	Arabidopsis		2264	74
550		thaliana	putative GTPase	810	42
	¥70400	Homo sapiens	Human cell-signalling protein-2.	429	68
551	AB048365	Homo sapiens	NEDD4-like ubiquitin ligase 1	8290	99
552	Y57880	Homo sapiens	HTMPN-4.	1112	95
553	AF119855	Homo sapiens		265	67
554	M17236	Homo sapiens	The same of arbitrary	1332	100
555	AL078468	Arabidopsis thaliana	putative protein	540	40
556	AC006963	Homo sapiens	similar to Kelch proteins; similar to BAA77027 (PID:g4650844)	515	44
557	AK024487	Homo sapiens	FLJ00086 protein	1623	98
558	M12140	Homo sapiens		117	48
559	W74825	Homo sapiens	Human secreted protein encoded by gene 97 clone HAQBF73.	225	56
560	X56681	Homo sapiens	junD protein	373	88
561	AF003136	Caenorhabdit is elegans	contains weak similarity to an AMP-binding motif	2926	54
562	AL109839	Homo sapiens	dJ1069P2.3.1 (novel PABPC1 (poly(A)-binding protein)	877	100
563	AF181640	Drosophila melanogaster	BcDNA.GH09817	289	42
564	AF052723	Peline leukemia virus	gag-pol precursor polyprotein gPr80	1547	43
565	AF161472	Homo sapiens	HSPC123	439	44
566	Y28817	Homo sapiens	pt326_4 secreted protein.	3338	100
567	U09848	Homo sapiens	zinc finger protein	1738	100
569	AF155113	Homo sapiens	NY-REN-55 antigen	3603	93
570	AF155113	Homo sapiens	NY-REN-55 antigen	3951	99
571	AL032821	Homo sapiens	dJ55C23.1 (vanin 1)	1821	98
572	M69181	Homo sapiens	non-muscle myosin B	7350	99
573	M69181	Homo sapiens	non-muscle myosin B	7311	98
574	¥59678	Homo sapiens	Secreted protein 108-008-5-0- E6-PL.	772	100
575	AL365234	Arabidopsis thaliana	putative protein	788	40
576	AL365234	Arabidopsis thaliana	putative protein	788	40
577	X06745	Homo sapiens	DNA polymerase alpha-subunit (AA 1 - 1462)	7619	99
578	AB041642	Homo sapiens	PAR-6	1342	100
579	D86984	Homo sapiens	similar to yeast adenylate cyclase (S56776)	2446	100
580	AF165124	Homo sapiens	gamma-aminobutyric acid A receptor gamma 2	2499	99
581	W88812	Homo sapiens	Polypeptide fragment encoded by gene 58.	2339	99
582	U82319	Homo sapiens	novel ORF	342	100
583	P92219	Homo sapiens (human)	CR1 protein.	11425	99
584	AJ223948	Homo sapiens	RNA helicase	6608	99
585	Y08612	Homo sapiens	88kDa nuclear pore complex protein	3874	99
586	Y42384	Homo sapiens	Amino acid sequence of lv310 7.	1007	37
587	AF129756	Homo sapiens	BAT4	1873	98

	ACCESSION	SPECIES	DESCRIPTION	SMITH-	
ID NO:	NUMBER			WATERMAN	IDENTITY
588	AF131775	<u> </u>		SCORE	
589	AJ250865	Homo sapiens		1929	99
591	Z98885	Homo sapiens		2348	100
"	230055	Homo sapiens	(~Zombaomazzz	4167	100
i		]	containing 1 (similar to peregrin, BR140))		1
592	L76571	Homo sapiens			
593	AF091622	Homo sapiens	PHD finger protein 3	1,355	100
594	X56807	Homo sapiens	desmocollin type 2a	9054	100
595	AL137802	Homo sapiens	dJ798A10.1 (novel protein)	4443	100
596	AL022329	Homo	bK407F11.2 (adrenergic, beta,	3653	55
		sapiens	receptor kinase 2)	3653	100
597	AF226048	Homo sapiens	GL003	2009	99
598	AJ278112	Homo	putative cell cycle control	335	23
		sapiens)	protein	333	23
		>Y49635	-		
	ł	Y49635 21-			
	-	OCT-1999 15-		1	
		APR-1998			]
		Human sdp3.5			ļ
	ļ	protein.			
		[Homo	<b>†</b>		
599	Y59741	sapiens Homo sapiens			
333	133/41	Homo sapiens		1574	99
600	L36531	Homo sapiens	derived protein 18.		
601	Y38458	Homo sapiens	Human secreted protein	5386	99
		nomo saptems	encoded by gene No. 20.	895	100
602	AF218584	Homo sapiens		3265	100
603	Y13115	Homo sapiens	serine/threonine protein	5071	99
_		•	kinase	3071	1 33
604	AL132776	Homo sapiens		2413	99
605	AL034452	Homo sapiens	dJ682J15.1 (novel Collagen	1979	100
			triple helix repeat		1
606			containing protein)	1	
607	Y14494 AJ001981	Homo sapiens	aralari	3465	99
608	X86098	Homo sapiens	OXA1L	2603	100
000	X00096	sapiens	binds directly to adenovirus	3069	100
610	AF163572	Homo sapiens	type 5 ElA protein Forssman glycolipid	<u> </u>	
	1 2055/2	nomo saprens	synthetase	1865	99
611	AF161503	Homo sapiens	HSPC154		
612	L41834	Ensis minor	nuclear protein	1261	97
613	Y91954	Homo sapiens	Human cytoskeleton associated	345 3668	30
		oo sapiena	protein 9 (CVSKP-9)	3000	100
614	AL022327	_	protein 9 (CYSKP-9).	L	
615		Homo sapiens	protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027)	361	94
615 616	AL022327 X85786 Y08319	Homo sapiens	protein 9 (CYSKP-9).	361 3203	94
615 616 617	AL022327 X85786 Y08319 D12644	Homo sapiens Homo sapiens	protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor	361 3203 3487	94 100 99
615 616	AL022327 X85786 Y08319	Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus	protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2	361 3203 3487 3609	94 100 99
615 616 617	AL022327 X85786 Y08319 D12644	Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus	protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT	361 3203 3487 3609 5936	94 100 99 97 89
615 616 617 618	AL022327 X85786 Y08319 D12644 U28789	Homo sapiens Homo sapiens Homo sapiens Mus musculus	protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein	361 3203 3487 3609	94 100 99
615 616 617 618 619	AL022327 X85786 Y08319 D12644 U28789 Y35914	Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus Homo sapiens	protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted	361 3203 3487 3609 5936	94 100 99 97 89
615 616 617 618	AL022327 X85786 Y08319 D12644 U28789	Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus	protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO.	361 3203 3487 3609 5936	94 100 99 97 89
615 616 617 618 619	AL022327 X85786 Y08319 D12644 U28789 Y35914 AB046382	Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus Homo sapiens	protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO. 163. testis-abundant finger protein	361 3203 3487 3609 5936 1684	94 100 99 97 89
615 616 617 618 619	AL022327 X85786 Y08319 D12644 U28789 Y35914	Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus Homo sapiens	protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO. 163. testis-abundant finger protein precursor polypeptide (AA -23	361 3203 3487 3609 5936 1684	94 100 99 97 89
615 616 617 618 619 620	AL022327 X85786 Y08319 D12644 U28789 Y35914 AB046382 Y00062	Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus Homo sapiens  Mus musculus	protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO. 163. testis-abundant finger protein precursor polypeptide (AA -23 to 1120)	361 3203 3487 3609 5936 1684	94 100 99 97 89 99
615 616 617 618 619 620	AL022327 X85786 Y08319 D12644 U28789 Y35914 AB046382 Y00062	Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus Homo sapiens  Mus musculus Homo sapiens	protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO. 163. testis-abundant finger protein precursor polypeptide (AA -23 to 1120) HDCMD38P	361 3203 3487 3609 5936 1684	94 100 99 97 89 99
615 616 617 618 619 620 621	AL022327 X95786 Y08319 D12644 U28789 Y35914 AB046382 Y00062 AF068286 X98248	Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus Homo sapiens  Mus musculus Homo sapiens  Homo sapiens	protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO. 163. testis-abundant finger protein precursor polypeptide (AA -23 to 1120) HDCMD38P sortilin	361 3203 3487 3609 5936 1684	94 100 99 97 89 99 23
615 616 617 618 619 620	AL022327 X85786 Y08319 D12644 U28789 Y35914 AB046382 Y00062	Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus Homo sapiens  Mus musculus Homo sapiens	protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO. 163. testis-abundant finger protein precursor polypeptide (AA -23 to 1120) HDCMD38P sortilin 75 kDa subunit NADH	361 3203 3487 3609 5936 1684	94 100 99 97 89 99 23
615 616 617 618 619 620 621 622 623 624	AL022327 X85786 Y08319 D12644 U28789 Y35914 AB046382 Y00062 AF068286 X98248 X61100	Homo sapiens Homo sapiens Homo sapiens Mus musculus Homo sapiens Mus musculus Homo sapiens Homo sapiens Homo sapiens Homo sapiens	protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO. 163. testis-abundant finger protein precursor polypeptide (AA -23 to 1120) HDCMD38P sortilin 75 kDa subunit NADH dehydrogenase precursor	361 3203 3487 3609 5936 1684 199 3440 861 4436 3734	94 100 99 97 89 99 23 99
615 616 617 618 619 620 621	AL022327 X95786 Y08319 D12644 U28789 Y35914 AB046382 Y00062 AF068286 X98248	Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus Homo sapiens  Mus musculus Homo sapiens  Homo sapiens	protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO. 163. testis-abundant finger protein precursor polypeptide (AA -23 to 1120) HDCMD38P sortiIin 75 kDa subunit NADH dehydrogenase precursor 75 kda infertility-related	361 3203 3487 3609 5936 1684 199 3440	94 100 99 97 89 99 23 99
615 616 617 618 619 620 621 622 623 624	AL022327 X85786 Y08319 D12644 U28789 Y35914 AB046382 Y00062 AF068286 X98248 X61100 S58544	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Homo sapiens  Mus musculus Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO. 163. testis-abundant finger protein precursor polypeptide (AA -23 to 1120) HDCMD38P sortilin 75 kDa subunit NADH dehydrogenase precursor 75 kda infertility-related sperm protein	361 3203 3487 3609 5936 1684 199 3440 861 4436 3734	94 100 99 97 89 99 23 99 100 99 99
615 616 617 618 619 620 621 622 623 624	AL022327 X85786 Y08319 D12644 U28789 Y35914 AB046382 Y00062 AF068286 X98248 X61100 S58544 AF151027	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO. 163. testis-abundant finger protein precursor polypeptide (AA -23 to 1120) HDCMD38P sortilin 75 kDa subunit NADH dehydrogenase precursor 75 kda infertility-related sperm protein HSPC193	361 3203 3487 3609 5936 1684 199 3440 861 4436 3734 2125	94 100 99 97 89 99 23 99 100 99 99
615 616 617 618 619 620 621 622 623 624	AL022327 X85786 Y08319 D12644 U28789 Y35914 AB046382 Y00062 AF068286 X98248 X61100 S58544 AF151027 X14968	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO. 163. testis-abundant finger protein precursor polypeptide (AA -23 to 1120) HDCMD38P sortilin 75 kDa subunit NADH dehydrogenase precursor 75 kda infertility-related sperm protein	361 3203 3487 3609 5936 1684 199 3440 861 4436 3734 2125 582 2079	94 100 99 97 89 99 23 99 100 99 99

SEO	ACCESSION	SPECIES			
ID	NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	TORNOTON
NO:		ļ		SCORE	IDENTITY
629	Y50911	Homo sapiens	Human fetal brain cDNA clone	1694	100
		<u> </u>	vb7 1 derived protein		
630	AF098786	Homo	17 beta-hydroxysteroid	1754	100
631	AL034555	sapiens	dehydrogenase type VII		
631	AL034555	Homo	dJ134019.3 (zinc finger	4273	100
632	W74826	sapiens	protein 151 (pHZ-67))		
1 032	W14026	Homo sapiens		794	96
1			encoded by gene 98 clone	ł	!
633	AF288288	Homo sapiens	HPT protein	2236	-
634	AF041429	Homo sapiens		823	.100
635	X66357	Homo sapiens		1589	100
	1		kinase	1303	100
636	Y11284	Homo sapiens	AFX1	2571	98
637	AB004884	Homo sapiens	PKU-alpha	3718	99
638	AJ002303	Homo sapiens	synaptogyrin lc	1020	100
639	AJ002304	Homo sapiens	synaptogyrin 1b	1002	100
640	AJ002303	Homo sapiens		933	94
641	D87682	Homo sapiens	similar to a C.elegans	2676	100
	1		protein encoded in cosmid	1	1
642	141.4550		T26A5.		
643	M14660 X06661	Homo sapiens	ISG-K54	2473	99
644	AF119900		calbindin (AA 1-261)	1358	100
645	AB031048	Homo sapiens Drosophila	PRO2822	185	76
015	ADOSTOGO	melanogaster	microtubule associated- protein orbit	738	27
646	AF250842	Drosophila	multiple asters	834	
		melanogaster	"marcible ascers	834	29
647	X86691	Homo sapiens	Mi-2 protein	10110	99
648	U67934	Homo sapiens	44.9 kDa protein C18B11	827	96
		_	homolog	""	1 -0
649	AF236061	Oryctolagus	RING-finger binding protein	3930	91
		cuniculus	_ <del></del>		
650	AL034553	Homo sapiens	dJ914P20.2 (KIAA0784 protein	5708	100
			similar to Mus musculus		
	ľ		activity-dependent		
	ì		neuroprotective protein (Adnp))		
653	X14766	Homo sapiens	GABA-A receptor alpha 1	2388	99
			subunit	2308	99
654	AC004614	Homo sapiens	similar to f-spondin proteins	3026	99
			AB006086 (PID:g2529225)		
655	Y5790B	Homo sapiens	Human transmembrane protein	608	99
			HTMPN-32.		
656	Z34975	Homo sapiens	ldlCp	3733	100
658 659	AL050306	Homo sapiens	dJ475B7.2 (novel protein)	1942	99
653	W76734	Homo	Human mDia Rho targeting	781	34
660	AF202724	sapiens Homo sapiens	protein.		
661	Z21966		Sadl unc-84 domain protein 1	2172	100
662	AJ242954	Mus musculus	mPOU homeobox protein dysferlin	1529	100
663	AF182316	Homo sapiens	myoferlin	4752	59
665	AL161516	Arabidopsis	hypothetical protein	6232 209	99
		thaliana	mypositered protein	***	30
667	X59303	Homo sapiens	valy1-tRNA synthetase	3393	99
668	Y13355	Homo sapiens	Amino acid sequence of	3692	100
		•	protein PRO220.		~00
669	AB010692	Arabidopsis	contains similarity to endo-	611	52
}		thaliana	beta-N-acetylglucosaminidase		
			gene		
671	X56123	Mus musculus	talin	4474	76
672	AB039371	Homo sapiens	mitochondrial ABC transporter	2902	99
	3706060		3		i
673 674	AF269223	Homo sapiens	TCP11	806	42
675	AF229633 L14463	Mus musculus	groucho-related protein 4	4053	99
· / -	T7.4407	Rattus	'transducin	3619	92

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
676	AC005757	Homo sapiens	R32611 1	2779	100
677	861069	Homo sapiens	reverse transcriptase	252	65
077	381005	NOMO Saprens	homolog=pol (retroviral element)	232	65
678	AF271388	Homo sapiens	CMP-N-acetyIneuraminic acid synthase	2273	100
679	X79066	Homo sapiens	ERF-1	1783	100
680	AF118566	Mus musculus	hematopoietic zinc finger protein	769	50
681	Y51415	Homo sapiens	Human wild type pKe83 . protein.	2621	99
682	AL133545	Homo sapiens	bA386N14.1 (novel protein similar to a dual specificity phosphatase)	700	68
683	Y86214	Homo sapiens	Nuclear transport protein clone hfb341 protein sequence.	5888	99 .
684	Y94952	Homo sapiens	Human secreted protein clone fhl16_11 protein sequence SEO ID NO:110.	354	98
685	AL021878	Homo sapiens	dJ257120.4 (transcription factor 20 (AR1) (KIAA0292) (isoform 2))	154	67
686	AE000198	Escherichia coli	orf, hypothetical procein	628	100
687	M58378	Homo sapiens	synapsin I	3730	99
688	AF039697	Homo sapiens	antigen NY-CO-31	508	98
689	009355	Oryctolagus cuniculus	protein phosphatase 2A1 B gamma subunit	2356	99
690	AF155106	Homo sapiens	NY-REN-36 antigen	265	50
691	AC004774	Homo sapiens	Dlx-5	1542	100
692	X90530	Homo sapiens	ragB	1926	99
693	X90530	Homo sapiens	ragB	1405	99
694	X90530	Homo sapiens	ragB	1590	85
695	G01563	Homo sapiens	Human secreted protein, SEQ ID NO: 5644.	330	100
696	AC011810	Arabidopsis thaliana Rattus	Putative methionine aminopeptidase	669	52 98
698	AB037901	norvegicus Homo	Collybistin I gene amplified in squamous	2455	99
699	Y99401	sapiens Homo sapiens	cell carcinoma-1 Human PRO1327 (UNQ687) amino	1386	100
701	AF221712	Homo	acid sequence SEQ ID NO:218. Smad- and Olf-interacting	6705	100
702	X83573	sapiens Homo sapiens	zinc finger protein ARSE	3184	99
703	AJ243274	Homo sapiens	AP-2rep protein	2078	99
704	Y71262	Homo sapiens	Human chondromodulin-like protein, Zchm1.	1697	94
705	Y71262	Homo sapiens	Human chondromodulin-like protein, Zchml.	1736	99
706	Y41257	Homo sapiens	Amino acid sequence of long human FAIM.	1060	100
707	AL022237	Homo sapiens	bK1191B2.3 (PUTATIVE novel Acyl Transferase similar to C. elegans C50D2.7) (isoform 1))	2030	100
708	AJ006266	Homo sapiens	AND-1 protein	5942	100
709	G01571	Homo sapiens	Human secreted protein, SEQ ID NO: 5652.	777	99
710	Y08698	Homo sapiens	ranbp3	2849	98
711	Y68770	Homo sapiens	Amino acid sequence of a human phosphorylation effector PHSP-2.	754	99

No.	SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	identity
13					SCORE	
Dox helicases   Dox helicases   S38   48		•			1	
10	713	AC004531	HOMO Sapiens		2715	99
Associated protein tyrosine phosphatase 2   100	714	D89016	Homo sapiens		538	48
National   Note   National   Na	715	Y92175	Homo sapiens	associated protein tyrosine	734	98
	716	AL137013	Homo sapiens		862	100
P40254 25-   OCT-1984 09-   APR-1983     Human 1gD.     Homo   Sapiens   Integrin beta 1 subunit     Precursor   Precursor     Precursor   Precurs			Mus musculus	alpha synthase	1696	93
T20	718	Y96290	P40254 25- OCT-1984 09- APR-1983 Human IgD. [Homo	Human IGFAM-2 immunoglobulin.	2345	85
			Homo sapiens		4347	99
W41565   Homo   Sapiens   SW41564   W		.1				1
Sapiens   W41564 08-   OCT-1997 05-   APR-1995   Human   calpain.   Homo   sapiens   HSPC078   1097   98		1.				
724 AF187318   Homo sapiens   F-box protein Fbx2   1607   100     725   AC006708   Caenorhabdit   contains similarity to   saccharomyces cerevisiae preminna splicing protein PRP31   (GS:272876)     726   AC006708   Caenorhabdit   contains similarity to   988   46     727   AC024818   Caenorhabdit   contains similarity to   Saccharomyces cerevisiae preminna splicing protein PRP31   (GB:272876)     727   AC024818   Caenorhabdit   contains similarity to Pfam   family Pf00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3     728   AJ005897   Homo sapiens   Human secreted protein   908   97     729   Y45377   Homo sapiens   Human secreted protein   908   97     730   G03931   Homo sapiens   Human secreted protein, SEQ   578   100     731   AB012720   Oncorhynchus   GTP-binding protein   3865   76     732   W73404   Homo sapiens   Human secreted protein   encoded by Gene No. 8   8.     733   G02650   Homo sapiens   Human secreted protein   SEQ   97     734   AC024813   Caenorhabdit   is elegans   Y54F10AL, a   152   24     735   AL035461   Homo sapiens   dJ967W21.6 (novel CDP-alcohol   1562   98     736   U00033   Caenorhabdit   is elegans   similar to S. cerevisiae YJU2   605   41     737   AF079098   Homo   argimine-tRNA-protein   2733   99			>W41564 W41564 08- OCT-1997 05- APR-1996 Human calpain. [Homo			
AC006708   Caenorhabdit   Sontains similarity to   Saccharomyces cerevisiae premark   Splicing protein PRP31   (GB:272876)   Saccharomyces cerevisiae premark   Splicing protein PRP31   (GB:272876)   Saccharomyces cerevisiae premark   Splicing protein PRP31   (GB:272876)   Saccharomyces cerevisiae premark   Splicing protein PRP31   (GB:272876)   Saccharomyces cerevisiae premark   Splicing protein PRP31   (GB:272876)   Saccharomyces cerevisiae premark   Splicing protein PRP31   (GB:272876)   Saccharomyces cerevisiae premark   Splicing protein PRP31   (GB:272876)   Saccharomyces cerevisiae premark   Splicing protein PRP31   (GB:272876)   Saccharomyces cerevisiae premark   Splicing protein PRP31   (GB:272876)   Saccharomyces cerevisiae premark   Splicing protein PRP31   (GB:272876)   Saccharomyces cerevisiae premark   Splicing protein PRP31   (GB:272876)   Saccharomyces cerevisiae premark   Splicing protein PRP31   Splicing protein PRP31   Splicing protein   Splicing Pr		AF161341	Homo sapiens	HSPC078	1097	98
is elegans   Saccharomyces cerevisiae pre- mRNA splicing protein PRP31   (GB:272876)   Saccharomyces cerevisiae pre- mRNA splicing protein PRP31   (GB:272876)   Saccharomyces cerevisiae pre- mRNA splicing protein PRP31   (GB:272876)   Saccharomyces cerevisiae pre- mRNA splicing protein PRP31   (GB:272876)   Saccharomyces cerevisiae pre- mRNA splicing protein PRP31   (GB:272876)   Saccharomyces cerevisiae pre- mRNA splicing protein PRP31   (GB:272876)   Saccharomyces cerevisiae pre- mRNA splicing protein PRP31   (GB:272876)   Saccharomyces cerevisiae pre- mRNA splicing protein PRP31   (GB:272876)   Saccharomyces cerevisiae pre- mRNA splicing protein PRP31   (GB:272876)   Saccharomyces cerevisiae pre- mRNA splicing protein PRP31   (GB:272876)   Saccharomyces cerevisiae protein PR931   (GB:272876)   Saccharomyces cerevisiae protein PR931   (GB:272876)   Saccharomyces cerevisiae protein PR931   (GB:272876)   Saccharomyces cerevisiae pro					1607	100
Saccharomyces cerevisiae premark splicing protein PRP31 (GB:Z72876)   Saccharomyces cerevisiae premark splicing protein PRP31 (GB:Z72876)   Saccharomyces cerevisiae premark splicing protein PRP31 (GB:Z72876)   Saccharomyces cerevisiae premark splicing protein PRP31 (GB:Z72876)   Saccharomyces cerevisiae premark splicing protein family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3   Saccharomyces cerevisiae premark splicing protein gene protein pragment encoded from gene protein protein protein protein masou   Saccharomyces cerevisiae protein	725	AC006708		Saccharomyces cerevisiae pre- mRNA splicing protein PRP31	1143	46
is elegans family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3  728 AJ005897 Homo sapiens JM5 831 47  729 Y45377 Homo sapiens Human secreted protein fragment encoded from gene 27.  730 G03931 Homo sapiens Human secreted protein, SEQ 578 100 ID NO: 8012.  731 AB012720 Oncorhynchus GTF-binding protein 3865 76 masou 862 97 encoded by Gene No. 8.  732 W73404 Homo sapiens Human secreted protein 862 97 encoded by Gene No. 8.  733 G02650 Homo sapiens Human secreted protein, SEQ 644 97 ID NO: 6731.  734 AC024813 Caenorhabdit Hypothetical protein is elegans Y54F10AL.a  735 AL035461 Homo sapiens dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase family member protein)  736 U00033 Caenorhabdit similar to S. cerevisiae YJU2 605 41 is elegans protein arginine-tRNA-protein 2733 99			is elegans	Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB: Z72876)	988	46
Y45377				family PF00400 (WD domain, G-beta repeat), score=81.8,	950	44
fragment encoded from gene 27.  730 G03931 Homo sapiens Human secreted protein, SEQ 578 100 ID NO: 8012.  731 AB012720 Oncorhynchus GTF-binding protein 3865 76 masou 3865 76 masou 40 Homo sapiens Human secreted protein 862 97 encoded by Gene No. 8.  732 W73404 Homo sapiens Human secreted protein 862 97 encoded by Gene No. 8.  733 G02650 Homo sapiens Human secreted protein, SEQ 644 97 ID NO: 6731.  734 AC024813 Caenorhabdit Hypothetical protein 152 24 is elegans 754F10AL.a  735 AL035461 Homo sapiens dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase family member protein)  736 U00033 Caenorhabdit similar to S. cerevisiae YJU2 605 41 is elegans protein 2733 99					831	47
G03931	729	¥45377	Homo sapiens	fragment encoded from gene	908	97
masou   Human secreted protein   862   97			Homo sapiens	Human secreted protein, SEQ	578	100
encoded by Gene No. 8.			masou	GTP-binding protein	3865	76
ID NO: 6731.				encoded by Gene No. 8.	862	97
is elegans Y54F10AL.a  735 AL035461 Homo sapiens dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase family member protein)  736 U00033 Caenorhabdit similar to S. cerevisiae YJU2 605 41 is elegans protein  737 AF079098 Homo arginine-tRNA-protein 2733 99				ID NO: 6731.		
phosphatidyltransferase family member protein)  736 U00033 Caenorhabdit similar to S. cerevisiae YJU2 605 41     is elegans protein  737 AF079098 Homo arginine-tRNA-protein 2733 99			is elegans	Y54F10AL.a	152	24
is elegans protein 737 AF07909B Homo arginine-tRNA-protein 2733 99			_	phosphatidyltransferase family member protein)	1562	98
and and and and and and and and and and			is elegans	similar to S. cerevisiae YJU2 protein		
	737	AF07909B		arginine-tRNA-protein transferase 1-1p; ATE1-1p	2733	99

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
738	AJ131712	Homo sapiens	nucleolar RNA-helicase	2793	100
739	AJ133115	Homo sapiens		2054	99
740	X98258	Homo sapiens		953	100
741	X98258	Homo sapiens	M-phase phosphoprotein 9	564	74
742	U97191	Caenorhabdit	strong similarity to the YPT1	960	85
743		is elegans	sub-family of RAS proteins		
744	X76057	Homo sapiens	phosphomannose isomerase	2191	100
	G03209	Homo sapiens	Human secreted protein, SEQ ID NO: 7290.	496	98
745	X97064	Homo sapiens	Sec23 protein	4034	99
746	W93946	Homo sapiens	Human regulatory molecule HRM-2 protein.	994	100
747	Y73388	Homo sapiens	HTRM clone 3376404 protein sequence.	1565	99
748	M19529	Sus scrofa	follistatin A	1.55	
749	AJ249457	Trichomonas		1906	98
		vaginalis	Centrin, putative	183	28
750	AC004410	Homo sapiens	fos39554_1	2094	100
751	AF074968	Homo sapiens	p47ING3 protein	2167	100
752	AF252284	Homo sapiens	transcription specificity factor Spl	4005	100
753	AB049629	Homo sapiens	phospholysine phosphohistidine inorganic pyrophosphate phosphatase	1375	99
754	D79205	Homo sapiens	ribosomal protein L39	160	77
755	AB008430	Homo sapiens	COEP	142	29
758	L32162	Homo sapiens	transcription factor	574	80
759	AF037204	Homo sapiens	RING zinc finger protein	295	54
760	Y44250	Homo sapiens	Human cell signalling protein-13.	625	100
761	AF218586	Homo sapiens	Cide-b	1136	100
762	U38934	Gallus gallus	histone H2A	625	97
763	AF226053	Homo sapiens	HSKM-B	606	32
764	X13403	Homo sapiens	Oct-1 protein (AA 1 - 743)	3626	100
765	D87446	Homo sapiens	Similar to a C.elegans protein encoded in cosmid C27F2 (U40419)	568	38
766	AL023828	Caenorhabdit is elegans	Y17G7B.14	200	27
767	¥82777	Homo sapiens	Human chordin related protein (Clone dw665 4).	2551	99
768	X92475	Homo sapiens	ITBA1	1429	100
769	Y42752	Homo sapiens	Human calcium binding protein	1426	100
770	X51416	Homo sapiens	3 (CaBP-3). hormone receptor hERR1 (AA 1-	2641	97
771	AJ006591	Homo sapiens	521)	L	
772	A08695	Homo sapiens	cysteine-rich protein	1793	100
773	Z12173	Homo sapiens	rap2 N-acetylglucosamine-6-	935 2970	100
774	Y91950	Homo sapiens	sulphatase Human cytoskeleton associated	565	43
776	AL023799	Homo sapiens	protein 5 (CYSKP-5). dJ322P7.1 (zinc finger)	855	56
777	AL023799	Homo sapiens	dJ322P7.1 (zinc finger)	855	56
778	G018B0	Homo sapiens	Human secreted protein, SEQ ID NO: 5961.	849	98
779	AJ012590	Homo sapiens	glucose 1-dehydrogenase	4155	99
780	AL078582	Homo sapiens	dJ130E4.2 (KIAAD796)	1321	68
781	Z75955	Caenorhabdit is elegans	similar to mitochondrial	384	34
782	AL109965	Homo sapiens	carrier protein dJ1121G12.2 (SCAN domain- containing 1 protein)	900	100
783	AF061262	Mus musculus	semaF cytoplasmic domain associated protein 2	1316	83
784	G03873		absociation process s	1	

TABLE 2

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	
ID	NUMBER	SPECIES	DESCRIPTION	WATERMAN	* IDENTITY
NO:				SCORE	IDENTITI
	<del> </del>		ID NO: 7954.	- COME	<del> </del>
785	Y84441	Homo sapiens	Amino acid sequence of a	2074	100
1			human RNA-associated		
			protein.		1
786	Y00918	Homo sapiens	Human Rab protein, RABP-1,	1048	99
		<u> </u>	protein sequence.		
787 788	297029	Homo sapiens	ribonuclease HI large subunit	1548	99
789	AB035384 AF024631	Homo sapiens		962	94
790	AJ006710	Homo sapiens	ANG2	2644	100
130	A0008710	norvegicus	phosphatidylinositol 3-kinase	4508	97
792	V00638	bacteriophag	reading frame eal0	600	100
,,,,	100000	e lambda	reading frame eart	600	100
793	AF049103	Homo sapiens	Huntingtin interacting	819	100
		•	protein	1025	100
795	Z26317	Homo sapiens	desmoglein 2	4810	99
796	Y76884	Homo sapiens	Retinoblastoma binding	5080	99
			protein-7sequence.		
797	U15155	Gallus	trypsinogen	372	37
		gallus			
798	U97189	Caenorhabdit	strong similarity to thw	227	28
799	AF112201	is elegans	P13/P14 family of kinases		
800	AF234765	·Homo sapiens	neuronal protein NP25	1053	100
800	AF 234/65	norvegicus	serine-arginine-rich splicing	958	63
801	AF267852	Homo sapiens	regulatory protein SRRP86 placental protein 13-like	743	99
•••	111201032	nomo saprens	protein	743	99
802	AF208851	Homo sapiens	BM-009	766	80
803	281097	Caenorhabdit	Similarity to Human	152	27
		is elegans	retinoblastoma-binding		• ′
	}	]	protein RBAP46 vk662d12.5		
		İ	comes from this gene		
804	G02113	Homo sapiens	Human secreted protein, SEQ	496	98
805			ID NO: 6194.		
806	AL121673 AC013483	Homo sapiens	bA305P22.1 (novel protein)	1160	100
806	AC013483	Arabidopsis thaliana	putative GTPase activator	264	30
807	AC013483	Arabidopsis	protein putative GTPase activator	264	
•••	110013103	thaliana	protein	204	3C
808	AB013885	Homo sapiens	beta-ureidopropionase	1494	100
809	AF078842	Homo sapiens	HOTTL protein	1581	99
810	AF161421	Homo sapiens	HSPC303	2134	96
811	AF261689	Homo sapiens	DNA polymerase epsilon p17	734	100
			subunit	1	
812	Z74029	Caenorhabdit	Similarity to C.elegans	610	71
		is elegans	alcohol dehydrogenase comes		
813	273497	Homo sapiens	from this gene cU240C2.2 (Core histone		
813	2/349/	nomo sapiens	H2A/H2B/H3/H4)	324	100
814	W87689	Homo	Human HTXFT19 polypeptide.	7.004	
		sapiens	ndman HIXFII3 polypeptide.	1484	99
815	X16282	Homo	zinc finger protein (217 AA)	1109	99
		sapiens	(1 is 2nd base in codon)		
816	Z92539	Mycobacteriu	pth	300	36
		m ·			=
		tuberculosis			j
818	AB030483	Mus musculus	В9	197	27
819	ለቤ117555	Homo sapiens	hypothetical protein	321	94
820	AC005328	Homo sapiens	R26660_2, partial CDS	865	97
821	G03951	Homo sapiens	Human secreted protein, SEQ	700	99
<del>.,,</del> -	T 74000		ID NO: 8032.		
822	L34807	Musca	transposase	174	20
823	G02928	domestica	YI		
	302720	Homo sapiens	Human secreted protein, SEQ ID NO: 7009.	558	78
824	Z99531	Schizosaccha	caffeine-induced death	104	29
		- Jan Bosacciia	Carrethe-Induced death	184	<b>4</b> 9

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
		romyces pombe	protein 1		<del>                                     </del>
825	AJ006692	Homo sapiens	ultra high sulfer keratin		
826	U23037	Oryctolagus	eIF-2Bepsilon	693	68
		cuniculus	1	3406	90
827	G03412	Homo sapiens	ID NO: 7493.	464	100
828	Y30827	Homo sapiens	Human secreted protein encoded from gene 17.	113	44
829	Y32199	Homo sapiens	Human receptor molecule (REC) encoded by Incyte clone 2022379.	1012	100
830	W78279	Homo sapiens	Fragment of human secreted protein encoded by gene 33.	1264	99
832	AB011542	Homo sapiens	MEGF9	2097	
833	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	2097	70
834	AF119664	Homo sapiens	transcriptional regulator	1574	100
835	AF119664	Homo sapiens	transcriptional regulator	1144	89
836	AF119664	Homo sapiens	transcriptional regulator	1448	94
837	X12517	Homo sapiens	protein HCNGP C protein (AA 1-159)	1	
838	U32865	Drosophila	linotte protein	918	100
839	AF067730	melanogaster		164	24
840	U27831	Homo sapiens	TLS-associated protein TASR-2	631	56
841	AF286366	Homo sapiens	striatum-enriched phosphatase	2840	98
842	G02309	Homo sapiens	CamKI-like protein kinase	1796	100
843			Human secreted protein, SEQ ID NO: 6390.	278	98
844	AE003615	Drosophila melanogaster	ade3 gene product	113	48
	G01350	Homo sapiens	Human secreted protein, SEQ ID NO: 5431.	629	100
845	U27838	Mus musculus	glycosyl-phosphatidyl- inositol-anchored protein homolog	3305	96
847	Y87788	Homo sapiens	Human RBP-26 protein.	2026	100
848	AF164794	Homo sapiens	Diff33 protein homolog	2398	100
849	U41315	Homo sapiens	ZNF127-Xp	2458	93
850	AF192784	Homo sapiens	makorin 1	2062	97
851	Y58628	Homo sapiens	Protein regulating gene expression PRGB-21.	1548	100
852	Z22968	Homo sapiens	M130 antigen	6205	100
853	222971	Homo sapiens	M130 antigen extracellular variant	6380	100
854	G03362	Homo sapiens	Human secreted protein, SEQ ID NO: 7443.	330	96
855	G03362	Homo sapiens	Human secreted protein, SEQ ID NO: 7443.	203	100
856	AF285118	Homo sapiens	CGI-203	452	100
857	AC006069	Arabidopsis	putative cleavage and	1383	55
		thaliana	polyadenylation specifity factor	1363	55
358	AL021546	Homo sapiens	Cytochrome C Oxidase Polypeptide VIa-liver precursor (EC 1.9.3.1)	593	100
359	L02956	Xenopus laevis	ribonucleoprotein	1664	85
360	AF201947		MEK binding partner 1	616	100
161	L31783		uridine kinase	1266	92
362	AF161472		HSPC123	602	73
363	Z49068		mitochondrial carrier protein	370	43
64	AF154108		tumor necrosis factor type 1	3559	99

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	IDENTIT
	<del></del>	-	receptor associated protein	SCORE	
865	AE001530	Helicobacter	putative	230	32
		pylori J99	<u></u>	230	32
866	X57807	Homo sapiens	chain	699	91
867	AL031673	Homo sapiens	dJ694B14.1 (PUTATIVE novel KRAB box protein with 18 C2H2 type Zinc finger domains)	4066	99
868	Y11652	Homo sapiens	phosphate cyclase	238	
869	AF192968	Homo sapiens	high-glucose-regulated	3041	1.00 99
870	AB020648	ļ.,	protein 8		1
871	AL031427	Homo sapiens		3237	99
872	AF151534			1608	100
873	AL021331	Homo sapiens	1	1866	100
		Homo sapiens	elegans UNC-93 (protein 1, C46F11.1) LIKE protein)	1129	100
874	X14608	Homo sapiens		3579	100
875	AL117334	Homo sapiens	dJ687F11.1 (novel protein (part of translation of cDNA	306	100
876	X79489	Combination	DKFZp434N061, Em:AL110249))		1.
		Saccharomyce s cerevisiae		446	35
877	Y53001	Homo sapiens	Human secreted protein clone dn834_1 protein sequence SEQ ID NO:8.	811	100
878	AF281064	Homo sapiens	CHMP1.5	957	100
879	X79417	Sus scrofa	40S ribosomal protein S12	687	100
880	AF001317	Saccharomyce s cerevisiae	Soilp	478	28
881	Y87275	Homo sapiens	Human signal peptide containing protein HSPP-52 SEQ ID NO:52	2547	100
882	M14036	Homo sapiens	C1-inhibitor	598	77
883	AB041261	Homo sapiens	calcium-independent phospholipase A2	2903	100
884	AF020313	Mus musculus	proline-rich protein 48	999	84
885	Y10936	Homo sapiens	hypothetical protein	1104	99
886	AF073997	Mus musculus	myotubularin related protein	B66	36
887	Y57893	Homo sapiens	Human transmembrane protein HTMPN-17.	1099	94
888	AL117635	Homo sapiens	hypothetical protein	929	99
889	AF210317	Homo sapiens	facilitative glucose transporter family member GLUT9	2046	99
890	Y36031	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 416.	583 .	100
391	¥36031	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 416.	192	57
392	AF237631	Homo sapiens	ubiquitous tropomodulin U- Tmod	1798	100
393	AF090929	Homo sapiens	PR00477p	653	99
194	AL031228	Homo sapiens	dJ1033B10.2 (WD40 protein BING4 (similar to S. cerevisiae YER082C, M. sexta MNG10 and C. elegans F28D1.1)	3196	100
95	AL031228	Homo sapiens	dJ1033B10.2 (WD40 protein BING4 (similar to S. cerevisiae YER082C, M. sexta	2825	96
ł	į.	Ī		. 1	
96	AF171102	Homo sapiens	MNG10 and C. elegans F28D1.1) retinal degeneration B beta	1302	95

No.   Second   Seco	SEQ	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-	*
100	NO:				WATERMAN SCORE	IDENTITY
390			Homo sapiens	DEAD Box Protein 5		100
900   297164   Homo saplens   KKEP   1902			Homo sapiens	EKE2	624	_1
901 A745587 Homo sapiens Kruppel-type zinc finger 1942 100 902 AF091034 Homo sapiens GTT-binding protein RAB22A 1011 100 802 AF0953 Homo sapiens GTT-binding protein RAB22A 1011 100 100 100 100 100 100 100 100 1	900	Z97184	Homo sapiens	HKE2	409	
100   100	901	AJ245587	Homo sapiens	Kruppel-type zinc finger		
100   100	902	AF091034	Homo sapiens	GTP-binding protein RAB22A	1011	,
104   104733   1000 sapiens   1000	903	R95953				
1904   1973   1900   1905					7.2.7	30
MESONSAI   DECOSOPILE   CG10984 gene product   Mesons	904	L04733	Homo sapiens	<u> </u>	1936	1 77
M55542   Homo sapiens   guanylate binding protein   2993   98	905	AE003540				1
M55542   Homo sapiens   Guanylate binding protein   2993   98   1907   M55542   Homo sapiens   Guanylate binding protein   2901   96   1907   M55542   Homo sapiens   Guanylate binding protein   2901   96   1908   M84085   Homo sapiens   Human membrane fusion protein   1889   100   100   MDProl.   This intracellular domain   647   100   10				Jene promoc	****	33
100   100	906	M55542		quanylate hinding protein	2003	100
907   M55542   Homo sapiens   Guanylate binding protein   2901   96   1906   1907   1908   1908   1908   1909				, , , , , , , , , , , , , , , , , , , ,	2333	36
Section   Sect	907	M55542	Homo sapiens		2001	<del>                                     </del>
100   100		1	nomo bapacino	isoform T	2901	1 96
WDProl.   WDPr	908	W84085	Homo caniene		1.000	<u> </u>
AF168676	,,,	101003	I IICANO BADIENS		1889	100
Sapiens   Interacting protein   100	909	AF160676	Uomo			
100   AB029150   Homo saplens   Ho	702	Ar 1000 / 0			647	100
HFBIOLL   Homo sapiens   Human secreted protein, SEQ   100	B10	32020150				
	310	A5029130	nomo sapiens		2196	100
10   10   10   10   10   10   10   10	011	C02021	172			
10   10   10   10   10   10   10   10	311	G02871	Homo sapiens		521	100
10   10   10   10   10   10   10   10	010	002160				
AJ243721   Homo   Sapiens   Sapien	912	G03162	Homo sapiens	Human secreted protein, SEQ	387	87
Sapiens	613	-				L
NF92508 13-   APR-2000 06-   OCT-1938   Human OXRE-5.   Home sapiens	913	AJ 243 /21			1710	100
Y92508 13				4-reductase	1	
APR-2000 06-OCT-1998				1	}	l
OCT-1998   Human OXRE   5. [Homo saplens   S. [Homo saplens   Method: conceptual translation supplied by authors   S. [Homo saplens   Method: conceptual translation supplied by authors   S. [Homo saplens   A human progesterone receptor complex p23-like protein.   S. [Homo saplens   A human progesterone receptor complex p23-like protein.   S. [Homo saplens   A human progesterone receptor complex p23-like protein.   S. [Homo saplens   A human progesterone receptor complex p23-like protein.   S. [Homo saplens   A human progesterone receptor complex p23-like protein.   S. [Homo saplens   A human progesterone receptor complex p23-like protein.   S. [Homo saplens   A human progesterone receptor receptor complex p23-like protein.   S. [Homo saplens   A human progesterone receptor receptor complex p24-like protein.   S. [Homo saplens   A human progesterone receptor receptor complex p24-like protein.   S. [Homo saplens   A human progesterone receptor peacetone protein   S. [Homo saplens   A human progesterone receptor protein   S. [Homo saplens   A human progesterone receptor protein   A human progesterone receptor protein   A human secretor protein   A human progesterone receptor protein   A human secretor protein   A human secretor protein   A human secretor protein   A human secretor protein   A human secretor protein   A human secretor protein   A human secretor protein   A human secretor protein   A human secretor protein   A human secretor protein   A human secretor protein   A human secretor protein   A human secretor protein   A human secretor protein   A human secretor   A human secretor protein   A human secretor   A human secretor   A human secretor   A human secretor   A human secretor   A human secretor   A human secretor   A human secretor   A human secretor   A human secretor   A human secretor   A human secretor   A human   A human   A human   A human   A human   A human   A human   A human   A human   A human   A human   A human   A human   A human   A human   A human   A human   A human   A human   A						
Humar OXRE   5. [Homo sapiens				1	<b>!</b>	
1				1	ł	i
Sapiens						
				· ·		
is elegans	014	77247.00	, -			
translation supplied by authors   A human progesterone receptor   843   99	714	024189			244	41
			is elegans			ł
		1	ł		1 .	
Complex p23-like protein.   Substitute   Complex p23-like protein.   Substitute   Complex p23-like protein.   Substitute   Complex p23-like protein.   Substitute   Complex p23-like protein.   Substitute   Complex p23-like protein.   Substitute   Complex p23-like protein.   Substitute   Complex p23-like protein.   Substitute   Complex p23-like protein.   Substitute   Complex p23-like protein.   Substitute   Complex p23-like protein.   Substitute   Complex p23-like protein.   Substitute   Complex p23-like protein.   Substitute   Complex p23-like protein.   Substitute   Complex p23-like protein.   Substitute   Complex p23-like p24-like p24-like p24-like p25-like p25-like p25-like p26-like	915	V02597	Yana and			
### AE000984   Archaeoglobu s fulgidus   Archaeoglobu s fulgidus   Archaeoglobu s fulgidus   Archaeoglobu s fulgidus   Archaeoglobu s fulgidus   Archaeoglobu s fulgidus   Archaeoglobu s fulgidus   Archaeoglobu s cricetus   DHFR-coamplified protein   163   30	J_J	102591	nomo sapiens		843	99
S fulgidus   Cricetus   Cricetus   Cricetus   Cricetus   Cricetus   Cricetus   Cricetus   Caenorhabdit   is elegans   Caenorhabdit   is elegans   Cricetus   Caenorhabdit   is elegans   Cricetus   Caenorhabdit   is elegans   Cricetus   Caenorhabdit   is elegans   Cricetus   Caenorhabdit   is elegans   Cricetus   Caenorhabdit   is elegans   Cricetus   Caenorhabdit   Caenorhabdit   Cricetus   Cricetus   Cricetus   Caenorhabdit   Cricetus	015	75000004	America and about			
	313	AEUUU984			171	26
M23159   Cricetus			s ruigiaus		ĺ	
Cricetus   Caenorhabdit   putative   1232   41	010	W22150	G-1			
12018   Caenorhabdit   is elegans   1232   41	210	453123	· ·	Dark-coamplified protein	163	30
is elegans    1232   31	010					
AF102177	コエラ	PT5018		putative	1232	41
AL096712   Homo sapiens   dJ744124.2 (similar to a novel human gene mapping to Activator)   Activator)	000	200				
novel human gene mapping to Activator   Activator			Homo sapiens			_ •
Activator   Acti	921	AL096712	Homo sapiens	dJ744I24.2 (similar to a	1017	78
Activator   Acti				novel human gene mapping to		
thaliana  AL161495 Arabidopsis putative WD-repeat protein  Caenorhabdit similar to schizosaccharomyces pombe  Els X71978 Mus musculus Fif 1503 95  Els M92288 Drosophila melanogaster  Els Y27575 Homo sapiens Human secreted protein encoded by gene No. 9.  Els Y22499 Homo sapiens Human secreted protein sequence clone mh703 1.  AJ224326 Homo sapiens ribulose-5-phosphate-epimerase			<u> </u>			
Thaliana	922	AL161495	Arabidopsis	putative WD-repeat protein	866	42
thaliana    124			thaliana	- * * * * * * * * * * * * * * * * * * *		
thaliana   Caenorhabdit   Similar to   Schizosaccharomyces pombe   Similar to   Schizosaccharomyces pombe   Similar to   Schizosaccharomyces pombe   Similar to   Schizosaccharomyces pombe   Similar to   Schizosaccharomyces pombe   Similar to   Schizosaccharomyces pombe   Similar to   Schizosaccharomyces pombe   Similar to   Schizosaccharomyces pombe   Similar to   Schizosaccharomyces pombe   Similar to   Schizosaccharomyces pombe   Similar to   Similar t	923	AL161495	Arabidopsis	putative WD-repeat protein	442	36
197001   Caenorhabdit   similar to   Schizosaccharomyces pombe   Schizosaccharomyces			thaliana			
1s elegans   Schizosaccharomyces pombe   1503   95	924	U97001		similar to	605	51
225   X71978   Mus musculus   Fif   1503   95     226						
M92288   Drosophila   melanogaster	925	X71978			1503	95
The content of the	926					
Y27575				man abacetti	-50	-J-L
encoded by gene No. 9.   100	927	Y27575		Human cograted assets	2202	300
28 Y22499 Homo sapiens Human secreted protein 2249 100 sequence clone mh703_1.  30 AJ224326 Homo sapiens ribulose-5-phosphate- 912 100 epimerase		**1313	TOUR Papteus		1392	700
sequence clone mh703_1.  sequence clone mh703_1.  AJ224326 Homo sapiens ribulose-5-phosphate- 912 100 epimerase	928	V22490	Homo ganier-		-2240	300
30 AJ224326 Homo sapiens ribulose-5-phosphate- 912 100 epimerase		166477	o.c sapiens		2249	700
epimerase	930	A.T224226	Homo essi			
		-WEZ4320	nomo sapiens		313	T00
caenornapdit   coded for by C. elegans cDNA   660   55		1139001	Chanastata			
	,,, t	020331	caenornabdit	coded for by C. elegans cDNA	660 .	55

SEQ ID NO:	ACCESSION NUMBER		DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
932	AL080065	is elegans	cm21c7		
933	G01884	Homo sapiens		210	25
934		Homo sapiens	ID NO: 5965.	767	98
	AJ276485	Homo sapiens	protein	1200	100
935	AL035681	Homo sapiens	similar to drosophila transcriptional repressor	1142	80
936	AB026808	Mus musculus	synaptotagmin XI	2142	95
937	AB015345	Homo sapiens	HRIHFB2216	2601	99
938	X65724	Homo sapiens		498	100
939	W89024	Homo sapiens	by gene 156.	1487	100
940	G04047	Homo sapiens	ID NO: 8128.	117	100
941	AF094583	Homo sapiens	putative HIV-1 infection related protein	452	100
942	AC024200	Caenorhabdit is elegans	contains similarity to several zinc finger proteins but not to the zinc finger domains	350	69
943	AF129756	Homo sapiens	G5c	273	100
944	M23765	Rattus norvegicus	alpha-tropomyosin	133	96
945	AC009917	Arabidopsis thaliana	Contains similarity to	583	47
946	AF223468	Homo sapiens	AD021 protein	551	44
947	AF055473	Homo sapiens	GAGE-8	273	51
948	X75756	Homo sapiens	protein kinase C mu	2019	68
949	AF143956	Mus musculus	coronin-2	2300	93
950	Y36729	Homo sapiens	Human PG1 protein sequence.	1861	99
951	W49041	Homo sapiens	Human low density lipoprotein binding protein LBP-2.	282	67
952	AB016881	Arabidopsis thaliana	gene_id:MXC17.7~	203	46
953	Y01785	Homo sapiens	Human ubiquitin-conjugating enzyme >Y25341 Y25341 01-JUL- 1999 12-AUG-1998 Human NCE-2 protein.	365	100
954	AF145615	Drosophila melanogaster	BcDNA.GH03377	823	46
955	U09410	Homo sapiens	zinc finger protein ZNF131	2483	99
956 957	U09410	Homo sapiens	zinc finger protein ZNF131	1853	99 .
957	AF195623	Homo sapiens	cholinephosphotransferase 1 alpha	2126	99
250	X94917	Drosophila melanogaster	head-elevated expression in 0.9 kb	155	32
959	U54807	Rattus norvegicus	GTP-binding protein	1167	97
960	AF058807	Bos taurus	GTP-binding protein rah	606	97
961	G03244	Homo sapiens	Human secreted protein, SEQ ID NO: 7325.	471	100
962	AF078850	Homo sapiens	steroid dehydrogenase homolog	583	40
963	AP001754	Homo sapiens	transient receptor potential- related channel 7, a novel putative Ca2+ channel protein	317	30
964	AL035419	Homo sapiens	dJ1100H13.1 (putative novel protein)	1129	100
965	X61381	Rattus rattus	interferon-induced protein	202	46
966	D38169	Homo sapiens	inositol 1,4,5-trisphosphate 3-kinase isoenzyme	3278	100
967	AL031432	Homo sapiens	dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1)	893	100
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SEQ	ACCESSION	SPECIES			
ID NO:	NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
968	U79275	Homo sapiens	unknown	611	100
969	AJ011306	Ното	guanine nucleotide exchange	2752	99
970	AF281134	sapiens	factor (long isoform)		
971	U53336	Homo sapiens		1186	100
		Caenorhabdit is elegans	region to myosin heavy chain	536	23
972	AC018749	Leishmania major	L8840.12	589	53
973	AF188504	Mus musculus	LNV	544	85
974	U25801	Homo sapiens		852	98
975	AF049523	Homo sapiens	huntingtin-interacting protein HYPA/FBP11	1390	97
976	AF161530	Homo sapiens	HSPC182	1040	100
977	G04020	Homo sapiens	Human secreted protein, SEQ ID NO: 8101.	626	100
978	AF164797	Homo sapiens	ribosomal protein L17 isolog	908	
979	U94991	Xenopus	transcription factor XLMO1	795	100 97
980	\$73775	laevis			
981	Y94888	Homo sapiens	calmitine; calsequestrine	2029	100
		sapiens	Human protein clone HP01462.	2501	100
982	AJ243191	Homo sapiens	heat shock protein	827	96
983	X65020	Bos taurus	PSST subunit of the NADH: ubiquinone oxidoreductase complex	964	85
984	AJ249207	Rhodococcus sp. AD45	putative racemase	351	43
985	Z30093	Homo sapiens	basic transcription factor 2, 35 kD subunit	1576	99
986	AB030835	Homo sapiens	contains two glutamine rich domains, three zinc-finger domains, and matrin 3 homologous domain 3 (MH3)	4697	99
987	AF227258	Bos taurus	RPGR-interacting protein-1	1262	
988	AL022238	Homo sapiens	dJ1042K10.2 (supported by GENSCAN, FGENES and GENEWISE)	4048	38 99
989	AL022238	Homo sapiens	dJ1042K10.2 (supported by	2321	99
990	AF161426	Homo sapiens	GENSCAN, FGENES and GENEWISE) HSPC308	<u> </u>	
991	AF161426	Homo sapiens	HSPC308	448	92
992	AF161426	Homo sapiens	HSPC308	453	92 92
993	AL023859	Schizosaccha romyces pombe	trna-splicing endonuclease subunit	172	42
994	AL049631	Homo sapiens	dJ513M9.1 (novel Homeobox domain protein)	241	47
995	AC005253	Homo sapiens	R26445 1	902	100
996	AF265206	Homo sapiens	MOG1 isoform A .	974	100
997	AJ248285	Pyrococcus abyssi	sarcosine oxidase, subunit beta (soxB)	195	28
998	AE003641	Drosophila melanogaster	BG:DS00941.3 gene product	218	58
999	W69343	Homo sapiens	Secreted protein of clone CR930 1.	1340	98
1000	AY007135	Homo sapiens	similar to bovine ADP/ATP translocase T1 mRNA with GenBank Accession Number M24102.1	1543	100
1001	Y73381	Homo sapiens	HTRM clone 1877278 protein sequence.	1668	100
1002	AF208844	Homo sapiens	BM-002	428	100
1003	AE004944	Pseudomonas aeruginosa	hypothetical protein	134	35
L004	AL031431 S45367	Homo sapiens Canis	dJ462023.2 (novel protein) centractin	2058	100

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	<del>-</del>
ID NO:	NUMBER		2200111101	WATERMAN SCORE	IDENTITY
1006	\$45367	Canis familiaris	centractin	1315	98
1007	AB022158	Mus musculus	chaperonin containing TCP-1 epsilon subunit	2649	96
1008	Y76332	Homo sapiens	protein encoded by gene 38.	1282	97
1009	AB011414	Homo sapiens	Kruppel-type zinc finger protein	1671	58
1010	Z68218	Caenorhabdit is elegans		269	67
1011	AB011414	Homo sapiens	protein	1671	58
1012	Z14000	Homo sapiens	RING1	2017	100
1013	G02841	Homo sapiens	ID NO: 6922.	332	93
1014	AF145659	Drosophila melanogaster	BcDNA.GH10333	1244	52
1015	Y02860	Homo sapiens	protein encoded by gene 65.	664	67
1016	Y02591	Homo sapiens	A human progesterone receptor complex p23-like protein.	772	97
1017	Y99448	Homo sapiens	Human PRO1759 (UNQ832) amino acid sequence SEQ ID NO:374.	2323	100
1018	X67250	Rattus norvegicus	n-chimaerin	1710	97
1019	AF183417	Homo sapiens	microtubule-associated proteins 1A/1B light chain 3	631	100
1020	AF164795	Homo sapiens	sex-regulated protein janus-a	674	100
1021	AF190625	Coturnix coturnix	qdgl-1	638	96
1022	AL133363	Arabidopsis thaliana	putative protein	155	37
1023	AB034912	Homo sapiens	WD-repeat like sequence	2483	100
1024	AY007091	Homo sapiens	similar to Homo sapiens mammalian inositol hexakisphosphate kinase 2 (IP6K2) mRNA with Ge	2243	100
1025	X69910	Homo sapiens	P63 protein	2958	99
1026	U80736	Homo sapiens	CAGF9	1657	100
1027	AB029333	Halocynthia roretzi	HrPET-1	1048	54
1028	AB032931	Homo sapiens	ubiquitin-conjugating enzyme isolog	1045	100
1029	G01797	Homo sapiens	Human secreted protein, SEQ ID NO: 5878.	749	98
1030	G01797	Homo sapiens	Human secreted protein, SEQ ID NO: 5878.	749	98
1031	AF193795 AJ222968	Homo sapiens	vacuolar sorting protein VPS29/PEP11	960	100
1032	281317	Mus musculus	L-periaxin	120	30
7033	5049T/	Schizosaccha romyces pombe	DNA2-NAM7 helicase family protein	685	31
1034	¥41519	Homo sapiens	Fragment of human secreted protein encoded by gene 75.	1321	99
1035	AJ276004	Mus musculus	Paxneb protein	1709	77
1036	AF025459	Caenorhabdit is elegans	H14A12.3 gene product	190	30
1037	U37251	Homo sapiens	Description: KRAB zinc finger protein; this is a splicing supplied by author	196	43
103B	W74580	Homo sapiens	Human membrane protein BA0306.	1921	97
1039	U88173	Caenorhabdit is elegans	weak similarity to Arabidopsis thaliana ubiquitin-like protein 8	331	80

TABLE 2

SEO	ACCESSION	SPECIES	DESCRIPTION		
ID NO:	NUMBER			SMITH- WATERMAN SCORE	IDENTITY
1040	AF290204	Homo sapiens	DOK1	1637	99
1041	¥96730	Homo sapiens	PRO539, a Costal-2 homologue.	162	22
1042	AF140683	Mus musculus	To the Bull and Tubb	2397	98
1043	AF151023	Homo sapiens	La caracteristic de la car	1104	100
1044	AF181631	Drosophila melanogaster		204	37
1045	¥77985	Homo sapiens	sequence.	1940	100
1046	AJ243972	Homo sapiens		1317	100
1047	AB035863	Homo sapiens	synthetase beta subunit precursor	2324	99
1048	AL034550	Homo sapiens	dJ1184F4.2 (novel protein similar to nucleolar protein 4 (NOLA) (NOLP))	981	92
1049	AF163825	Homo sapiens	pre-B lymphocyte protein 3	634	100
1050	AF201949	Homo sapiens	60S ribosomal protein L30 isolog	868	100
1051	AF190624	Mus musculus	mdgl-1	236	85
1052	AE003529	Drosophila melanogaster	CG6151 gene product	160	44
1053	G01191	Homo sapiens	Human secreted protein, SEQ ID NO: 5272.	646	98
1054	AL162756	Neisseria meningitidis	Glu-tRNA(Gln) amidotransferase subunit A	682	44
1055	AF181856	Rattus norvegicus	tRNA selenocysteine associated protein	1525	99
1056	U89649	Chlamydomona s reinhardtii	Mr19,000 outer arm dynein light chain	244	34
1057	AF159141	Homo sapiens	breast cancer metastasis- suppressor 1	663	53
1058	AF230929	Homo sapiens	keratinocyte annexin-like protein pemphaxin	1710	99
1059	AJ270952	Homo sapiens	putative membrane protein	1363	100
1050	AF224263	Heterodontus francisci	HoxD8	742	83
1061	X63417	Homo sapiens	IRLB	1037	100
1062	AL079345	Streptomyces coelicolor A3(2)	hypothetical protein	143	27
1063	Y71112	Homo sapiens	Human Hydrolase protein-10 (HYDRL-10).	2547	100
1064	AF363614	Homo sapiens	acetyl-CoA synthetase	3493	99 .
1065	Y13356	Homo sapiens	Amino acid sequence of protein PRO221.	1363	100
1066	AC006153	Homo sapiens	similar to Aquifex aeolicus GTP-binding protein; similar to AE000771 (PID:g2984292)	662	98
1067	Y18930	Sulfolobus solfataricus	hypothetical protein	162	29
1068	R65969	Homo sapiens T98G	Glioblastoma-derived polypeptide.	887	100
1069	Y07964	Homo sapiens	Human secreted protein fragment	863	96
1070	AF177476	Rattus norvegicus	CDK5 activator-binding protein	1995	86
1071	AF245505	Homo sapiens	adlican	3109	99
1072	U92794	Mus musculus	alpha glucosidase II, beta subunit	147	36
1073	G03889	Homo sapiens	Human secreted protein, SEQ ID NO: 7970.	698	98
1074	U15779	Homo sapiens	p70	380	28
1075	Y13392	Homo sapiens	Amino acid sequence of	1271	91

TABLE 2

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	윰
ID NO:	NUMBER			WATERMAN	IDENTITY
NO:			770000	SCORE	ļ
1076	AF161457	Homo sapiens	protein PRO328.	ļ <u>.</u>	I
1077	Y79509	Homo sapiens		2151	100
10,,	1/3309	Homo saprens	protein CRBAP-5.	2151	98
1078	AF223466	Homo sapiens	1	831	66
1079	AL132965	Arabidopsis	putative WD-40 repeat-protein	286	29
		thaliana			1
1080	AB024937	Homo sapiens		1284	100
1081	Y14768	Homo sapiens		579	100
	1		protein		1
1082	AF016416	Caenorhabdit	F29A7.4 gene product	141	31
1083	L13291	is elegans Homo sapiens	ADD I beautiful by		
1084	AB041541	Mus musculus		802 151	45
1085	G01922	Homo sapiens	Human secreted protein, SEQ	202	97
	002322	TOMO Bapiens	ID NO: 6003.	202	9'
1086	AB030814	Homo sapiens	H-REV107 protein homolog	833	100
1087	AF151638	Homo sapiens	phosphatidylcholine transfer	1142	100
			protein	1176	100
1088	Y84432	Homo sapiens	Amino acid sequence of a	2783	100
		1	human RNA-associated	] -	
		<u> </u>	protein.		
1089	Y94867	Ното	Human protein clone HP10563.	613	100
1000		sapiens			
1090	AK023982	Homo sapiens	unnamed protein product	130	49
1091	AB041586	Mus musculus	unnamed protein product	1103	81
1092	Y71277 U34973	Homo sapiens	Human Zlipo3 protein.	606	100
1093	0349/3	Mus musculus	protein tyrosine phosphatase-	1131	95
1094	Y66677	Homo	Membrane-bound protein	522	
	1000//	sapiens	PRO828.	522	56
1095	Y87276	Homo sapiens	Human signal peptide	1029	99
			containing protein HSPP-53	1025	33
			SEQ ID NO:53.		
1096	Y87276	Homo sapiens	Human signal peptide	863	98
	ĺ		containing protein HSPP-53	1	İ
			SEQ ID NO:53.	]	
1097 1098	AF161455	Homo sapiens	HSPC337	742	98
1098	U80029	Caenorhabdit	similar to thioredoxin	242	39
1099	AJ005866	is elegans Homo sapiens	0 3 1/1		
1100	AJ005866	Homo sapiens	Sqv-7-like protein Sqv-7-like protein	1321	99
1101	AJ005866	Homo sapiens	Sqv-7-like protein	1118 891	99
1102	AJ005866	Homo sapiens	Sqv-7-like protein	1016	99
1103	AL110244	Homo sapiens	hypothetical protein	299	31
1104	AF242194	Drosophila	brakeless-B	147	52
		melanogaster			
1105	AL031010	Homo sapiens	dJ422F24.1 (PUTATIVE novel	968	100
			protein similar to C. elegans		
1106	172000		C02C2.5)		
1106	U28016	Mus musculus	parathion hydrolase	1624	87
	,		(phosphotriesterase) -related		
1107	AJ278150	Homo sapiens	protein putative lipid kinase		
1108	G03733	Homo sapiens	Human secreted protein, SEQ	2207	99
	/	sabrens	ID NO: 7814.	495	98
1109	AF217287	Drosophila	G protein RhoBTB	834	54
		melanogaster		~~~	J-2
1110	Y28921	Homo	Human regulatory protein	941	48
		sapiens	HRGP-7.		
1111	Y28921	Homo	Human regulatory protein	1331	51
1		sapiens	HRGP-7.		
1112	AF176704	Homo sapiens	F-box protein FBX9	2027	99
1113	AF182076	Homo	glioma tumor suppressor	2418	100
- 1		sapiens	candidate region protein 2		
114	G04039	Homo sapiens			

TABLE 2

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	*
NO:				SCORE	IDENTITY
1115	AF229439	Mus musculus	ID NO: 8120.		
1116	L40357	Homo sapiens		1697	91
1117	L40357	Homo sapiens		509	100
1118	A12155	Homo sapiens	, - ,	404	85
1119	AL161542	Arabidopsis	isomerase like protein	1673	100
1120	AL023754	thaliana		607	53
		Homo sapiens	Ca2+/Calmodulin dependent Protein Kinase LIKE protein)	2341	98
1121	Y57901	Homo sapiens	ETMPN-25.	321	36
1122	Z14122	Xenopus laevis	XPGPS	455	77
1123	AF225418	Homo sapiens	lipase	1531	97
1124	Y06518	Homo sapiens	Zen GTPase interacting protein ZIP.	3227	100
1125	AL035690	Homo sapiens		952	100
1126	AJ000217	Homo sapiens		1286	199
1127	AB030505	Mus musculus	UBE-1c2	1069	79
1128	Y73375	Homo sapiens	HTRM clone 1427838 protein sequence.	874	100
1129	Y78941	Homo sapiens	Cyclophilin-type peptidyl prolyl cis/trans isomerase amino acid sequence.	877	100
1130	AL023553	Homo sapiens		557	100
1131	Y91945	Homo sapiens	Human chaperone protein 6 (HCHP-6).	1408	100
1132	Z68197	Schizosaccha romyces pombe	putative nuclear pore protein	596	39
1133	Z68197	Schizosaccha romyces pombe	putative nuclear pore protein	389	35
1134	AF180681	Homo sapiens	guanine nucleotide exchange factor	3597	100
1135	AF079765	Mus musculus	enhancer of polycomb	264	41
1136	M62419	Mus musculus	clathrin-associated protein	2189	99
1137	AJ006219	Drosophila melanogaster	clathrin-associated protein	1254	78
1138	Y76218	Homo sapiens	Human secreted protein encoded by gene 95.	440	98
1139	W88104	Homo	A Rab protein designated	1065	99
		sapiens	HRABS-2.		
1140	Y13401	Homo sapiens	Amino acid sequence of protein PRO339.	3979	98
1141	W85026	Chimeric - Homo sapiens	Green fluorescent protein- Zap70 fusion product.	3309	100
1142	Y13402	Homo sapiens	Amino acid sequence of protein PRO310.	1694	99
1143	G03875	Homo sapiens	Human secreted protein, SEQ ID NO: 7956.	660	99
1144	Y12917	Homo sapiens	Amino acid sequence of a	750	98
1145	¥12917	Homo sapiens	human secreted peptide.  Amino acid sequence of a	1096	100
1146	AL022157	Homo sapiens	human secreted peptide.  SPIN (SPINDLIN HOMOLOG	1233	100
1147	AL022157	Homo sapiens	(PROTEIN DXF34)) SPIN (SPINDLIN HOMOLOG	1233	100
1148	G02548	Homo sapiens	(PROTEIN DXF34)) Human secreted protein, SEQ	370	98
1149	¥73338	Homo sapiens	ID NO: 6629. HTRM clone 2019742 protein	1492	100
1150	W74841	Homo sapiens	sequence. Human secreted protein		55
			encoded by gene 113 clone		

TABLE 2

NO	SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	7 · · · · ·
No:   HBANKSO.   SCORE	ID					IDENTITY
1.151	NO:		ļ	1		
1.152			1	HEAAR60.		<del>                                     </del>
1152	1151	AF044201	Rattus	neural membrane protein 35;	1570	92
Sapiens	_	j	norvegicus	NMP35		
AL18501   Romo sapiens   GJ151N16.1 (A novel protein   872   64	1152	AF156774	Homo		1855	99
			sapiens	acyltransferase-gammal		
DKF2D565A0946, Em:AL050069)   100	1153	AL118501	Homo sapiens		872	64
1154						
1185					i	ľ
aspiens   sequence.   Sequen				,		100
1156   G04036	1155	Y41705			1381	97
157					1	
1157	1156	G04036	Homo sapiens		607	99
1.158				L		
1158	1157	AF112444		L-asparaginase	287	43
1159					<u> </u>	<u> </u>
1160		1				1
1161   Y87330   Homo sapiens   Human signal peptide   Containing protein   HSPP-107   SEQ   IN Oc.107.						
1161   Y87330	1160	AB001773		PEM-6	196	33
Containing Protein HSPP-107   SEQ ID NO:107.   SEQ ID NO:107.   SEQ ID NO:107.   SEQ ID NO:107.   T46   83   SEQ ID NO:107.   SEQ ID NO:107.   T46   SEQ ID NO						1
SEQ ID NO.1407.	1161	¥87330	Homo sapiens		746	83
1162   Y87330   Homo sapiens   Human signal peptide containing protein   HSPP-107   SEQ   ID NO:107.   SEQ		ľ	ľ		1	ſ
Containing protein HSPP-107   SEQ ID No.1207.						L
163	1162	Y87330	Homo sapiens		746	83
1163						1
1164   AF232226   Danio rerio   Deddi   191   41     1165   AL118501   Homo sapiens   duli91N.6.1 (A novel protein (translation of the cDNA (translation of the cDNA DKF2p566A0946, Em:AL050069))     1166   AL118501   Homo sapiens   duli91N16.1 (A novel protein (translation of the cDNA DKF2p566A0946, Em:AL050069))     1167   AF187733   Homo sapiens   DKF2p566A0946, Em:AL050069))     1168   AB019415   Homo sapiens   DKF2p566A0946, Em:AL050069))     1169   AF064604   Homo sapiens   DRSpholipase   951   55     1169   AF064604   Homo sapiens   Folypeptide fragment encoded   Dy gene 6   Drospholipase   D	43.25					
1165   AL18501   Homo sapiens   GUISINI6.1 (A novel protein (translation of the cDNA   DKFZp566A0946, Em. AL050069))   1166   AL18501   Homo sapiens   GJISINI6.1 (A novel protein (translation of the cDNA   DKFZp566A0946, Em. AL050069))   1167   AF187733   Homo sapiens   Syntaphilin   831   42   42   43   42   43   42   43   43						
(translation of the cDNA DKF2p566A0946, Em:AL050069))  1166 AL118501 Homo sapiens dJ1191N16.1 (A novel protein (translation of the cDNA DKF2p566A0946, Em:AL050069))  1167 AF187733 Homo sapiens Syntaphilin 831 42  1168 AB019415 Homo sapiens Phospholipase 951 55  1169 AF064604 Homo sapiens F0lypeptide fragment encoded 1191 100 by gene 6.  1170 Y01164 Homo sapiens Polypeptide fragment encoded 1191 100 by gene 6.  1171 L03188 Saccharomyce putative 180 22  1172 AF113751 Mus musculus nuclear pore membrane 3941 81 slycoprotein POM210  1173 AJ245417 Homo sapiens G5b protein 794 100 1174 AL022238 Homo sapiens dJ1042K10.3 (novel protein) 1285 100 1175 U41278 Caenorhabdit is elegans T-cell receptor V-alpha-J-salpha region 1177 AC012680 Arabidopsis putative protein phosphatase 209 37 thaliana 2C; 55455-56414  1178 G01345 Homo sapiens Dytative protein phosphatase 209 17 NO: 5426.  1180 AF039716 Caenorhabdit is elegans chain for similar to worm, Arabidopsis and pine proteins similar to worm, Arabidopsis and pine proteins 1342 100 similar to worm, Arabidopsis and pine proteins 1342 100 similar to worm, Arabidopsis and pine proteins 1342 100 similar to worm, Arabidopsis and pine proteins 1342 100 similar to worm, Arabidopsis and pine proteins 1342 100 similar to worm, Arabidopsis and pine proteins 1342 100 similar to worm, Arabidopsis and pine proteins 1342 100 similar to worm, Arabidopsis and pine proteins 1342 100 similar to worm, Arabidopsis and pine proteins 1342 100 similar to worm, Arabidopsis and pine proteins 1342 100 similar to worm, Arabidopsis and pine proteins 1342 100 similar to worm, Arabidopsis and pine proteins 1342 100 similar to worm, Arabidopsis and pine proteins 1342 100 similar to worm, Arabidopsis and pine proteins 1342 100 similar to worm, Arabidopsis and pine proteins 1342 100 similar to worm, Arabidopsis and pine proteins 1342 100 similar to worm, Arabidopsis 1342 100 100 100 100 100 100 100 100 100 10			L			
DKFZp566A0946, Em:AL050059)	1165	AL118501	Homo sapiens		1051	71
1166						
(translation of the cDNA   NFE25566A0946, Em:AL050059)   1167   AF187733   Homo sapiens   Syntaphilin   831   42   1168   AB019435   Homo sapiens   Phospholipase   951   55   1159   AF064604   Homo sapiens   Folypeptide fragment encoded   1191   100   1170   Y01164   Homo sapiens   Polypeptide fragment encoded   1191   100   1171   L03188   Saccharomyce   putative   180   22   1172   AF113751   Mus musculus   nuclear pore membrane   3941   81   1173   AJ245417   Homo sapiens   G5b protein   794   100   1174   AL022238   Homo sapiens   dJ1042K10.3 (novel protein)   1285   100   1175   U41278   Caenorhabdit   is elegans   T-call receptor V-alpha-J-   284   83   28   1176   M35617   Homo sapiens   T-call receptor V-alpha-J-   284   83   20   37   20   20   37   20   20   37   20   20   20   37   20   20   20   20   20   20   20   2						
DKFZp566A0946, Em:AL050069)	1166	AL118501	Homo sapiens		945	76
1167   AF187733   Homo sapiens   Syntaphilin   831   42     1168   AE019435   Homo sapiens   Phospholipase   951   55     1169   AF664604   Homo sapiens   KE03 protein   324   33     1170   Y01164   Homo sapiens   Folypeptide fragment encoded   1191   100     1171   L03188   Saccharomyce   Sucrevisiae   Saccharomyce   Sucrevisiae   Saccharomyce   Sucrevisiae   Saccharomyce   Sucrevisiae   Saccharomyce   Sucrevisiae   Saccharomyce   Sucrevisiae   Saccharomyce   Sucrevisiae   Saccharomyce   Sucrevisiae   Saccharomyce   Sucrevisiae   Saccharomyce   Sucrevisiae   Saccharomyce   Sucrevisiae   Saccharomyce   Sucrevisiae   Saccharomyce   Sucrevisiae   Saccharomyce   Sucrevisiae   Saccharomyce   Sucrevisiae   Saccharomyce   Saccharomyce   Sucrevisiae   Saccharomyce						
1168	1167	200.0000				
1169		I			(	
1170   Y01164						
Dy gene 6.		1				
1171	11/0	TOTIER	Homo sapiens		1191	100
S   Cerevisiae   S   Cerevisiae   S   S   S   S   S   S   S   S   S	1171	102100	Coastanas		1	
1172	TT 1 T	1703199		putative	180	22
Section   Sect	1172	NP113751		nual care novo mombres	3043	0.1
1173	11,2	AF113731	Mus musculus		3941	87
1174	1173	A.7245417	Homo ganiene		704	100
1175					-	
18   18   18   18   18   18   18   18						
1176   M35617   Homo sapiens   T-cell receptor V-alpha-J-alpha region   284   83     1177   AC012680   Arabidopsis   putative protein phosphatase   209   37     1178   G01345   Homo sapiens   Human secreted protein, SEQ   692   99     1179   AL096767   Homo sapiens   dJ579N16.3 (novel protein similar to worm, Arabidopsis and pine proteins)     1180   AF039716   Caenorhabdit is elegans   chain   1342   100     1181   Y11710   Homo sapiens   Collagen type XIV   1048   97     1182   X82240   Homo sapiens   T cell leukemia/lymphoma 1   617   100     1180   AF03974   R94974   R94974 09-MAY-1996 27-OCT-1994   Human TCL-1		32.270		199612.3 gene product	عدد	20
Ac012680   Arabidopsis   putative protein phosphatase   209   37   20; 55455-56414	1176	M35617		T-cell recentor V-alpha-J-	284	82
1177   AC012680   Arabidopsis thaliana   2C; 55455-56414   2C; 55455-56414   2C; 55455-56414   37   37   37   37   37   37   37   3			Julia Suprens		207	03
thaliama 2C; 55455-56414  1178 G01345 Homo sapiens Human secreted protein, SEQ 692 99  ID NO: 5426.  1179 AL096767 Homo sapiens dJ579N16.3 (novel protein similar to worm, Arabidopsis and pine proteins)  1180 AF039716 Caenorhabdit similar to ATP synthase B 496 55 is elegans chain  1181 Y11710 Homo sapiens collagen type XIV 1048 97  1182 X82240 Homo T cell leukemia/lymphoma 1 617 100 sapiens) >R94974 R94974 09-MAY-1996 27-OCT-1994 Human TCL-1	1177	AC012680	Arabidopsis		209	37
1178   G01345   Homo sapiens   Human secreted protein, SEQ   10 NO: 5426.   1179   AL096767   Homo sapiens   dJ579N16.3 (novel protein similar to worm, Arabidopsis and pine proteins)   1180   AF039716   Caenorhabdit is elegans   Chain   1181   Y11710   Homo sapiens   Collagen type XIV   1048   97   1182   X82240   Homo sapiens   T cell leukemia/lymphoma 1   617   100						٥,
ID NO: 5426.	1178	G01345			692	99
AL096767   Homo sapiens   dJ579N16.3 (novel protein similar to worm, Arabidopsis and pine proteins)   1342   100					[	
Similar to worm, Arabidopsis and pine proteins	1179	AL096767	Homo sapiens		1342	100
and pine proteins			•	similar to worm. Arabidopsis		
1180 AF039716 Caenorhabdit is elegans chain  1181 Y11710 Homo sapiens collagen type XIV 1048 97  1182 X82240 Homo T cell leukemia/lymphoma 1 617 100  sapiens) >R94974 R94974 09- MAY-1996 27- OCT-1994 Human TCL-1			i			
is elegans chain    1181   Y11710   Homo sapiens   Collagen type XIV   1048   97	1180	AF039716	Caenorhabdit	similar to ATP synthase B	496	55
1181 Y11710 Homo sapiens collagen type XIV 1048 97  1182 X82240 Homo T cell leukemia/lymphoma 1 617 100  sapiens) >R94974 R94974 09- MAY-1996 27- OCT-1994 Human TCL-1					} ""	-
1182 X82240 Homo T cell leukemia/lymphoma 1 617 100 sapiens) >R94974 R94974 09- MAY-1996 27- OCT-1994 Human TCL-1	1181	Y11710			1048	97
sapiens) >R94974 R94974 09- MAY-1996 27- OCT-1994 Human TCL-1	1182					
>R94974 R94974 09- MAY-1996 27- OCT-1994 Human TCL-1						
R94974 09- MAY-1996 27- OCT-1994 Human TCL-1					ĺ	
MAY-1996 27- OCT-1994 Human TCL-1						
OCT-1994 Human TCL-1		1				•
Human TCL-1	İ		1			
		I			]	

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	<del></del>
ID	NUMBER		DESCRIPTION	WATERMAN	IDENTITY
NO:				SCORE	
		[Homo		·   · · · · · · ·	
1183	U42841	sapiens   Caenorhabdit		<u> </u>	
1.00	012011	is elegans	short region of weak similarity to collagen	161	33
1185	AJ131613	Homo sapiens		1470	99
1186	L27645	Danio rerio	growth-associated protein	130	36
1187	Y02738	Homo sapiens	Human secreted protein	636	100
ł	ł	•	encoded by gene 89 clone	1 020	1 200
	1		HLHFP03.		
1188	AF217544	Xenopus laevis	ornithine decarboxylase-2	1459	60
1189	AL136307	Homo sapiens	dJ380B8.2 (Neuritin, a	182	33
			protein which promotes		
			neurite outgrowth)		1
1190	X89602	Homo sapiens	rTSbeta	197	100
1191	U32828	Haemophilus	ribosomal protein S6	268	31
	1	influenzae	modification protein (rimK)	}	1
1192	AF154831	Rd			
1132	AF154831	Rattus norvegicus	PV-1	1403	60
1193	Y50926	Homo sapiens	Human fetal brain cDNA clone	<del> </del>	
	130320	none saprens	vc16 1 derived protein.	918	100
1194	AF026530	Rattus	stathmin-like-protein splice	1093	97
		norvegicus	variant RB3'	1033	] "
1195	U35244	Rattus	vacuolar protein sorting	2981	96
		norvegicus	homolog r-vps33a		
1196	¥70470	Homo sapiens	Human p53 target molecule,	1680	100
1197	374570	- <u> </u>	PRG3 protein.		
1198	AF157318 AF125443	Homo sapiens	AD-017 protein	912	47
1130	AF125443	Caenorhabdit is elegans	contains similarity to S.	460	39
	1	15 Clegans	pombe phosphatidyl synthase (GB: 228295)		
1199	AF201934	Homo sapiens	DC12	1649	88
1200	AL031775	Homo sapiens	dJ30M3.3 (novel protein	1902	100
	1	"	similar to C. elegans	1	[
			Y63D3A.4)	1	ļ
1201	M21103	Ovis aries	BIIIB4 high-sulfur keratin	484	82
1202	285986	Homo sapiens	dJ108K11.3 (similar to yeast	1143	75
1203	U18762	Rattus	suppressor protein SRP40)		
1203	010702	norvegicus	retinol dehydrogenase type I	890	52
1204	U35730	Mus musculus	jerky	2235	76
1205	AB002327	Homo sapiens	KIAA0329	151	24
1206	AB019233	Arabidopsis	ubiquinone/menaquinone	762	56
		thaliana	biosynthesis		30
			methyltransferase-like		
1207	AL136307	Homo sapiens	dJ380B8.2 (Neuritin, a	742	100
			protein which promotes		
1208	AF207989	77.	neurite outgrowth)		
0	עמנייט איבה	Homo sapiens	orphan G-protein coupled	2326	100
1209	Z97630	Homo sapiens	receptor dJ466N1.4 (novel protein		
		Gupicis	similar to ANK3 (ankyrin 3,	181	44
			node of Ranvier (ankyrin	]	
		İ	G)))		1
1210	U21549	Mus musculus	Ac39/physophilin	1280	68
1211	Y27700	Homo sapiens	Human secreted protein	1267	100
			encoded by gene No. 12.		
1212	AF117814	Mus musculus	odd-skipped related 1 protein	945	66
1213	AF277233	Naegleria	calcineurin B	222	39
1214	D14849	fowleri			
47	213013	Mus musculus	meiosis-specific nuclear	1950	77
1215	G03022	Homo sapiens	structural protein 1 Human secreted protein, SEQ	590	300
			ID NO: 7103.	390	100
1216	272510	Caenorhabdit	similarity to yeast UTR3	634	49

SEQ	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	IDENTITY
NO:				SCORE	IDENTITY
		is elegans	protein (Swiss Prot accession		<del></del>
			yk677h11.5 comes from this gene		
1217	Z49703	Saccharomyce s cerevisiae	unknown	134	22
1218	AC013430	Arabidopsis thaliana	F3F9.18	199	29
1219	L10910	Homo sapiens	splicing factor	1026	71
1220	270750	Caenorhabdit is elegans	similar to vanadate resistance protein transmembranous comes from this gene	965	58
1221	AL163815	Arabidopsis thaliana	putative protein	653	61
1222	AF155100	Homo sapiens	zinc finger protein NY-REN-21 antigen	2261	100
1223	J05071	Bos taurus	GTP-binding regulatory protein gamma-6 subunit	356	100
1224	Y73364	Homo sapiens	HTRM clone 2765991 protein sequence.	1169	99
1225	AL050170	Homo sapiens	hypothetical protein	714	100
1226 .	X64002	Homo sapiens	RAP74	2661	99
1227	X04085	Homo sapiens	catalase	2846	100
1228	AJ005620	Mus musculus	skeletal muscle-specific gene	1416	90
1229	AF045564	Rattus norvegicus	development-related protein	1715	93
1230	X97571	Mus musculus	HCMV-interacting protein	479	96
1231	L0B239	Homo sapiens	located at OATL1	2274	100
1232 1233	AF121863	Homo sapiens	sorting nexin 14	1964	100
1234	AF121863 AC024805	Homo sapiens Caenorhabdit	sorting nexin 14	1203	84
1235	AC006634	is elegans	contains similarity to TR:004595	744	31
		Caenorhabdit is elegans	contains similarity to Saccharomyces cerevisiae probable membrane protein YLR418c (GB:U20162)	357	33
1236	Y18101	Mus musculus	macrophage actin-associated- tyrosine-phosphorylated protein	1559	87
1237	AB042646	Homo sapiens	TGIF2	1224	100
1238	AB026264	Homo sapiens	IMPACT	1694	100
1239 1240	AB026264 G00429	Homo sapiens	IMPACT	1123	100
1241	Y76144	Homo sapiens	Human secreted protein, SEQ ID NO: 4510.	324	100
L241 L242	AL035602		Human secreted protein encoded by gene 21.	1363	53
243	X76483	Arabidopsis thaliana	putative protein	499	28
.es3	A/0403	Gallus gallus	Yes-associated protein (65kDa)	574	48
1244	AF220186	Homo sapiens	uncharacterized hypothalamus protein HT012	503	100
1245	AL021453	Homo sapiens	dJ821D11.3 (PUTATIVE protein)	856	100
246	AJ276003	Homo sapiens	GAR1 protein	1216	100
.247	Y57910	Homo sapiens	Human transmembrane protein HTMPN-34.	1369	98
.248	AC004874	Homo sapiens	similar to N- acetylgalactosaminyltransfera se; similar to Q07537 (PID:g1171989)	957	100
249	AF199597	Homo sapiens	A-type potassium channel modulatory protein 1	1139	100
1250	Y13148	Rattus norvegicus	PAG608	1350	88
251	M24852	Rattus norvegicus	neuron-specific protein PEP- 19	124	46

SEQ ID NO: 1252	ACCESSION NUMBER AF146738	SPECIES	DESCRIPTION	SMITH- WATERMAN	*
1252	AF146738	1			IDENTITY
	111 110 110	Rattus	testis specific protein	SCORE 771	83
1253	<u> </u>	norvegicus	-	//1	83
	G02725	Homo sapiens	Human secreted protein, SEQ ID NO: 6806.	419	97
1254	W44375	Homo sapiens	Human ubiquitin-conjugating enzyme polypeptide.	1045	99
1255	AC006538	Homo sapiens	1	831	78
1256	AB004316	Bos taurus	mitochondrial methionyl-tRNA	1556	88
1257	235094	Homo sapiens	transformylase	125	
1258	Y13362	Homo sapiens	Amino acid sequence of	1354 2383	97
	1 - 2000	none sapiens	protein PRO214.	2383	100
1259	AC006014	Homo sapiens	similar to RFP transforming	1299	100
			protein; similar to P14373 (PID:q132517)		
1260	AC005099	Homo sapiens	match to AI222572	469	100
			(NID:g3804775)	1	
1261	V00507	Homo sapiens	coding sequence of DHFR (1 is 1st base in codon) (561 is 3rd base in codon)	984	100
1262	X15443	Rattus sp.	gamma-glutamyltranspeptidase	697	32
1263	20222		(AA 1-568)		
1264	AF173871 AF178983	Mus musculus	neuronal PAS3	977	94
1265	X70473	Homo sapiens	Ras-associated protein Rapl Human cyclic nucleotide-	433	97
		nomo saptens	associated protein-1 (CNAP-	2785	99
1266	Y41738	Homo sapiens	Human PRO541 protein sequence.	1622	100
1267	AF061346	Mus musculus	Edpl protein	1077	64
1268	U97006	Caenorhabdit is elegans	C13F10.4 gene product	154	23
1269	AF233582	Mus musculus	GTPase Rab37	942	95
1270	AF195951	Homo sapiens	signal recognition particle	3127	98
1271	AL031177	Homo sapiens	dJ889M15.3 (novel protein)	1150	55
1272 1273	AF201933 AF201933	Homo sapiens	DC11	650	100
1274	AL021710	Homo sapiens Arabidopsis	DC11	346	98
		thaliana	putative protein	348	49
1275	AC004449 Y86295	Homo sapiens	R33683_3	556	100
1276	186295	Homo sapiens	Human secreted protein HL2AG87, SEQ ID NO:210.	1920	100
1277	Y71111	Homo sapiens	Human Hydrolase protein-9 (HYDRL-9).	1576	99
1278	S94421	Homo sapiens	T cell receptor eta-exon	478	100
1279	Y66695	Homo	Membrane-bound protein	1909	100
1280	AF161380	sapiens	PRO1344.		
		Homo sapiens	HSPC262	772	100
1281	Y48610	Homo sapiens	Human breast tumour- associated protein 71.	779	100
1282	AC015446	Arabidopsis thaliana	Similar to AIG1 protein	406	35
1283	AK024432	Homo sapiens	FLJ00022 protein	403	35
1284	W96153	Homo sapiens	Human FADD-interacting	1825	81
1285	AJ001019	Varia as	protein (FIP).		
1286	AE003823	Homo sapiens Drosophila	ring finger protein	1301	100
		melanogaster	CG13178 gene product	195	29
1287	AF178632	Homo sapiens	FEM-1-like death receptor binding protein	3261	100
1288	AC006033	Homo sapiens	similar to MLN 64; similar to I38027 (PID:g2135214)	1195	100
1289	AC006033	Homo sapiens	similar to MLN 64; similar to I38027 (PID:g2135214)	668	93
1290	AB023811	Homo sapiens	TU3A	351	54

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	
ID No:	NUMBER		22508777708	WATERMAN	IDENTITY
1291	273424	Caenorhabdit is elegans		235	36
1292	Y94871	Homo sapiens	Human protein clone HP02551.	1222	100
1293	AF190425	Homo sapiens	protein RAP140	489	29
1294	G03856	Homo sapiens	ID NO: 7937.	538	99
1295	AF133670	Mus musculus	, p	367	51
1296	AJ249735	Homo sapiens		1142	100
1297	X57560	Escherichia coli	pspE protein	535	100
1298	AF169284	Homo sapiens	protein 1	1997	100
1299	U41023	Caenorhabdit is elegans	yk61f1.3; coded for by C. yk109h8.5	324	29
1300	AB024523	Homo sapiens		1206	100
1301	X55989	Homo sapiens	eosinophil cationic-related protein	737	99
1302	AF007151	Homo sapiens	unknown	1481	100
1303	X52904	Escherichia coli	open reading frame (AA 1-65)	359	100
1304	U19577	Escherichia coli	galactonate dehydratase	242	93
1305	AF266508	Mus musculus		1409	97
1306	Y57901	Homo sapiens	HTMPN-25.	932	100
1307	U58750	Caenorhabdit is elegans	similar to the mitochondrial carrier family	365	54
1308	AF044774	Homo sapiens	breakpoint cluster region protein 2	2681	99
1309	AL078593	Homo sapiens	dJ21081.1 (KIAA0680)	267	34
1310	X82693	Homo sapiens		620	96
1311	282263	Caenorhabdit is elegans	C47A4.1	283	35
1312	AF131213	Homo sapiens	chromosome 16 open reading frame 5	1493	100
1313	Y41763	Homo sapiens	Human PRO938 protein sequence.	1636	100
1314	AF196972	Homo sapiens	JM24 protein	2239	100
1315	AF053356	Homo sapiens	insulin receptor substrate	228	97
1316	¥66695	Homo sapiens	Membrane-bound protein PRO1344.	1909	100
1317	AF153127	Gallus gallus	SAPK interacting protein	2442	89
1318	AF153127	Gallus gallus	SAPK interacting protein	1477	83
1319	AF153127	Gallus gallus	SAPK interacting protein	1651	86
1320	X56932	Homo sapiens	23 kD highly basic protein	1044	100
1321	AF174605	Homo	F-box protein Fbx25	467	70
		sapiens) >Y83086 Y83086 09- MAR-2000 28- AUG-1998 F- box protein FBP-18. [Homo sapiens	- BOX process reasons	467	76
1322	M61732	Trypanosoma cruzi	neuraminidase	214	24
1323	Y17013	porcine	pol	304	64
	<u>-</u>	endogenous			

SEQ					,
ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-	*
NO:	NOMBER			WATERMAN SCORE	IDENTITY
NO.		retrovirus	ļ - ·	SCORE	ļ
1324	AL138655	Arabidopsis	putative protein	1174	37
		thaliana	pacacave process	11,3	13'
1325	AL138655	Arabidopsis	putative protein	946	35
		thaliana	Facation Process	1	
1326	AL133215	Homo sapiens	bA108L7.2 (novel protein	1322	99 ~
		· •	similar to rat tricarboxylate		
			carrier)		
1327	AF161541	Homo sapiens	HSPC056	1357	99
1328	Y73346	Homo sapiens	HTRM clone 619699 protein	785	96
		Ĺ	sequence.		İ
1329	L10910	Homo sapiens	splicing factor	912	82
1330	AF146568	Homo sapiens	MIL1 protein	1936	100
1331	W87772	Homo sapiens	Human serum glucocorticoid-	232	39
			regulated kinase (H-SGK2)	i	
			polypeptide.		
1332	¥41741	Homo	Human PRO704 protein	1860	100
1333	3.000000	sapiens	sequence.		
1334	AF295096 Z82271	Homo sapiens	zinc-finger protein ZBRK1	411	91
1334	2822/1	Caenorhabdit is elegans	Similarity to Mouse kinensin- like protein KIF4 comes from	578	44
		is elegans	this gene		
1335	AE000810	Methanobacte	conserved protein	290	43
1000	ABOUGIO	rium	Conserved procesn	1 2 90 '	43
		thermoautotr		i	
		ophicum			
1336	Y68779	Homo sapiens	Amino acid sequence of a	1019	91
		-	human phosphorylation		
			effector PHSP-11.	ļ	
1337	AB027003	Mus musculus	protein phosphatase	378	84
1338	U64856	Caenorhabdit	Weak similarity to TPR	215	40
		is elegans	domains		<u> </u>
1339	AE001394	Plasmodium	protein of the YMR7 family	170	29
1340	X76717	falciparum Homo sapiens	MT-11 protein	204	89
1341	AC011914	Arabidopsis	putative mutT protein; 68398-	289	45
	110011311	thaliana	67881	209	4.5
1342	AJ276171	Homo sapiens	ASPIC	2122	100
1343	AF187016	Homo sapiens	myosin regulatory light chain	2303	99
		•	interacting protein MIR		
1344	AC006963	Homo sapiens	similar to Kelch proteins;	894	35
		:	similar to BAA77027		
			(PID:g4650844)	<u> </u>	
1345	AF257466	Homo sapiens	N-acetylneuraminic acid	1880	99
			phosphate synthase		
1346	Y25896	Homo sapiens	Human secreted protein	1148	100
			fragment encoded from gene	}	1
1347	AJ272073	Torpedo	male sterility protein 2-like	1664	58
1011	20212013	marmorata		1004	30
1348	AF161548	Homo sapiens	HSPC063	1018	98
1349	W78128	Homo sapiens	Human secreted protein	11117	100
		Dapacins	encoded by gene 3 clone	!	-00
			HOSBI96.	İ	ł
1351	G02144	Homo sapiens	Human secreted protein, SEQ	418	100
		•	ID NO: 6225.		
1352	D90869	Escherichia	similar to	2047	100
		coli			
1353	A12029	Homo sapiens	MRP-14	613	100
1354	AC005328	Homo sapiens	R26660_1, partial CDS	870	74
1355	AC024876	Caenorhabdit	contains similarity to	829	61
		is elegans	SW:RPB1_CRIGR		
1356	AF077226	Homo sapiens	copine III	1876	64
1359	AF217188	Mus musculus	YIP1B	801	63
1360	AC074331	Homo sapiens	ZNF234	3869	100
1361	AL163279	Homo sapiens	homolog to cAMP response	5035	99

SEQ ID	ACCESSION	SPECIES	DESCRIPTION	SMITH- WATERMAN	% IDENTITY
NO:				SCORE	IDENTITY
	•		element binding and beta transducin family proteins		
1362	Z48475	Homo sapiens		3160	99
1363	Z48475	Homo sapiens	glucokinase regulator	2682	97
1364	AF195764	Homo sapiens	megakaryocyte-enhanced gene	2055	99
			transcript 1 protein; MEGT1 protein		
1365	AF116609	Homo sapiens	PRO0915	581	100
1366	AF116609	Homo sapiens		581	100
1367	AL117352	Homo sapiens	dJ876B10.3 (novel protein similar to C. elegans T19B10.6 (Tr:022557))	2581	99
1368	Y34124	Homo sapiens	Human potassium channel K+Hnovl5.	1342	100
1369	AJ245621	Homo sapiens	CTL2 protein	3728	99
1370	AF008220	Bacillus subtilis	YtaG	429	45
1371	X05562	Homo sapiens	alpha-2 chain precursor (AA - 25 to 1018) (3416 is 2nd base in codon)	5908	99
1372	Z98048	Homo sapiens	dJ408N23.4 (novel DnaJ domain protein)	1296	99
1373	AF154415	Homo sapiens	FLASH	10253	100
1374	U20286	Rattus norvegicus	lamina associated polypeptide	1567	69
1375	U53445	Homo sapiens	DOCI	1645	46
1376	AL117337	Homo sapiens	bA393J16.1 (zinc finger protein 33a (KOX 31))	250	60
1377	AC005328	Homo sapiens	R26660 1, partial CDS	1126	100
1378	U35113	Homo sapiens	metastasis-associated gene	1823	69
1379	L15313	Caenorhabdit is elegans	putative	858	58
1380	Y25756	Homo sapiens	Human secreted protein encoded from gene 46.	1508	100
1381	AB037360	Homo sapiens	ANKHZN	5734	95
1382	AB037360	Homo sapiens	ANKHZN	959	97
1383 1384	AF237676	Mus musculus	,	1721	96
1385	AF237676 Y58793	Mus musculus	G beta-like protein GBL	1043	70
		Homo sapiens	Human calcium regulatory protein CaREG-1.	715	100
1386 1387	AF212162	Homo sapiens	ninein	10369	99
1388	AL031685 AC004890	Homo sapiens		337	33
1305	AC004890	Homo sapiens	similar to zinc finger proteins; similar to BAA24380 >W06316 W06316 03-OCT-1996 27-APR-1995 TRP-1 protein.	542	86
1389	AF187989	Homo sapiens		2665	99
1390 -	AC035150	Homo sapiens	Zinc finger protein ZNF221	3459	100
1391	AF287894	Homo sapiens	PIST	1410	97
1392	AF282265	Homo sapiens	inner centromere protein INCENP	1794	99
1393	X90840	Homo sapiens	axonal transporter of synaptic vesicles	4584	99
1394	AF076249	Homo sapiens	zinc finger protein SBBIZ1	3208	99
1395	G02224	Homo sapiens	Human secreted protein, SEQ ID NO: 6305.	299	75
1396	AC004809	Arabidopsis thaliana	Similar to	130	34
1398	AF242519	Homo sapiens	zinc finger protein SBZF3	181	66
1399	AL133396	Homo sapiens	dJ1068H6.4 (prion protein like protein doppel)	962	100
1400	Y48611	Homo sapiens	Human breast tumour- associated protein 72.	817	99
1401	AC004472	Homo sapiens	P1.11659 5	280	54
1402	X91489	Saccharomyce	putative HMG box	164	27
		s cerevisiae			

TABLE 2

SEQ	ACCESSION	SPECIES	DEMONTRACE	- Charmy	
ID	NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	IDENTITY
NO:				SCORE	IDENTITY
1403	Y79222	Homo	Human transferase TRNSPS-14.	2842	100
		sapiens			
1404	X81058	Mus musculus	tex261	1010	99
1405	AB012084	Mus musculus	ITM	194	29
	AB030251	Homo sapiens	GTPase activating protein	3233	99
1407	AJ010585	Rattus rattus	PTB-like protein	2684	99
1408	X75760	Drosophila melanogaster	LRR47	364	29
1409	076618	Mus musculus	N-RAP	804	48
1410	AC005578	Homo sapiens	F20887_1, partial CDS	835	63
1411	AE000284	Escherichia coli	orf, hypothetical protein.	360	100
1412	X01563	Escherichia coli	L5 (rplE) (aa 1-179)	911	100
1413	W78279	Homo sapiens	Fragment of human secreted	1264	99
1 4 7 4	1		protein encoded by gene 33.		
1414	AB031051	Homo sapiens	Organic anion transporter OATP-E	3832	100
1415	M17466	Homo sapiens	coagulation factor XII	3455	100
1416	AF097994	Homo	L-kynurenine/alpha-	2202	99
		sapiens	aminoadipate aminotransferase		
1417	AF151077 Y09945	Homo sapiens	HSPC243	1262	99
1418	109945	Rattus norvegicus	putative integral membrane transport protein	1098	61
1419	U13152	Mesocricetus	guanine nucleotide-binding	2179	7.0
1417	013132	auratus	protein beta 5	21/9	76
1420	AL162458	Homo sapiens	bA465L10.5 (KIAA1176 (novel	5696	100
	120230	licino bapacino	protein, presumed ortholog	3036	100
			of mouse K-Cl cotransporter		
			KCC2))	1	
1421	Y99426	Homo sapiens	Human PRO1604 (UNQ785) amino acid sequence SEQ ID NO:308.	152	29
1422	Y94923	Homo sapiens	Human secreted protein clone	4039	99
			qs14_3 protein sequence SEQ ID NO:52.		
1423	AF177388	Homo	cancer-amplified	10748	99
		sapiens	transcriptional coactivator . ASC-2		
1424	Y48517	Homo sapiens	Human breast tumour- associated protein 62.	1851	99
1425	AF208848	Homo sapiens	BM-006	1454	89
1426	AF208848	Homo sapiens	BM-006	853	79
1427	AF112886	Bos taurus	differentiation enhancing	4693	95
			factor 1	)	
1428	U41387	Homo sapiens	Gu protein	1372	63
1429	AF161534	Homo sapiens	HSPC049	2853	78
1430	AF125043	Mus musculus	bisphosphate 3'-nucleotidase	275	30
1431	¥66718	Homo	Membrane-bound protein	1886	100
1432	NE102612	sapiens	PRO1106.		
1432	AF193613	Homo sapiens	cell recognition molecule Caspr2	568	100
1433	AB044560	Mus musculus	Gliacolin	192	34
1434	R99900	Homo sapiens	NTII-1 nerve protein,	707	51
			facilitates regeneration of nerve cells.		
1435	AF220530	Homo sapiens	myo-inositol 1-phosphate synthase Al	2904	100
1436	X70944	Homo sapiens	PTB-associated splicing factor	1261	72
1437	AF271732	Homo sapiens	bridging integrator-3	1282	100
1438	Y30811	Homo sapiens	Human secreted protein	595	98
1439			encoded from gene 1.		
1440	AJ293659 AF219138	Homo sapiens	mucolipidin	628	97
1441	AF219138 AF219138	Homo sapiens	GGA3 long isoform	3083	100
-44T	WE 413138	Homo sapiens	GGA3 long isoform	3346	100

SHIII 6	SEO	ACCESSION	SPECIES	200000000000000000000000000000000000000		
No.			SPECIES	DESCRIPTION		*
1442   AB039669   Homo sapiens   ALKX   3944   100		NOMBER	1		1	IDENTITY
1444		78039660	Vama contona	20199		
Mart			, -			
1444	1443	AF23//11			191	27
1446	2000	3 701 7 0 0 5	_			
1446				Nail beta protein		
APP003924   Homo sapiens   ANC 2001   2645   39					1	
1449	1446	AF214114	Homo sapiens		3999	99
1448	<u></u>					1
1449					2645	99
1449	1448	AF003136			2843	52
1450   Y95004						
No.					1184	89
1451	1450	Y95004	Homo sapiens		985	100
1452				vc54_1, SEQ ID NO:48.		
1453   Z38011   Mus musculus   DNR-NS		1	Homo sapiens	ataxin 2-binding protein	688	57
1453   X90568		AF107203	Homo sapiens	ataxin 2-binding protein	456	78
ALO35409   Homo sapiens   ALO35409   Homo sapiens   ADST/98MBL/Heidelberg.DE   ADST/98MBL/PROPERD.DE   ADST/98MBL/PROPERD.DE   ADST/98MBL/PROPERD.DE   ADST/98MBL/PROPERD.DE   ADST/98MBL/PROPERD.DE   ADST/98MBL/PROPERD.DE   ADST/98MBL/PROPERD.DE   ADST/98MBL/PROPERD.DE   ADST/98MBL/PROPERD	1453	Z38011	Mus musculus		882	56
ALOS5409   Homo sapiens   AJS54W11.3 (similar to   1356   100   1456   D44480   Mus musculus   MATH-7 protein   272   100   1458   AF141326   Homo sapiens   RNA helicase HDB/D-CE1   478   45   478   478   45   478   45   478   45   478   45   478   45   478   45   478   45   478   45   478   45   478   45   478   45   478   478   45   478   45   478   45   478   45   478   45   478   45   478   45   478   45   478   45   478   45   478   45   478   478   45   478   45   478   45   478   45   478   45   478   45   478   45   478   45   478   45   478   47	1454	X90568	Homo sapiens	Protein sequence and	510	
LABETTSEMBL-Heidelberg.DE   1356   100		ĺ	1			
1455		1				
1456   D44480   Mus musculus   MATE-2 protein   272   100     1458   AF141326   Homo sapiens   RNA helicase HDB/DICE1   478   45     1459   AF242552   Gallus   retinovin   945   34     1460   U11036   Homo sapiens   Ibd1   724   84     1461   AB025258   Mus musculus   granuphilin-a   545   39     1462   Y08134   Homo sapiens   acid sphingomyelinase-like   2428   99     1463   AC004997   Homo sapiens   match to ESTS 243979   869   98     1464   AC004997   Homo sapiens   match to ESTS 243979   Robert	1455	AL035409	Homo sapiens		1356	100
1456		1			12300	100
1458	1456	D44480	Mus musculus		272	100
1459	1458	AF141326				1
1460   Uli036   Homo sapiens   Ibd1   724   84   84   84   84   84   84   84	1459					
1460	[			12021100211	1 242	1 34
1461	1460	1111036		That	1704	
1462   Y08134	L					
1463   AC004997   Homo sapiens   match to ESTs 243879   Reference   Match to ESTs 243879   Reference   Match to ESTs 243879   Reference   Match to ESTs 243879   Reference   Match to ESTs 243879   Reference						
1463   AC004997   Homo sapiens   match to ESTS 243979   R19699   R171,95730371)   R19699   R171,95730371)   R19699   R171,95730371)   R19699   R171,95730371   R19699   R171,95730371   R19699   R171,95730371   R19699   R171,95730371   R19699   R171,95730371   R19699   R171,95730371   R19699   R171,95730371   R19699   R171,95730371   R19699   R171,95730371   R19699   R171,95730371   R19699   R171,95730371   R19699   R171,95730371   R19699   R171,95730371   R19699   R171,95730371   R19699   R171,95730371   R19699   R171,95730371   R19699   R171,95730371   R19699   R171,95730371   R19699   R171,95730371   R19699   R19699   R19699   R19699   R19699   R19699   R196999   R196999   R196999   R1969999   R1969999   R19699999999999999999999999999999999999		100134	AOMO Saprens		2428	99
1464   AC004997   Homo sapiens   match to ESTS 243979   869   98	1463	AC004997	Wome contone		-	
1464   AC004997   Homo sapiens   match to ESTS 243979   869   98	1200	ACOUST	nomo saptens		869	98
1464   AC004997   Homo sapiens   Match to ESTs Z43979   869   98			ļ		1	1
NND:g573097), R19699 (NID:g774333)   Solution	1454	7004007	 			
1465   U32743	1404	ACOULSS	nomo sapiens		869	98
1465   U32743					1	
influenzae Rd  1466 Y09022 Homo sapiens Not56-like protein 2342 100  1467 AC003034 Homo sapiens Homolog of rat kidney-specific (KS) gene 1072 99  1468 AF071544 Spinacia ribulose-l,5-bisphosphate oleracea carboxylase/oxygenase small subunit N-methyltransferase I (	3465	***************************************	1,,		<u> </u>	
Rd   1466   Y03022	1465	032743		fucose operon protein (fucU)	315	50
1466   Y09022						
1467   AC003034   Homo sapiens   Homolog of rat kidney-specific (KS) gene   1072   99	7.455	1/4444			<u> </u>	
Specific (KS) gene			Homo sapiens	Not56-like protein		
1468	1467	AC003034	Homo sapiens		1072	99
Coleracea   Carboxylase/oxygenase small   Subunit N-methyltransferase I   1469   Y57930   Homo sapiens   Human transmembrane protein   HTMPN-54.   1053   100   HTMPN-54.   1470   AF032666   Rattus   norvegicus   Ruman membrane channel   protein-17   (MECHP-17).   1471   Y70467   Homo sapiens   Human membrane channel   protein-17   (MECHP-17).   1472   AL031033   Homo sapiens   C321D2.1 (Ribosomal Large   1694   100   100   1473   AF177292   Homo sapiens   G321D2.1 (Ribosomal Large   1694   100   1474   S45936   Homo sapiens   HTS1   1101   50   1475   Y86241   Homo sapiens   Human secreted protein   1879   98   1476   AJ010317   Fugu						
Subunit N-methyltransferase	1468	AF071544		ribulose-1,5-bisphosphate	333	26
1469         Y57930         Homo sapiens         Human transmembrane protein         1053         100           1470         AF032666         Rattus norvegicus         rsec5         4504         93           1471         Y70467         Homo sapiens         Human membrane charnel protein-17 (MECHP-17).         452         74           1472         AL031033         Homo sapiens         C321D2.1 (Ribosomal Large Subunit Pseudouridine Synthase protein)         1694         100           1473         AF177292         Homo sapiens         HTS1         1101         50           1474         S45936         Homo sapiens         HTS1         1101         50           1475         Y86241         Homo sapiens         Human secreted protein HOABR60, SEQ ID NO:156.         1879         98           1476         AJ010317         Fugu rubripes         Sand         1278         68           1477         U42831         Caenorhabdit is elegans         coded for by C. elegans cDNA yk99b4.3; similar to human transforming protein (PIR:322157)         846         44           1478         X62447         Homo sapiens         PR 264         543         61           1479         X82209         Homo sapiens         MN1         7116         100		1	oleracea		ŀ	
HTMPN-54.   100						
1470         AF032666         Rattus norvegicus         rsec5         4504         93           1471         Y70467         Homo sapiens         Kuman membrane charnel protein-17 (MECHP-17).         452         74           1472         AL031033         Homo sapiens         C321D2.1 (Ribosomal Large Subunit Pseudouridine Synthase protein)         1694         100           1473         AF177292         Homo sapiens Genethonin 3         4026         98           1474         S45936         Homo sapiens HTS1         1101         50           1475         Y86241         Homo sapiens Homan secreted protein HOABR60, SEQ ID NO:156.         1879         98           1476         AJ010317         Fugu rubripes         Sand Sand Sand Sand Sand Sand Sand Sand	1469	Y57930	Homo sapiens		1053	100
1471   Y70467   Homo sapiens   Human membrane charnel   protein-17 (MECHP-17).     1472   AL031033   Homo sapiens   C321D2.1 (Ribosomal Large Subunit Pseudouridine Synthase protein)     1473   AF177292   Homo sapiens   G9nethonin 3   4026   98     1474   S45936   Homo sapiens   HTS1   1101   50     1475   Y86241   Homo sapiens   Human secreted protein   1879   98   HOABR60, SEQ ID NO:156.     1476   AJ010317   Fugu rubripes   Sand   1278   68     1477   U42831   Caenorhabdit is elegans   Caenorhabdit is elegans   Caenorhabdit is elegans   Caenorhabdit is elegans   FR 264   543   61   1479   X82209   Homo sapiens   MN1   7116   100     100     100   1				L .	!	
1471         Y70467         Homo sapiens         Human membrane charnel protein-17 (MECHP-17).         452         74           1472         AL031033         Homo sapiens         C321D2.1 (Ribosomal Large Subunit Pseudouridine Synthase protein)         1694         100           1473         AF177292         Homo sapiens         genethonin 3         4026         98           1474         S45936         Homo sapiens         HTS1         1101         50           1475         Y86241         Homo sapiens         Human secreted protein HOABR60, SEQ ID NO:156.         1879         98           1476         AJ010317         Fugu rubripes         Sand         1278         68           1477         U42831         Caenorhabdit is elegans yk99b4.3; similar to human transforming protein (PIR:S22157)         846         44           1478         X62447         Homo sapiens         PR 264         543         61           1479         X82209         Homo sapiens         MN1         7116         100	1470	AF032666		rsec5	4504	93
Protein-17 (MECHP-17).				<u>L</u>		
1472       AL031033       Homo sapiens       C321D2.1 (Ribosomal Large Subunit Pseudouridine Synthase protein)       1694       100         1473       AF177292       Homo sapiens Genethonin 3       4026       98         1474       S45936       Homo sapiens HTS1       1101       50         1475       Y86241       Homo sapiens Human secreted protein HOABR60, SEQ ID NO:156.       1879       98         1476       AJ010317       Fugu rubripes       Sand       1278       68         1477       U42831       Caenorhabdit is elegans yk99b4.3; similar to human transforming protein (PIR:S22157)       846       44         1478       X62447       Homo sapiens PR 264       543       61         1479       X82209       Homo sapiens MN1       7116       100	1471	¥70467	Homo sapiens	Human membrane charnel	452	74
1472       AL031033       Homo sapiens       C321D2.1 (Ribosomal Large Subunit Pseudouridine Synthase protein)       1694       100         1473       AF177292       Homo sapiens Genethonin 3       4026       98         1474       S45936       Homo sapiens HTS1       1101       50         1475       Y86241       Homo sapiens Human secreted protein HOABR60, SEQ ID NO:156.       1879       98         1476       AJ010317       Fugu rubripes       Sand       1278       68         1477       U42831       Caenorhabdit is elegans yk99b4.3; similar to human transforming protein (PIR:S22157)       846       44         1478       X62447       Homo sapiens PR 264       543       61         1479       X82209       Homo sapiens MN1       7116       100				protein-17 (MECHP-17).		i i
Subunit Pseudouridine   Synthase protein	1472	AL031033	Homo sapiens		1694	100
Synthase protein			-			
1473         AF177292         Homo sapiens         genethonin 3         4026         98           1474         S45936         Homo sapiens         HTS1         1101         50           1475         Y86241         Homo sapiens         Human secreted protein HOABR60, SEQ ID NO:156.         1879         98           1476         AJ010317         Fugu rubripes         Sand         1278         68           1477         U42831         Caenorhabdit is elegans         coded for by C. elegans cDNA 						ŀ
1474         S45936         Homo sapiens         HTS1         1101         50           1475         Y86241         Homo sapiens         Human secreted protein         1879         98           1476         AJ010317         Fugu rubripes         Sand         1278         68           1477         U42831         Caenorhabdit is elegans         coded for by C. elegans cDNA yk99b4.3; similar to human transforming protein (PIR:S22157)         846         44           1478         X62447         Homo sapiens         PR 264         543         61           1479         X82209         Homo sapiens         MN1         7116         100	1473	AF177292	Homo sapiens		4026	98
1475         Y86241         Homo sapiens         Human secreted protein         1879         98           1476         AJ010317         Fugu rubripes         Sand         1278         68           1477         U42831         Caenorhabdit is elegans yk99b4.3; similar to human transforming protein (PIR:S22157)         846         44           1478         X62447         Homo sapiens         PR 264         543         61           1479         X82209         Homo sapiens         MN1         7116         100	1474				1	
HOABR60, SEQ ID NO:156.   1278   68   1476   AJ010317   Fugu rubripes   Sand   1278   68   1477   U42831   Caenorhabdit is elegans   Caenorhabdit transforming protein (PIR:322157)   1478   X62447   Homo sapiens   PR 264   543   61   1479   X82209   Homo sapiens   MN1   7116   100						
1476     AJ010317     Fugu rubripes     Sand     1278     68       1477     U42831     Caenorhabdit is elegans yk99b4.3; similar to human transforming protein (PIR:S22157)     846     44       1478     X62447     Homo sapiens PR 264     543     61       1479     X82209     Homo sapiens MN1     7116     100	_			HOARRED, SEO ID NO.156	2019	00
Tubripes   Tubripes	1476	AJ010317	Film		1270	
1477 U42831 Caenorhabdit coded for by C. elegans cDNA is elegans yk99b4.3; similar to human transforming protein (PIR:S22157)  1478 X62447 Homo sapiens PR 264 543 61  1479 X82209 Homo sapiens MN1 7116 100	<b>-</b>			Juliu	14/0	08
is elegans yk99b4.3; similar to human transforming protein (PIR:S22157)  1478 X62447 Homo sapiens PR 264 543 61  1479 X82209 Homo sapiens MN1 7116 100	1477	TT42831		godod for his C	L	
transforming protein (PIR:S22157)  1478 X62447 Homo sapiens PR 264 543 61  1479 X82209 Homo sapiens MN1 7116 100	/				546	44
1478     X62447     Homo sapiens     PR 264     543     61       1479     X82209     Homo sapiens     MN1     7116     100		l	To eredams			ļ
1478     X62447     Homo sapiens     PR 264     543     61       1479     X82209     Homo sapiens     MN1     7116     100	ļ					!
1479 X82209 Homo sapiens MN1 7116 100	1470	V62442	77			
/110						
Fan paniscus MHC Class I A 675 84	_				1	
	-300 J	010330	Fan paniscus	PHU.CISSS I A	675	84

SEO	ACCESSION	SPECIES	DESCRIPTION	CVIDI	
ID NO:	NUMBER			SMITH- WATERMAN SCORE	IDENTITY
	AL078599	Homo sapiens	dJ991C6.1 (novel protein similar to C. elegans F55A12.9 (Tr:P91086))	1274	65
1482	298977	Schizosaccha romyces pombe	putative vacuolar protein	256	29
1483	AB005662	Mus musculus	JNK/SAPK-associated protein-1	4968	92
1484	AL050120	Homo sapiens	hypothetical protein	716	100
1485	M27878 Y69161	Homo sapiens		1006	53
1485	X84156	Homo sapiens	partial protein kinase.	575	99
1488	AF038963	Saccharomyce s cerevisiae	ATHL	341	29
1489	U56966	Homo sapiens Caenorhabdit		446	34
		is elegans	coded for by C. elegans cDNA yk30b3.5; coded for by C. elegans cDNA yk30b3.3	620	42
1490	AE000989	Archaeoglobu s fulgidus	enoyl-CoA hydratase (fad-4)	533	46
1491	M80633	Rattus norvegicus	adenylyl cyclase type IV	707	95
1492	¥73342	Homo sapiens	HTRM clone 2709055 protein sequence.	3513	99
1493	Y17220	Homo sapiens	Human secreted protein (clone fj283-11).	462	37
1494	AF133670	Mus musculus	ARL-6 interacting protein-2	701	97
1495	¥94897	Homo sapiens	Human protein clone HP10574.	1371	100
1496 1497	AL049699	Homo sapiens	dJ747H23.2 (novel protein)	1550	100
1497	AF037447 AL445067	Homo sapiens Thermoplasma	ribosomal S6 protein kinase	2427	100
		acidophilum	putative target YPL207w of the HAP2 transcriptional complex related protein	269	35
1499	AB039947	Homo sapiens	X11L-binding protein 51	227	36
1500 1501	AJ277750 AL050333	Homo sapiens	UBASH3A protein	3509	100
1502	AF179896	Homo sapiens Homo sapiens	dJ93K22.1 (novel protein (contains DKFZP564B116))	2439	100
1503	AF178948	Homo sapiens	TALE homeobox protein Meis2b TALE homeobox protein Meis2a	1140	100
1504	¥53005	Homo sapiens	Human secreted protein clone pm749_8 protein sequence SEQ ID NO:16.	1442	99
1505	X82494	Homo sapiens	fibulin-2	3580	99
1506 1507	X98296	Homo sapiens	ubiquitin hydrolase	783	42
1507	AL034548 Y76144	Homo sapiens	dJ1103G7.6 (novel protein)	1098	100
1509	AF220182	Homo sapiens	Human secreted protein encoded by gene 21. uncharacterized hypothalamus	1736	100
1510	U64601		protein HT008	1181	98
1511	AL356192	is elegans	Gene probably begins in the next cosmid	415	58
		Neurospora crassa	related to MDM1 protein	196	29
1512	D17629	Homo sapiens	N-acetylgalactosamine 6- sulfate sulfatase (GALNS)	1829	100
1513	AF168717	Homo sapiens	x 009 protein	694	99
1514	AJ243531	Homo sapiens	nM15 protein	735	100
1515	AC003672	Arabidopsis thaliana	putative C3HC4-type RING zinc finger protein	407	30
1516	AF115435	Rattus norvegicus	syntaxin 17	1374	90
1517	AF003140	Caenorhabdit is elegans	C44E4.5 gene product	274	31
1518 1519	AB002584	Rattus norvegicus	beta-alanine-pyruvate aminotransferase	2238	82
	AL121764	Schizosaccha	yeast atp12 protein precursor	270	30

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	
ID NO:	NUMBER			WATERMAN SCORE	IDENTITY
		romyces	homolog		
1520	AF255910	Homo sapiens	vascular endothelial junction-associated molecule	547	100
1521	D31764	Homo sapiens	KIAA0064	170	27
1522	Y66634	Homo	Membrane-bound protein	985	100
1523	Y94450	sapiens Homo sapiens	PRO190.	1050	
	1	_	protein	250	43
1524	AC000107	Arabidopsis thaliana	F17F8.22	277	37
1525	AF109377	Mus musculus		1277	83
1526	AL031427	Homo sapiens		1432	99
1527	Y08135	Mus musculus	acid sphingomyelinase-like phosphodiesterase	1496	79
1528	AK024423	Homo sapiens		611	100
1529	AF154502	Homo sapiens	quiescent cell proline	679	100
			dipeptidase		1
1530	AF205598	Homo sapiens		1368	100
1531	AF251039	Homo sapiens		1420	50
1532	W74805	Homo sapiens	Human secreted protein encoded by gene 77 clone HOEAS24.	493	57
1533	AF039023	Homo sapiens	Ran-GTP binding protein; RanBP6	5707	99
1534	AC007190	Arabidopsis thaliana	F23N19.9	374	37
1535	AB027564	Homo sapiens		4482	100
1536	Y36178	Homo sapiens	Human secreted protein	377	87
1537	Y50907	Homo sapiens	Human fetal brain cDNA clone vb3_1 derived protein.	3693	99
1538	AF017368	Mus musculus	faciogenital dysplasia protein 2	177	47
1539	AF266756	Homo sapiens	sphingosine kinasc	2011	99
1540	Z48804	Homo sapiens	OA1	2238	100
1541	AF000195	Caenorhabdit is elegans	Contains similarity to Pfam domain: PF30169 (PH), Score=20.6, E-value=1.9e-05, N=1	379	42
1542	¥71159	Homo sapiens	Human phosphodiesterase interacting protein, myomegalin.	9415	99
1543	X76092	Homo sapiens	DNA binding protein RFX3	3327	100
1544	AB015330	Homo sapiens	HRIHFB2007	631	50
1545 1546	AF198487 AF016417	Homo sapiens	transcription factor LBP-1b	2822	100
		Caenorhabdit is elegans	Similar to BZIP transcription factor	518	42
1547	X55885	Homo sapiens	KDEL receptor	1106	100
1548	AB035495	Carassius auratus	ubiquitin-activating enzyme	836	42
1549	AL021707	Homo sapiens	dJ508I15.4 (KIAA0668)	3688	100
1550	AJ223978	Bacillus subtilis	YvqK protein	292	42
1551	AF145615	Drosophila melanogaster	BcDNA.GH03377	822	44
1552	AL157734	Schizosaccha romyces pombe	putative mannosyltransferase involved in N-glycosylation	435	37
			IER5		63
1553	AF079527	Mus musculus			
1553 1554	AF079527 AB026291	Rattus	acetoacetyl-CoA synthetase	1099	88
1554 1555	AB026291 Y44722	Rattus norvegicus Homo sapiens			
1554	AB026291	Rattus norvegicus	acetoacetyl-CoA synthetase Human immune system molecule,	1099	88

TABLE 2

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	T &
ID	NUMBER	""	DESCRIPTION	WATERMAN	IDENTITY
NO:			·	SCORE	IDENTITI
		<del>                                     </del>	protein, MTRP-1.	JCOKS	<del> </del>
1558	Y71056	Homo sapiens	Human membrane transport	1975	99
			protein, MTRP-1.	12372	
1559	Y71056	Homo sapiens	Human membrane transport	1894	97
		-	protein, MTRP-1.		1 "
1560	AF092050	Mus musculus	beta-1,3-N-	262	44
			acetylglucosaminyltransferase	1	1 **
1561	AL109827	Homo sapiens	dJ309K20.2 (acrosomal protein	1607	97
			ACR55 (similar to rat sperm	1 1007	" '
	j		antigen 4 (SPAG4)))		
1562	AJ131890	Homo sapiens	DNA polymerase lambda	3002	100
1563	AL035424	Homo sapiens	dA22D12.1 (novel protein	3015	
	1	nomo supremo	similar to Drosophila Kelch	3012	100
		ļ	proteins)		1
1564	AC002400	Homo sapiens	Gene product with similarity	1.550	L
2001	110002400	TOWN BUDIENTS	to Ubiquitin binding enzyme	2790	100
1565	AC005306	Homo sapiens	R27216 1	<u> </u>	
1566	AF000195			919	82
7200	WE OF OTAR	Caenorhabdit	Contains similarity to Pfam	550	45
		is elegans	domain: PF00169 (PH),	}	1
			Score=20.6, E-value=1.9e-05,	1	
1555			N=1		
1567	AB033281	Homo	F-box and WD-repeats protein	2879	100
		sapiens	beta-TRCP2 isoform C		
1568	D49473	Mus musculus	truncated form of Sox17	1047	78
1569	AK025270	Homo sapiens	unnamed protein product	210	91
1570	X75756	Homo sapiens	protein kinase C mu	4797	99
1571	AF145713	Homo sapiens	SCHIP-1	2388 .	100
1572	AE003831	Drosophila	CG18445 gene product	180	31
		melanogaster			
1573	AF074603	Streptomyces	NonF	205	38
		griseus	· ·		
	ľ	subsp.		ļ	İ
		griseus	ĺ		
1574	U28993	Caenorhabdit	F22D3.3 gene product	144	27
		is elegans	·		
1575	AF129507	Homo sapiens	transcription factor ICBP90	287	68
1576	X64878	Homo sapiens	oxytocin receptor	2002	100
1577	AF237711	Drosophila	Diablo	421	54
		melanogaster			-
1578	G00975	Homo sapiens	Human secreted protein, SEQ	480	100
		-	ID NO: 5056.	***	
1579	AF248744	Cryptosporid	thrombospondin-related	123	33
		ium parvum	adhesive protein	122	33
1580	AL121782	Homo sapiens	dJ585I14.2 (novel protein	663	100
			(translation of cDNA	003	100
			Em: AK000219))		
1581	AF041853	Homo sapiens	kinesin family member protein	345	
			KIF3A	323	33
1582	AF025441	Homo sapiens	Opa-interacting protein OIP5	1198	100
1583	AE001803	Thermotoga			100
		maritima	glycerate kinase, putative	349	34
1584	AF252283		V-1-6-146-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1		
1585		Homo sapiens	Kelch-like 1 protein	3973	100
7203	AF169675	Homo	leucine-rich repeat	3494	99
1506	3714 00	sapiens	transmembrane protein FLRT1		
1586	AF118274	Homo sapiens	DNb-5	2628	97
1587	X79440	Homo sapiens	NADP+-dependent malic enzyme	3167	99
1588	X99802	Homo sapiens	ZYG homologue	3966	99
1589	AF169803	Homo sapiens	flavohemoprotein b5+b5R	2563	100
1590	Y29861	Homo sapiens	Human secreted protein clone	181	47
		_	cb98 4.		
1591	225535	Homo sapiens	nuclear pore complex protein	7567	99
	ŀ	•	hnup153		
1592	X13293	Homo sapiens	B-myb protein (AA 1-700)	3678	99
1592 1593	X13293 M74027	Homo sapiens	B-myb protein (AA 1-700) mucin	3678	99 27
			B-myb protein (AA 1-700) mucin hypothetical protein	3678 242 235	99 27 54

TABLE 2

SEO	ACCESSION	SPECIES	DESCRIPTION		
ID	NUMBER	3120225	DESCRIPTION	SMITH- WATERMAN	TDENMERON
NO:				SCORE	IDENTITY
		pombe		SCORE	
1595	W78324	Homo sapiens	Fragment of human secreted	1318	98
		_	protein encoded by gene 81.	2020	1 -0
1596	Y94906	Homo sapiens	Human secreted protein clone	2236	98
}			rb649_3 protein sequence SEQ		
			ID NO:18.		
1597	AF174605	Homo sapiens		1408	99
1598	AB032254	Homo	bromodomain adjacent to zinc	9676	98
1599	X73114	sapiens	finger domain 2A		
1600	X82200	Homo sapiens		5568	95
1601	¥00876	Homo sapiens		2305	100
	100070	sapiens	Human LAPH-1 protein sequence.	1149	98
1602	AJ223351	Homo sapiens	HIRA-interacting protein 3	2821	
1603	AJ222801	Homo sapiens	neutral sphingomyelinase	2268	99
1604	AJ222801	Homo sapiens	neutral sphingomyelinase	1601	99
1605	AF185576	Mus musculus	POZ/zinc finger transcription	3435	97
L.	1	1	factor ODA-8	1 3 3 3 3	"'
1606	AF093744	Homo sapiens	unknown	131	100
1607	A12142	synthetic	IFN-pseudo-omega 2	800	98
		construct			
1608	¥57949	Homo sapiens	Human transmembrane protein	1868	100
1609	AF151044	<u> </u>	HTMPN-73.		
1610	X15218	Homo sapiens	HSPC210	681	97
1611	Y08200	Homo sapiens	ski protein (AA 1 - 728)	3765	100
1	100200	Homo sapiens	rab geranylgeranyl transferase	2976	100
1612	AF220560	Homo sapiens	B/K protein	2.40.4	
1613	AC004481	Arabidopsis	nodulin-like protein	2486 371	99
		thaliana	moddiin-like procein	371	26
1614	Y09501	Homo sapiens	NADH-cytochrome-b5 reductase	1607	100
1615	Y15521	Homo sapiens	start position 1	3150	97
1616	AJ010750	Rattus	Castration induced prostatic	890	62
ĺ	İ	norvegicus	apoptosis related protein-1,	100	""
			(CIPAR-1)	ŀ	
1617	X58079	Homo sapiens	\$100 alpha protein	481	100
1018	¥66678	Homo	Membrane-bound protein	967	100
1619	AJ242973	sapiens	PRO1009.		
1015	AU242973	Homo sapiens	peptide methionine sulfoxide reductase	929	100
1620	AF150733	Homo sapiens	AD-014 protein		
1621	AJ007509	Homo sapiens	E1B-55kDa-associated protein	288 4646	100 98
1622	X64177	Homo sapiens	metallothionein	380	100
1623	AE001045	Archaeoglobu	A. fulgidus predicted coding	240	36
		s fulgidus	region AF0859	210	30
1624	AL355013	Schizosaccha	mitochondrial carrier protein	403	34
		romyces	-		i
1625	Y66746	pombe			
1025	100/40	Homo	Membrane-bound protein	1184	100
1626	D90053	sapiens Sus scrofa	PRO1198. destrin	<u> </u>	
1627	Y35954	Homo sapiens	Extended human secreted	863	100
			protein sequence, SEQ ID NO.	756	100
		l	203.	1	1
1628	AL031775	Homo sapiens	dJ30M3.2 (novel protein)	470	100
1629	AF132484	Mus musculus	unknown	286	68
1630	AF017096	Drosophila	similar to C. elegans	493	61
		melanogaster	R10H10.6 and S. cerevisiae		
7.75			YD8419.03c	]	1
1631	X03077	Homo sapiens	lactate dehydrogenase-A	1704	100
1632	AF151084	Homo sapiens	HSPC250	763	100
1633	AJ001874	Homo sapiens	orf	255	97
1034	AC012187	Arabidopsis	Contains weak similarity to	143	38
i		thaliana	GATA-6 DNA-binding protein		1
	ļ		gb H36135, gb Z26200 come from this gene.	}	I
			LLOW CIIID YELE.		

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	-6-
ID	NUMBER	SFECIES	DESCRIPTION	WATERMAN	IDENTITY
NO:				SCORE	152
1635	AF'026246	Homo sapiens	HERV-E integrase	411	90
1636	Y50943	Homo sapiens	Human adult brain cDNA clone	1126	95
			ve8_1 derived protein.		
1637	AF134593	Homo sapiens	L-pipecolic acid oxidase	2068	99
1638	AJ238247 Y94942	Mus musculus	putative phosphatase subunit	1948	96
1639	¥94942	Homo sapiens	Human secreted protein clone yk251 1 protein sequence SEQ	1320	100
	1		ID NO:90.	1	
1640	AF235030	Homo sapiens	BM88 antigen	766	99
1641	AF233288	Drosophila	WDS	358	26
		melanogaster		330	1 20
1642	M19351	Mus musculus	immunoglobulin heavy chain	145	34
			binding protein		
1643	Y70452	Homo sapiens	Human membrane channel	1352	1.00
			protein-2 (MECHP-2).	}	
1644	AF176520	Mus musculus	WD repeat-containing F-box	2676	88
			protein FBW5	<u> </u>	
1645	W67B16	Homo sapiens	Human secreted protein	1156	100
l .		1	encoded by gene 10 clone		
1646	X67155	Homo sapiens	HCEMU42.	4.55	
1647	M63180	Homo sapiens	mitotic kinase-like protein-l threonyl-tRNA synthetase	1040	99 61
1648	Y87342	Homo sapiens	Human signal peptide	1566	93
1 -0.0	10,342	2101110 Saptelle	containing protein HSPP-119	1200	93
	1	1	SEQ ID NO:119.		
1649	R95332	Homo sapiens	Tumor necrosis factor	4137	100
		•	receptor 1 death domain	1	
			ligand (clone 3TW).		
1650	AC007136	Homo sapiens	Putative map kinase	856	99
1000			interacting kinase		1
1651	AB015346 AL161576	Homo sapiens Arabidopsis	Eps15R	4464	99
1052	WD1012/0	thaliana	putative protein	1341	48
1653	AC005313	Arabidopsis	putative calmodulin	288	28
1	1.00000	thaliana	pacacive carmodatin	200	20
1654	AL031428	Homo sapiens	dJ184J9.1 (KIAA0601 protein)	3526	100
1655	AL031428	Homo sapiens	dJ184J9.1 (KIAA0601 protein)	3526	100
1656	AB017910	Dictyosteliu	myoM	297	32
		m discoideum			
1657	Y28919	Homo	Human regulatory protein	2251	99
1658	AF056191	sapiens Homo sapiens	HRGP-5. TPA inducible protein		
1659	U76846	Arabidopsis	ubiquitin-specific protease	2744 137	98
~~~	070540	thaliana	dbidgitiu-specific brocease	137	35
1660	AL078627	Schizosaccha	actin-like protein; (2 actin	320	34
		romyces	domains)	320	[ ] ]
		pombe .			
1662	X52022	Homo sapiens	collagen type VI, alpha 3	16274	99
			Chain		
1663	AF300648	Homo	guanine nucleotide binding	1811	100
	7701100	sapiens	protein beta subunit 4		
1664	AF214736	Homo sapiens	EH domain containing protein	2774	100
1665	Z48613	Saccharomyce	2 unknown		
1005	240013	s cerevisiae	unknown	138	26
1666	AF177385	Homo	cytochrome c oxidase assembly	1395	99
		sapiens	protein isoform 2		13
1667	AC007842	Homo sapiens	BC331191 1	1581	47
1668	S67513	Borna	p40	397	43
] ]		disease	-		
		virus BDV,	·	ļ	
		WT-1, Halle			
		Bl/91, horse			ł
		brain, field isolate,	ĺ		
	1	Peptide, 370	l		

TABLE 2

SEQ	ACCESSION	SPECIES		T	
ID NO:	NUMBER		DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
1669	299753	aa			
		Schizosaccha romyces pombe	nucleolar protein	569	47
1670	G03130	Homo sapiens	ID NO: 7211.	427	97
1671	M96625	Gallus gallus	cardiac muscle tensin	1185	54
1672	AF174482	Homo sapiens		2005	99
1673	Y51846	Homo sapiens	Human 18.1 homolog protein fragment.	233	29
1674	AF255334	Homo sapiens	EXP35	152	29
1675	Y94867	Homo sapiens	Human protein clone HP10563.	109	30
1676	¥25712	Homo sapiens	Human secreted protein encoded from gene 2.	3043	99
1677	Y25712	Homo sapiens		1580	91
1678	AF163151	Homo sapiens	dentin sialophosphoprotein precursor	170	17
1679	AF163151	Homo sapiens	dentin sialophosphoprotein precursor	170	17
1680	AK024453	Homo sapiens	FLJ00045 protein	1349	
1681	AF019236	Dictyosteliu m discoideum	TipD	613	34
1682	AJ243459	Leishmania	proteophosphoglycan	153	26
1683	Z69369	Schizosaccha romyces pombe	putative GTP-binding protein	560	46
1684	X94910	Homo sapiens	ERp28		
1685	AF286475	Takifugu rubripes	retinitis pigmentosa GTPase regulator-like protein	1334	100
1686	AF191298	Homo sapiens	vacuolar sorting protein 35	4087	100
1687	AJ275986	Homo sapiens	transcription factor	2958	100
1688	AJ275986	Homo sapiens	transcription factor	1886	88
1689	X07311	Drosophila melanogaster	heat shock protein	138	43
1690	AF240463	Rattus norvegicus	LIS1-interacting protein NUDE1	1383	83
1691	AJ272078	Homo sapiens	APOBEC-1 stimulating protein	1256	68
1692	AJ272079	Homo sapiens	APOBEC-1 stimulating protein	1336	60
1693	AF177942	Xenopus laevis	katanin p60	1664	66
1694	AP263539	Homo sapiens	arginine N-methyltransferase	1774	100
1695	AF222689	Homo sapiens	protein arginine N- methyltransferase 1-variant 2	1182	81
1696 1697	AK000193	Homo sapiens	unnamed protein product	1060	100
	AB041035	Homo sapiens	kidney superoxide-producing NADPH oxidase	3122	100
1698	AB041035	Homo sapiens	kidney superoxide-producing NADPH oxidase	2181	100
1699	AF025772	Homo sapiens	C2H2 zinc finger protein	488	54
1700	Y44676	Homo sapiens	Human ARF-Related Protein-1 (HARP-1).	938	97
1701	AK022407	Homo sapiens	unnamed protein product	315	98
1702 1703	AB024574	Homo sapiens	GTP-binding like protein 2	1172	100
1703	AF055078 AF198092	Homo sapiens	zinc finger protein 42	421	52
1704	AE003573	Mus musculus Drosophila	RP42 CG12474 gene product	1057	77 33
1706	AB036345	Drosophila melanogaster	aquaporin	164	24
1707	Y55927	Homo sapiens	Human STLK2 protein.	2146	100
1708	U27121	Danio rerio	G12		47
1709	AL391710	Arabidopsis	putative protein		50
			F		1

SEQ	ACCESSION	SPECIES	DECCRIPMION	C Grands	·
ID	NUMBER	SECTES	DESCRIPTION .	SMITH- WATERMAN	*
NO:				SCORE	IDENTITY
	·	thaliana		SCORE	
1710	B01311	Homo sapiens	Human PRC241 polypeptide.	1649	97
1711	U40750	Mus musculus	formin binding protein 30	4561	85
1712	AJ011118	Mus musculus	skeletal muscle and cardiac	1490	89
			protein	1 230	1 83
1713	AF255303	Homo	membrane-associated nucleic	4416	99
L		sapiens	acid binding protein		""
1714	AF255303	Homo	membrane-associated nucleic	2960	100
		sapiens	acid binding protein		1
1715	U08227	Rattus	Ras-related protein	511	151
		norvegicus	_		
1716	AF168795	Rattus	schlafen-4	1129	44
		norvegicus			
1717	AF196304	Homo sapiens	SUMO-1-specific protease	5804	99
1718	AL355737	Homo sapiens	HMG20A	1782	100
1719	AB029333	Halocynthia	HrPET-1	1069	46
		roretzi			
1720	AF071317	Mus musculus	COP9 complex subunit 7b	1297	97
1721	AJ272215	Homo sapiens	HEYL protein	1681	99
1722	G01982	Homo sapiens	Human secreted protein, SEQ	718	100
			ID NO: 6063.	1	
1723	AL032643	Caenorhabdit	similar to Uncharacterized	825	41
		is elegans	protein family UPF0034,	1	
1724	G01972	Homo sapiens	Human secreted protein, SEQ	586	92
			ID NO: 6053.		
1725	Y94441	Homo	Human Adipose Specific	1231	100
		sapiens	Protein 1.		•
1726	AF255443	Homo sapiens	CGI-201 protein	4397	99
1727	AF183426	Homo sapiens	HT004 protein	1810	99
1728	D10884	Bos taurus	neurocalcin	1002	99
1729	Z18529	Gallus	tensin	1411	84
_		gallus			
1730	273423	Caenorhabdit	cDNA EST EMBL: Z14908 comes	233	41
		is elegans	from this gene-cDNA EST this		ŀ
			gene		
1732	AF090891	Homo sapiens	PRO0105	470	30
1733	AJ277724	Homo sapiens	histone deacetylase 8	2015	100
1734	G04050	Homo sapiens	Human secreted protein, SEQ	503	95
			ID NO: 8131.		
1735	D45913	Mus musculus	leucine-rich-repeat protein	3531	94
1736	AF096709	Drosophila	failed axon connections	276	32
1737		virilis	protein		·
	AF195120	Homo sapiens	dynactin p62 subunit	2417	99
1738	L15314	Caenorhabdit	contains similarity to Pfam	206	37
1739	VE4612	is elegans	family PF01772 N=1	<u>                                      </u>	
T139	X54618	Listeria	phosphadidylinositol specific	134	27
	i i	monocytogene	phospholipase C		1
1740	AL031658	S			1
1/40	VP03192B	Homo sapiens	dJ310013.4 (novel protein	123	31
			similar to predicted C.		•
			elegans an C. intestinalis	]	İ
1741	Y35924	172-2	proteins)	<u> </u>	
~/ <del>*</del> 1	133324	Homo sapiens	Extended human secreted	1013	99
			protein sequence, SEQ ID NO.		
1742	AC013354	Drob-da -	173.		
1146	AC013354	Arabidopsis	F15H18.15	202	32
1743	W75771	thaliana		<u> </u>	
1/23	W/3//1	Homo	Human GTP binding protein	1932	59
1744	W75771	sapiens	APDOB.		
T/44	W75771	Homo	Human GTP binding protein	1854	61
1745	AF221098	sapiens	APD08.		
T/43	PL751038	Homo	Ral guanine nucleotide	1224	70
1746	Y99372	sapiens	exchange factor RalGPS1A		
71.20	127312	Homo sapiens	Human PRO1430 (UNQ736) amino	1332	99
1747	Y94294	Vone co-	acid sequence SEQ ID NO:116.		
	-212,74	Homo sapiens	Human coenzyme A-utilising	842	100

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	IDENTITY
10:	<del></del>	<del></del>		SCORE	
1748	AK024436	Homo sapiens	enzyme CoAEN-2. FLJ00026 protein		
1749	AE000877	Methanobacte	conserved protein	1619	100
		rium thermoautotr ophicum		231	36
1750	AF101361	Drosophila melanogaster	Abnormal X segregation	193	33
1751	¥15067	Homo sapiens		889	100
1752 1753	AF251038	Homo sapiens	GAP-like protein	822	100
	AC003093	Homo sapiens	OXYSTEROL-BINDING PROTEIN; 45% similarity to P22059 (PID:g129308)	352	57
1754	X69089	Homo sapiens	165kD protein	5703	99
1755	AL049795	Homo sapiens	dJ622L5.3 (novel protein)	1039	100
1756	AL031393	Homo sapiens	dJ733D15.1 (Zinc-finger protein)	2765	100
1757	AB040672	Homo sapiens	UDP-GalNAc: polypeptide N- acetylgalactosaminyltransfera se	2020	99
1758	AL022238	Homo sapiens	dJ1042K10.4 (novel protein)	776	43
1759	AF117653	Homo sapiens	double homeobox protein	375	54
1760	¥12065	Homo sapiens	hNop56	2959	99
1761	AL049712	Homo sapiens	dJ686C3.2 (nucleolar protein hNop56)	2595	99
1762	AC002394	Homo sapiens	Gene product with similarity to dynein beta subunit	1542	51
1763	AF169017	Homo sapiens	formiminotransferase cyclodeaminase	877	100
1764	U91541	Homo sapiens	human formiminotransferase cyclodeaminase (ftcd)protein, carboxy-terminal end	596	100
1765	AB013365	Bacillus halodurans	YlqF	350	34
1766	¥38421	Homo sapiens	Human secreted protein encoded by gene No. 36.	145	71
1767	AC009176	Arabidopsis thaliana	putative ribulose-1,5- bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I	216	27
1768	AK000647	Homo sapiens	unnamed protein product	737	99
1769	AJ238982	Homo sapiens	VNN3 protein	2665	99
1770	U73522	Homo sapiens	AMSH	1214	56
1771 1772	U89435	Mus musculus	unknown	829	86
1773	S70011 AL035086	Rattus sp.	tricarboxylate carrier	1604	95
1774	Y99426	Homo sapiens	dJ44A20.2 (novel protein)	2036	100
1775	AF110330		Human PRO1604 (UNQ785) amino acid sequence SEQ ID NO:308.	1057	99
1776	AJ269529	Homo sapiens	glutaminase glycerol 3-phosphate permease	3146	100
1777	Z81579	Caenorhabdit	cDNA EST yk76f1.5 comes from	2787	100 31
1778	AY007239	is elegans Homo sapiens	monooxygenase X	1055	
1779	AL109608	Schizosaccha romyces	oxysterol-binding protein family	1875 644	99 38
		pombe	- -		İ
1780	AF254260	Homo sapiens	tuftelin 1	1729	100
1781	L07924	Mus musculus	guanine nucleotide dissociation stimulator	247	50
1782	AF295773	Homo sapiens	ral guanine nucleotide dissociation stimulator	142	49.
1783	AK024475	Homo sapiens	FLJ00068 protein	4333	100
L784		Homo sapiens	FLJ00068 protein	3996	93
L785		Homo sapiens	Human secreted protein, SEQ ID NO: 8014.	570	100
1786	S82637	Homo sapiens	Ig lambda-like gene/beta-	247	100

# TABLE 2

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	*
ID	NUMBER			WATERMAN	IDENTITY
NO:				SCORE	
			glucuronidase exon 11 homolog		

TRADOCS:1416280.1(%CT401!.DOC)

TABLE 3

SEQ ID NO		DESCRIPTION	RESULTS*
2	NO. BL00240	Receptor tyrosine kinase	BL00240B 24.70 8.250e-
		class III proteins.	12 157-181
3	PR00109	TYROSINE KINASE CATALYTIC DOMAIN	PR00109D 17.04 8.085e-
		SIGNATURE	25 550 501
4	BL00028	Zinc finger, C2H2 type,	BL00028 16.07 9.400e-
		domain proteins.	10 1129-1146 BL00028
			837
5	BL00023	Type II fibronectin collagen-binding domain	BL00023 24.31 8.920e- 33 413-450 BL00023
		proteins.	24.31 4.545e-27 353-
-	77.00003		390
6	BL00023	Type II fibronectin collagen-binding domain	BL00023 24.31 8.920e- 33 413-450 BL00023
		proteins.	24.31 4.545e-27 353-
7	BL00023	Type II fibronectin	390 BL00033 34 31 8 0305
•	5500023	collagen-binding domain	BL00023 24.31 8.920e- 33 413-450 BL00023
		proteins.	24.31 4.545e-27 353-
8	BL00023	Type II fibronectin	390 BL00023 24.31 8.920e-
		collagen-binding domain	33 413-450 BL00023
		proteins.	24.31 4.545e-27 353- 390
9	BL01160	Kinesin light chain	BL01160B 19.54 5.119e-
10	Phones	repeat proteins.	09 863-917
10	PR00464	E-CLASS P450 GROUP II SIGNATURE	PR00464D 17.40 6.182e- 12 294-312 PR00464G
			12.41 4.231e-11 377-
11	PR00734	GLYCOSYL HYDROLASE	393 PR00734I 11.46 4.296e~
		FAMILY 7 SIGNATURE	09 502-520
12	PF00023	Ank repeat proteins.	PF00023B 14.20 6.500e-
			14.20 2.636e-09 56-66
14	DM00031	IMMUNOGLOBULIN V REGION.	DM00031B 15.41 3.848e-
15	PR00208	GLIADIN AND LMW GLUTENIN	09 79-113 PR00208A 12.59 9.868e-
		SUPERFAMILY SIGNATURE	10 517-535 PR00208A
	1		12.59 2.233e-09 520- 538
17	PD00066	PROTEIN ZINC-FINGER	PD00066 13.92 8.200e-
	1	METAL-BINDI.	14 282-295 PD00066
			13.92 9.400e-14 477- 490 PD00066 13.92
			6.500e-13 505-518
			PD00066 13.92 9.500e- 13 254-267 PD00066
			13.92 1.429e-12 393-
			406 PD00066 13.92
18	BL00845	CAP-Gly domain proteins.	6.571e-12 421-434 PL00845 16.43 2.200e-
20	DI COCCE		25 55-80
20	BL00487	IMP dehydrogenase / GMP reductase proteins.	BL00487E 16.12 5.737e- 26 154-199 BL00487F
			18.79 8.984e-22 235-
			276 BL00487G 26.82 4.082e-12 287-329
21	BL00487	IMP dehydrogenase / GMP	BL00487E 16.12 5.737e-
		reductase proteins.	26 154-199 BL00487F
			18.79 8.984e-22 235- 276 BL00487G 26.82
			4.082e-12 348-390
22	BL00107	Protein kinases ATP-	BL00107A 18.39 3.250e-
		binding region proteins.	26 302-333

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
23	BL00107	Protein kinases ATP-	BL00107A 18.39 3.250e-
1		binding region proteins.	26 302-333
25	BL00115	Bukaryotic RNA	BL00115T 8.45 7.273e-
	İ	polymerase II	29 1208-1242 BL00115Q
	1 .	heptapeptide repeat	18.08 2.776e-21 953-
		proteins.	983 BL00115Y 11.86
1			8.000e-17 1604-1650
}			BL00115M 19.19 8.130e-
			16 731-774 BL00115H
			14.34 9.392e-16 463-
ł			496 BL00115A 15.44
1			7.414e-15 43-82
Ī			BL00115R 6.50 6.128e-
			14 983-1010 BL00115J
			16.71 9.289e-14 591-
Ì			617 BL00115I 8.33
			4.336e-13 535-590
			BL00115L 12.25 5.939e-
			13 662-694 BL00115G
	1	I	11.65 6.011e-13 435-
	1		463 BL00115K 15.03
	1		3.417e-10 617-659
			BL001150 16.76 5.805e-
		1	10 863-913 BL00115P
	1		11.54 7.538e-10 913-
			953 BL00115S 18.24
	1	İ	7.968e-10 1010-1052
	1		BL00115U 10.34 4.475e-
	1		09 1242-1265
26	BL00420	Speract receptor repeat	BL00420A 20.42 4.109e-
		proteins domain	11 81-110 BL00420A
		proteins.	20.42 8.820e-10 84-113
27	BL00050	Ribosomal protein L23	BL00050A 23.71 9.250e-
		proteins.	27 94-127 BL00050B
		•	14.81 8.125e-12 133-
		<b>}</b>	147
28	PR00925	NONHISTONE CHROMOSOMAL	PR00925B 3.73 3.089e-
		PROTEIN HMG17 FAMILY	10 41-54
		SIGNATURE	
29	PF00756	Putative esterase.	PF00756C 14.12 1.108e-
	L		09 486-516
32	BL00557	FMN-dependent alpha-	BL00557D 17.76 5.065e-
		hydroxy acid	37 274-316 BL00557A
		dehydrogenases proteins.	35.08 8.909e-29 24-73
	}		BL00557C 15.59 1.000e-
	!		28 227-257 BL00557B
	[		21.27 8.898e-22 130-
			169
34	PR00629	SHC PHOSPHOTYROSINE	PR00629E 9.90 5.886e-
	İ	INTERACTION DOMAIN	35 299-328 PR00629F
		SIGNATURE	10.95 8.364e-32 334-
		1	361 PR00629B 13.66
		1	3.786e-27 224-247
		1	PR00629A 13.45 8.364e-
		i	21 206-222 PR00629C
i	İ	1	3.80 4.000e-12 249-261
		1	PR00629D 12.45 3.739e-
			11 276-286
35	PD01270	RECEPTOR FC	PD01270A 17.22 1.000e-
		IMMUNOGLOBULIN AFFIN.	40 39-79 PD01270B
		<b>i</b>	22.18 2.875e-38 94-131
			PD01270D 24.66 3.700e-
			34 171-207 PD01270C
			19.54 3.455e-30 137-
			166
36	PD01270	RECEPTOR FC	PD01270A 17.22 1.000e-
ļ		IMMUNOGLOBULIN AFFIN.	40 39-79 PD01270B
J			22.18 2.875e-38 94-131
		<del></del>	

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			PD01270D 24.66 3.700e- 34 171-207 PD01270C 19.54 3.455e-30 137- 166
37	BL00412	Neuromodulin (GAP-43) proteins.	BL00412C 10.28 9.241e- 10 264-298
38	BL00412	Neuromodulin (GAP-43) proteins.	BL00412C 10.28 9.241e- 10 264-298
39	BL00412	Neuromodulin (GAP-43) proteins.	BL00412C 10.28 9.241e- 10 264-298
40	PR00380 .	KINESIN HEAVY CHAIN SIGNATURE	PR00380B 12.64 7.366e- 14 342-360 PR00380C 13.18 6.927e-13 375- 394 PR00380D 9.93 2.180e-12 429-451 PR00380A 14.18 5.154e- 12 143-165
44	BL00345	Ets-domain proteins.	BL00345B 21.28 1.000e- 40 239-290 BL00345A 13.96 2.452e-14 204- 223
45	BL00345	Ets-domain proteins.	BL00345B 21.28 1.000e- 40 215-266 BL00345A 13.96 2.452e-14 180- 199
46	DM01551	kw OSTEOINDUCTIVE YOPM MEMBRANE OUTER.	DM01551A 15.63 3.538e- 26 172-202 DM01551C 14.62 3.571e-17 232- 252 DM01551B 8.84 4.750e-11 214-226
47	PR00876	NEMATODE METALLOTHIONEIN SIGNATURE	PR00876B 7.66 9.328e- 11 246-260
48	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 4.231e- 33 6-45
50	BL00972	Ubiquitin carboxyl- terminal hydrolases family 2 proteins.	BL00972D 22.55 7.750e- 19 994-1019 BL00972A 11.93 7.120e-18 216- 234 BL00972E 20.72 9.471e-14 1020-1042 BL00972C 16.48 7.000e- 13 360-375 BL00972B 9.45 8.269e-10 302-312
51	BL00972	Ubiquitin carboxyl- terminal hydrolases family 2 proteins.	BL00972D 22.55 7.750e- 19 990-1015 BL00972A 11.93 7.120e-18 216- 234 BL00972E 20.72 9.471e-14 1016-1038 BL00972C 16.48 7.000e- 13 360-375 BL00972B 9.45 8.269e-10 302-312
52	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 3.063e- 14 10-54
53	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 8.500e- 17 20-38 PR00988F 12.23 7.828e-15 196- 210 PR00988C 13.64 6.108e-14 104-120 PR00988E 8.27 3.872e- 11 174-186 PR00988D 5.95 6.878e-10 160-171 PR00988B 11.60 2.915e- 09 57-69
55	PR00762	CHLORIDE CHANNEL SIGNATURE	PR00762C 9.29 4.682e- 21 294-314 PR00762D 11.29 4.103e-19 509- 530 PR00762A 14.22 9.333e-18 199-217

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			PR00762F 15.12 3.100e- 16 563-583 PR00762B 12.12 6.063e-16 230- 250 PR00762E 12.07 2.286e-15 545-562 PR00762G 14.13 6.276e- 13 601-616
56	BL00216	Sugar transport proteins.	BL00216B 27.64 8.800e- 10 153-203
58	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 2.049e- 10 1080-1135
59	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 2.049e- 10 1062-1117
61	PD01929	KINASE TYPE RESISTANCE ANTIBIOTIC TRANSFERASE AM.	PD01929E 10.75 9.018e- 09 206-221
68	PR00360	C2 DOMAIN SIGNATURE	PR00360A 14.59 7.395e- 09 680-693
69	PR00360	C2 DOMAIN SIGNATURE	PR00360A 14.59 7.395e- 09 670-683
70	PF00551	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 8.714e- 10 51-64
72	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 5.304e- 09 108-118
73	BL00239	Receptor tyrosine kinase class II proteins.	BL00239B 25.15 7.075e- 12 118-166
74	BL00790	Receptor tyrosine kinase class V proteins.	BL00790N 13.25 6.116e- 10 93-120
76	DM00471	0 PROKARYOTIC DNA TOPOISOMERASE I.	DM00471A 11.73 9.357e- 13 53-66 DM00471B 8.45 4.857e-12 70-81
80	PD02876	DECARBOXYLASE PHOSPHATIDYLSERINE.	PD02876C 8.80 2.723e- 13 223-236 PD02876D 12.13 2.588e-12 334- 351
81	PD02876	DECARBOXYLASE PHOSPHATIDYLSERINE.	PD02876C 8.80 2.723e- 13 282-295 PD02876D 12.13 2.588e-12 393- 410
83	BL00708	Prolyl endopeptidase family serine proteins.	BL00708B 24.91 7.197e-
84	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE	PR00014C 15.44 8.043e- 09 985-1004
86	PR00678	PI3 KINASE P85 REGULATORY SUBUNIT SIGNATURE	PRO0678H 9.13 1.379e- 09 246-269
89	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 8.200e- 09 264-279 PR00320B 12.19 8.650e-09 264- 279
93	BL00455	Putative AMP-binding domain proteins.	BL00455 13.31 2.588e- 14 316-332
95	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 4.000e- 10 123-154
96	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 4.000e- 10 212-243
97	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE	PR00081B 10.38 6.318e- 13 134-146 PR00081A 10.53 2.500e-12 54-72
98	.PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 5.500e- 24 401-423 PR00380D 9.93 7.188e-20 613-635 PR00380B 12.64 7.517e- 16 529-547 PR00380C 13.18 2.756e-13 560- 579

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102	PR00300	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT SIGNATURE	PR00300A 9.56 7.545e- 14 289-308
104	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 6.786e- 18 298-314 BL00479A 19.86 4.913e-16 155- 178 BL00479A 19.86 4.300e-13 272-295 BL00479B 12.57 6.294c- 12 181-197
106	BL01019	ADP-ribosylation factors family proteins.	BL01019A 13.20 8.013e- 12 43-83
107	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 5.000e- 16 403-416
108	BL00191	Cytochrome b5 family, heme-binding domain proteins.	3L00191K 17.38 4.951e- 27 238-282 BL00191J 11.37 6.447e-17 182- 204
109	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 4.938e- 37 8-47
110	BL01138	Scorpion short toxins proteins.	BL01138A 10.96 8.297e- 10 38-50
113	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 5.800e- 23 156-187 BL00107B 13.31 9.100e-14 225- 241
117	BL00214	Cytosolic fatty-acid binding proteins.	BL00214B 26.51 1.000e- 17 46-91 BL00214A 21.17 7.052e-11 5-31
118	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 8.560e- 13 36-67
119	PR00529	GONADOTROPHIN RELEASING HORMONE RECEPTOR SIGNATURE	PR00529C 11.03 7.506e- 10 158-177
120	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 9.400e-
121	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 9.400e- 09 80-95
127	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 7.158e- 13 216-241
128	BL01032	Protein phosphatase 2C proteins.	BL01032C 6.14 3.195e- 12 147-157 BL01032H 11.25 5.680e-11 318- 331 BL01032G 8.33 8.932e-11 282-296 BL01032T 10.42 8.902e- 09 379-389
129	BL01310	ATPIG1 / PLM / MAT8 family proteins.	BL01310 14.74 6.694e- 26 28-64
130	PR00990	RIBOKINASE SIGNATURE	PR00990B 12.32 9.534e- 15 47-67 PR00990A 16.23 5.500e-14 20-42 PR00990C 12.62 2.412e-
133	BL00880	Acyl-CoA-binding protein.	09 119-133 BL00880 17.52 5.576e- 26 72-122
L34	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 9.308e- 14 18-37
135	PR00215	NEUROMODULIN SIGNATURE	PR00215C 13.98 6.779e- 10 475-496
.36	BL01310	ATP1G1 / PLM / MATS family proteins.	BL01310 14.74 2.432e- 29 71-107
.40	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.882e- 14 214-231 BL00028 16.07 9.471e-14 102- 119 BL00028 16.07 2.800e-13 18-35

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			BL00028 16.07 5.500e- 13 74-91 BL00028 16.07 9.100e-13 186- 203 BL00028 16.07 8.043e-12 46-63 BL00028 16.07 8.435e- 12 130-147 BL00028 16.07 9.217e-12 270- 287 BL00028 16.07 6.192e-11 242-259 BL00028 16.07 4.000e- 10 158-175
141	BL00501	Signal peptidases I serine proteins.	BL00501D 16.69 9.538e- 14 113-133 BL00501C 9.61 8.688e-10 89-101
143	BL01020	SAR1 family proteins.	BL01020C 15.35 7.722e- 20 79-130
146	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 6.400e- 25 335-374
149	BL00126	3'5'-cyclic nucleotide phosphodiesterases proteins.	BL00126C 22.07 1.450e- 25 509-550 BL00126E 35.22 3.951e-16 654- 709 BL00126D 25.50 1.360e-15 565-604 BL00126B 15.20 8.200e- 11 483-495 BL00126A 27.56 8.269e-11 442- 479
151	BL00632	Ribosomal protein S4 proteins.	BL00632 23.79 5.271e- 20 106-149
154	BL00559	Eukaryotic molybdopterin oxidoreductases proteins.	BL00559Y 13.63 5.304e- 19 29-58 BL00559K 13.17 2.957e-18 172- 199 BL00559J 19.63 8.385e-13 99-151 BL00559L 13.60 5.814e- 12 241-259
155	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 1.692e- 13 13-35
157	BL00406	Actins proteins.	BL00406D 12.58 2.547e- 18 275-330 BL00406A 9.95 5.776e-16 15-50 BL00406B 5.47 7.429e- 12 69-124 BL00406C 6.75 9.682e-12 128-183
160	BL00132	Zinc carboxypeptidases, zinc-binding region 1 proteins.	BL00132A 26.07 7.000e- 14 22-63 BL00132C 21.35 3.466e-12 104- 145
165	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 9.043e- 13 139-158
168	BL00362	Ribosomal protein S15 proteins.	BL00362 24.67 9.700e- 15 129-172
169	BL00039	DEAD-box subfamily ATP- dependent helicases proteins.	BL00039D 21.67 1.000e- 35 640-686 BL00039A 18.44 1.964e-13 212- 251 BL00039B 19.19 4.553e-13 378-404 BL00039C 15.63 8.773e- 12 465-489
175	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 3.72le- 12 14-36
178	BL01310	ATPIG1 / PLM / MAT8 family proteins.	BL01310 14.74 2.432e- 29 133-169
179	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-	PD01066 19.43 9.455e- 36 6-45

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		BINDING NU.	
180	PR00007	COMPLEMENT CIQ DOMAIN SIGNATURE	PRO0007B 14.16 7.429e- 20 160-180 PR00007A 19.33 4.938e-19 133- 160 PR00007C 15.60 1.225e-15 206-228 PR00007D 9.64 6.885e-
1.81	BL00027	'Homeobox' domain proteins.	11 238-249 BL00027 25.43 9.526e-
182	BL00027	'Homeobox' domain proteins.	24 280-323 BL00027 26.43 9.526e- 24 263-306
183	BL00027	'Homeobox' domain proteins.	BL00027 26.43 9.526e- 24 280-323
184	BL00027	'Homeobox' domain proteins.	BL00027 26.43 9.526e-
188	PR00929	AT-HOOK-LIKE DOMAIN SIGNATURE	24 263-306 PR00929C 5.26 3.328e-
189	PR00929	AT-HOOK-LIKE DOMAIN SIGNATURE	09 460-471 PR00929C 5.26 3.328e-
190	BL00383	Tyrosine specific protein phosphatases proteins.	09 440-451  BL00383F 15.51 7.188e- 17 666-682 BL00383A 13.34 8.714e-17 162- 177 BL00383E 10.35 1.000e-14 333-344 BL00383E 10.35 7.300e- 14 628-639 BL00383F 15.51 1.720e-13 371- 387 BL00383C 10.10 3.000e-13 217-228 BL00383D 11.92 7.000e-
191	FR00450	RECOVERIN FAMILY	13 295-308 BL00383B 7.61 1.692e-11 187-196 BL00383C 10.10 1.750e- 09 509-520 BL00383D 11.92 4.000e-09 589- 602 BL00383B 7.61 8.000e-09 479-488 PR00450C 12.22 7.911e- 15 83-105 PR00450C
193	PF00564	Octicosapeptide repeat	12.22 6.286e-13 47-69 PF00564B 24.74 6.164e-
		proteins.	16 227-278
194	PR00503	BROMODOMAIN SIGNATURE	PR00503D 20.81 9.156e- 15 204-224 PR00503B 9.96 9.571e-13 170-187
195	BL00901	Cysteine synthase/cystathionine beta-synthase P- phosphate att.	BL00901C 20.63 3.429e- 18 67-117
197	BL00636	Nt-dnaJ domain proteins.	BL00636A 8.07 6.211e- 17 40-57 BL00636B
198	PR00690	ADHESIN FAMILY SIGNATURE	15.11 2.000e-13 67-88 PR00690A 10.86 9.866e- 09 463-482
199	BL01131	Ribosomal RNA adenine dimethylases proteins.	BL01131A 26.62 2.343e-
201	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	12 84-130 PR00910A 2.51 8.352e-
103	DM00215	PROLINE-RICH PROTEIN 3.	12 509-522 DM00215 19.43 2.286e- 10 39-72
06	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE	PRO0261A 11.02 4.462e- 19 65-87 PR00261C 11.37 9.308e-19 65-87 PR00261D 12.47 2.667e- 18 65-87 PR00261B 14.12 4.000e-18 143- 165 PR00261A 11.02

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	NO.	-200 CK21 11 ON	RESULTS*
			4.833e-18 143-165 PR00261D 12.47 7.500e- 18 143-165 PR00261B 14.12 5.065e-16 65-87 PR00261C 11.37 8.967e- 16 143-165 PR00261F 11.57 4.938e-13 143- 165 PR00261E 11.08
			7.188e-13 65-87 PR00261F 11.57 7.188e- 13 65-87 PR00261E 11.08 1.643e-11 143-
209	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors	PF00791B 28.49 6.143e- 13 118-173 PF00791C 20.98 7.680e-10 132-
211	PR00007	COMPLEMENT C10 DOMAIN SIGNATURE	PR00007A 19.33 5.761e- 19 131-158 PR00007B 14.16 4.115e-18 158- 178 PR00007C 15.60 1.675e-15 201-223 PR00007D 9.64 7.231e-
212	BL00183	Ubiquitin-conjugating	11 233-244 BL00183 28.97 1.545e-
213	BL00183	enzymes proteins. Ubiquitin-conjugating	30 43-91 BL00183 28.97 1.545e-
215	BL00039	enzymes proteins.  DEAD-box subfamily ATP-dependent helicases proteins.	30 43-91 BL00039D 21.67 1.900e- 29 568-614 BL00039A 18.44 1.871e-23 21-60 BL00039C 15.63 1.720e- 11 364-388 BL00039B 19.19 4.064e-11 277-
217	BF00100	Chloramphenicol acetyltransferase	303 BL00100D 17.22 8.484e- 09 68-106
219	PR00213	proteins. MYELIN PO PROTEIN	PR00213C 15.94 3.969e-
222	BL00678	SIGNATURE Trp-Asp (WD) repeat	11 199-227 BL00678 9.67 1.947e-09
224	PR00875	proteins proteins.  MOLLUSC METALLOTHIONEIN SIGNATURE	PR00875A 5.83 1.000e-
225	BL00636	Nt-dnaJ domain proteins.	09 901-913 BL00636B 15.11 8.200e-
226	BL00636	Nt-dnaJ domain proteins.	19 18-39 BL00636A 8.07 1.000e- 21 21-38 BL00636B 15.11 8.200e-19 45-66
229	PR00301	70 KD HEAT SHOCK PROTEIN SIGNATURE	PR00301F 13.98 7.563e- 13 329-346 PR00301G 13.78 4.300e-12 361-
230	BL00460	Glutathione peroxidases selenocysteine proteins.	382 BL00460A 28.67 8.773e- 20 35-70 BL00460B 9.73 7.429e-16 78-96 BL00460C 14.35 2.831e- 12 111-134 BL00460D 16.89 8.773e-11 140- 160
231	PR00647	SENR ORPHAN RECEPTOR SIGNATURE	PR00647B 10.19 8.522e-
233	BL00292	Cyclins proteins.	09 273-287 BL00292B 20.31 7.429e- 27 244-275 BL00292A 22.87 7.750e-27 201-
34	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 6.308e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			17.27 4.462e-11 47-70 PR00449D 10.79 7.120e
235	PR00019	LEUCINE-RICH REPEAT SIGNATURE	11 109-123 PR00019B 11.36 7.300e 10 251-265 PR00019B 11.36 5.320e-09 119- 133 PR00019B 11.36
236	PR00019	LEUCINE-RICH REPEAT SIGNATURE	1.000e-08 229-243 PR00019B 11.36 7.300e 10 245-259 PR00019B 11.36 5.320e-09 113-
237	PD00289		127 PR00019B 11.36 1.000e-08 223-237
240	PR00011	PROTEIN SH3 DOMAIN REPEAT PRESYNA. TYPE III EGF-LIKE	PD00289 9.97 8.448e-09
241	PR00011	SIGNATURE	PR00011D 14.03 3.492e- 10 616-635
244	BL00903	TYPE III EGF-LIKE SIGNATURE	PR00011D 14.03 3.492e- 10 616-635
	2500303	Cytidire and deoxycytidylate deaminases zinc-binding region s.	BL00903 12.93 8.941e- 12 54-64
245	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 8.043e-
248	BL00246	Wnt-1 family proteins.	BL00246D 23.97 1.000e- 40 186-239 BL00246E 20.32 1.000e-40 305- 351 BL00246B 13.69 4.176e-36 105-140 BL00246A 15.75 2.286e- 24 70-90 BL00246C 15.56 4.857e-22 150-
250	PR00927	ADENINE NUCLEOTIDE	175 PR00927E 14.93 5.114e-
254	BL00674	TRANSLOCATOR 1 SIGNATURE AAA-protein family proteins.	10 253-275 BL00674B 4.46 1.000e-
255	PD01796	PROTEIN TRANSMEMBRANE COBALT ZINC CADMIU.	09 223-245 PD01796 15.01 6.045e-
256	BL50002	Src homology 3 (SH3) domain proteins profile.	09 61-88 BL50002B 15.18 2.800e- 10 421-435
250	PR00094	ADENYLATE KINASE SIGNATURE	PR00094C 12.94 2.200e- 18 87-104 PR00094D 12.52 2.731e-14 161- 177 PR00094A 10.31 5.500e-14 11-25 PR00094B 11.01 4.115e- 13 39-54 PR00094E 11.25 7.333e-13 178-
59	BL00892	HIT family proteins.	BL00892A 18.17 5.500e-
62	BL00388	Proteasome A-type subunits proteins.	13 60-91 BL00388A 23.14 1.000e- 40 8-54 BL00388B 31.38 3.864e-33 66-108 BL00388D 20.71 1.000e- 21 153-184 BL00388C 18.79 8.147e-16 126-
64	BL00903	Cytidine and deoxycyticylate deaminases zinc-binding	148 BL00903 12.93 5.821e- 09 91-101
	BL00107	region s.  Protein kinases ATP- binding region proteins.	BL00107B 13.31 1.529e- 09 241-257
70	BL00226	Intermediate filaments proteins.	BL00226D 19.10 1.000e- 37 362-409 BL00226B

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		
		·	23.86 8.043e-35 196- 244 BL00226C 13.23 7.000e-20 261-292 BL00226A 12.77 6.143e- 15 96-111
271	PD02952	KINASE TRANSFERASE CHOLINE PROTEIN MULTIGENE FAMI.	PD02952C 15.76 9.731e- 16 235-265 PD02952B 15.57 5.625e-09 215-
272	PD02929	ADHESION GLYCOPROTEIN PRECURSOR I.	PD02929A 28.27 1.000e- 40 106-160 PD02929B 18.36 8.800e-17 179- 199
274	BL01027	Glycosyl hydrolases family 39 proteins.	BL01027B 15.34 3.486e-
275	PR00424	ADENOSINE RECEPTOR SIGNATURE	PR00424D 14.32 6.451e-
277	BL00052	Ribosomal protein S7 proteins.	BL00052A 27.85 6.000e- 13 137-184 BL00052B 15.17 5.143e-12 208- 235
279	BL00790	Receptor tyrosine kinase class V proteins.	BL00790N 13.25 5.659e- 13 267-294
280	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319D 11.64 6.625e- 23 107-125 PR00319C 13.41 1.000e-21 89-105 PR00319A 15.27 8.364e- 21 51-68 PR00319B
281	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	11.47 8.200e-19 70-85 PR00319D 11.64 6.625e- 23 94-112 PR00319C 13.41 1.000e-21 76-92 PR00319A 15.27 8.364e- 21 38-55 PR00319B
287	PF00929	Exonuclease.	11.47 8.200e-19 57-72 PF00929D 16.17 7.366e-
291	BL00326	Tropomyosins proteins.	09 149-163 BL00326A 14.01 2.360e- 09 93-127
292	BL00326	Tropomyosins proteins.	BL00326A 14.01 2.360e-
294	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	09 93-127 PD00066 13.92 8.714e- 12 203-216
295	BLUOUZA	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 5.500e- 15 322-339 BL00028 16.07 9.471e-14 433- 450 BL00028 16.07 4.600e-13 648-665 BL00028 16.07 5.500e- 13 760-777 BL00028 16.07 9.550e-13 788- 805 BL00028 16.07 3.348e-12 704-721 BL00028 16.07 6.478e- 12 461-478 BL00028 16.07 8.435e-12 844- 861 BL00028 16.07 1.692e-11 593-610 BL00028 16.07 2.038e- 11 211-228 BL00028 16.07 5.154e-11 732- 749 BL00028 16.07 5.846e-11 377-394 BL00028 16.07 6.885e- 11 816-833 BL00028 16.07 7.231e-11 676-

SEQ ID N	O: ACCESSION NO.	DESCRIPTION	RESULTS*
			BL00028 16.07 4.086e- 09 517-534 BL00028 16.07 7.429e-09 489- 506
296	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 8.333e- 16 111-136 BL00215A 15.82 2.723e-11 10-35 BL00215B 10.44 9.526e- 11 152-165 BL00215B 10.44 7.375e-10 59-72 BL00215A 15.82 9.824e-
302	PF00953	Glycosyl transferase.	10 205-230 PF00953C 19.70 8.773e- 34 236-269 PF00953A 19.68 5.000e-25 102- 129 PF00953B 6.17
304	PF00152	tRNA synthetases class	1.000e-13 182-194 PF00152D 21.30 8.364e- 28 422-461 PF00152C 28.03 9.250e-21 220- 257 PF00152B 15.67 2.658e-13 159-184 PF00152A 19.68 5.714e-
305	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	11 44-67 PD01066 19.43 8.250e- 35 37-76
305	PD02784	PROTEIN NUCLEAR RIBONUCLEOPROTEIN.	PD02784B 26.46 5.840e-
307	PR00454	ETS DOMAIN SIGNATURE	09 92-135 PR00454C 11.24 7.808e- 09 1167-1186
308	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237E 13.03 5.091e- 13 188-212 PR00237G 19.63 7.207e-13 268- 295 PR00237A 11.48 4.375e-11 24-49 PR00237C 15.69 3.057e- 10 101-124 PR00237D 8.94 4.750e-10 137-159 PR00237F 13.57 5.364e- 10 230-255 PR00237B 13.50 9.438e-10 57-79
309	BL00522	DNA polymerase family X proteins.	BL00522C 11.90 7.577e- 24 315-339 BL00522F 14.90 1.310e-15 470- 494 BL00522A 25.52 1.265e-14 179-226 BL00522E 19.63 8.615e- 14 430-460 BL00522B 27.30 9.625e-12 267- 313
	BL00326	Tropomyosins proteins.	BL00326D 8.76 5.235e- 10 856-897
312	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 4.706e- 14 151-174 BL00290B 13.17 9.000e-12 211- 229
313	BL00345	Ets-domain proteins.	BL00345B 21.28 1.000e- 40 34-85 BL00345A 13.96 9.217e-16 1-20
315	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 5.091e- 15 63-76
317	BL01020	SAR1 family proteins.	BL01020C 15.35 3.198e- 17 79-130
318	BL00216	Sugar transport proteins.	BL00216B 27.64 4.696e-
120	PR00109	TYROSINE KINASE CATALYTIC DOMAIN	11 164-214 PR00109B 12.27 4.814e-

SEQ ID NO:	ACCESSION No.	DESCRIPTION	RESULTS*
	DY 00000	SIGNATURE	
321	BL00027	'Homeobox' domain proteins.	BL00027 26.43 5.688e- 10 329-372
322	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 8.765e- 12 558-577
324	BL01241	Link domain proteins.	BL01241 35.81 8.313e- 30 183-236 BL01241 35.81 3.222c-13 282- 335
326	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 4.000e- 12 515-566 BL00412D 16.54 5.705e-11 516- 567 BL00412D 16.54 7.848e-10 518-569 BL00412D 16.54 1.827e- 09 514-565 BL00412D 16.54 1.918e-09 513- 564 BL00412D 16.54 2.102e-09 520-571
328	BL00232	Cadherins extracellular repeat proteins domain proteins.	BL00232B 32.79 9.557e- 20 151-199 BL00232B 32.79 2.246e-18 41-89 BL00232B 32.79 5.985e- 18 370-418 BL00232B 32.79 5.500e-16 258- 306 BL00232B 32.79 9.384e-15 475-523 BL00232C 10.65 2.537e- 12 256-274 BL00232C 10.65 4.326e-11 368- 386 BL00232C 10.65 7.261e-11 473-491 BL00232C 10.65 7.457e- 11 39-57
330	PR00454	ETS DOMAIN SIGNATURE	PR00454C 11.24 7.808e-
331	BL00598	Chromo domain proteins.	BL00598 14.45 8.393e- 18 27-49
333	BL01016	Glycoprotease family proteins.	BL01016C 22.84 3.925e- 32 70-115 BL01016E 14.88 5.286e-19 149- 177 BL01016H 13.71 7.577e-13 291-301 BL01016D 8.86 3.298e- 11 127-140 BL01016G 7.14 5.622e-10 261-271 BL01016A 5.65 7.167e- 10 4-19 BL01016F 13.34 1.563e-09 200- 212 BL01016B 8.93 8.855e-09 38-50
339	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 5.500e- 11 17-61
340	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 1.231e- 33 10-49
341	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 5.042e- 09 55-109
342	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 2.400e- 30 16-55
343	DM00031	IMMUNOGLOBULIN V REGION.	DM00031A 16.80 1.000e- 40 20-68
346	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 4.764e- 11 135-154
347	PR00109	TYROSINE KINASE	PR00109B 12.27 4.764e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
<del></del>	10.	CATALYTIC DOMAIN	11 135-154
		SIGNATURE	
351	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.	BL01187B 12.04 1.783e- 13 100-116 BL01187B 12.04 8.435e-13 276- 292 BL01187B 12.04 8.800e-11 13-29 BL01187B 12.04 7.429e- 10 54-70 BL01187B 12.04 5.725e-09 231- 247 BL01187A 9.98 7.000e-09 255-267
352	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 5.950e- 10 366-379 PD00078B 13.14 4.522e-09 168- 181
354	BL00380	Rhodanese proteins.	BL00380F 9.76 6.694e-
355	PF00628	PHD-finger.	PF00628 15.84 1.000e-
356	PR00587	SOMATOSTATIN RECEPTOR TYPE 1 SIGNATURE	PR00587A 8.06 9.700e-
359	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 4.462e- 15 261-274 PD00066 13.92 6.500e-13 233- 246 PD00066 13.92 4.300e-09 289-302
361	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 9.604e- 13 54-109 PF00791B 28.49 1.095e-12 21-76 PF00791A 27.85 1.432e- 09 71-126 PF00791B 28.49 7.440e-09 184- 239
362	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 2.273e- 11 279-334
363	PR00450	RECOVERIN FAMILY SIGNATURE	PR00450C 12.22 5.080e- 10 73-95 PR00450C 12.22 3.278e-09 109- 131
364	PF00242	DNA polymerase (viral) N-terminal domain proteins.	PF00242Q 13.51 2.328e- 09 22-68
365	PF00242	DNA polymerase (viral) N-terminal domain proteins.	PF00242Q 13.51 2.328e- 09 22-68
366	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 6.644e- 09 1038-1092
367	PR.00019	LEUCINE-RICH REPEAT SIGNATURE	PRO0019B 11.36 1.360e- 09 229-243 PR00019B 11.36 6.040e-09 91-105 PR00019A 11.19 8.667e- 09 370-384
368	PR00011	TYPE III EGF-LIKE SIGNATURE	PRO0011D 14.03 9.000e- 15 30-49 PRO0011A 14.06 9.830e-15 30-49 PRO0011B 13.08 4.500e- 14 30-49 PRO0011C 24.25 5.143e-09 6-35
369	BL01032	Protein phosphatase 2C proteins.	BL01032H 11.25 4.150e-
372	BL00478	LIM domain proteins.	BL00478B 14.79 7.750e-
373	PD01066	ZINC-FINGER METAL-	12 410-425 PD01066 19.43 9.757e- 34 26-65
376	PR00170	BINDING NU. SODIUM CHANNEL SIGNATURE	PR00170E 6.48 2.739e-

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO -		
380	BL00107	Protein kinases ATP-	10 88-118
	1-200207	binding region proteins.	BL00107A 18.39 1.000e- 23 276-307 BL00107B
		Total Process.	13.31 1.692e-12 342-
			358
381	BL00455	Putative AMP-binding	BL00455 13.31 5.714e-
		domain proteins.	12 50-66
382	PR00624	HISTONE H5 SIGNATURE	PR00624G 4.08 4.900e-
			09 524-544
384	PD00078	REPEAT PROTEIN ANK	PD00078B 13.14 5.950e-
		NUCLEAR ANKYR.	10 366-379 PD00078B
	-	j	13.14 4.522e-09 168-
385			181
303	PR00511	TEKTIN SIGNATURE	PR00511D 7.11 5.371e-
386	PD02870		09 67-80
300	PD02870	RECEPTOR INTERLEUKIN-1	PD02870B 18.83 6.000e-
388	PD00066	PRECURSOR.	10 97-130
200	FD00008	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 5.000e-
389	BL00290	Immunoglobulins and	13 516-529
		major histocompatibility	BL00290A 20.89 7.657e-
	1	complex proteins.	09 151-174
390	BL00215	Mitochondrial energy	BL00215A 15.82 5.200e-
		transfer proteins.	15 221-246 BL00215A
			15.82 7.618e-14 20-45
			BL00215A 15.82 8.851e-
		l	11 123-148 BL00215B
			10.44 9.526e-11 69-82
			BL00215B 10.44 7.300e-
•	}		09 272-285 BL00215B
	1		10.44 8.500e-09 165-
394	BL00674	AAA-protein family	178
	2200074	proteins.	BL00674B 4.46 2.723e-
397	PR00048	C2H2-TYPE ZINC FINGER	16 299-321
		SIGNATURE	PR00048A 10.52 8.579e- 11 141-155
398	PR00761	BINDIN PRECURSOR	PR00761B 9.93 6.764e-
		SIGNATURE	09 55-74
399	BL00240	Receptor tyrosine kinase	BL00240B 24.70 7.907e-
		class III proteins.	10 118-142
401	PF00676	Dehydrogenase E1	PF00676B 24.71 8.071e-
		component.	18 331-369 PF00676D
		·	14.40 3.854e-15 486-
			506 PF00676C 16.88
402	DIOOFIA		9.182e-14 454-478
7V4	BL00514	Fibrinogen beta and	BL00514C 17.41 4.673e-
		gamma chains C-terminal	28 4432-4469 BL00514G
		domain proteins.	15.98 6.092e-14 4555-
			4585 BL00514D 15,35
		1	2.532e-12 4473-4486
l		1	BL00514F 11.65 4.288e-
1	,	1	10 4519-4534 BL00514H 14.95 4.955e-10 4584-
		]	4609
403	PF00992	Troponin.	PF00992A 16.67 5.974e-
			09 105-140
104	PR00019	LEUCINE-RICH REPEAT	PR00019B 11.36 1.450e-
Į.		SIGNATURE	10 73-87 PR00019A
		1	11.19 8.043e-10 76-90
1			PR00019B 11.36 1.000e-
1		1	09 50-64 PR00019B
05	D1 000==	<u> </u>	11.36 1.000e-09 96-110
05	BL00232	Cadherins extracellular	BL00232B 32.79 9.557e-
1		repeat proteins domain	20 139-187 BL00232B
1		proteins.	32.79 2.246e-18 29-77
ı			BL00232B 32.79 5.985e-
		1	18 358-406 BL00232B
		I I	32.79 5.500e-16 246-

NO.     294 BL00232B 32.79   9.384e-15 463-511   BL00232C 10.55 2.537c-12 244-262 BL00232C 10.55 2.537c-12 244-262 BL00232C 10.55 3.74 BL00232C 10.65 7.457c-11 266-13 161-479   BL00232C 10.65 7.457c-11 27-45   BL00232C 10.65 7.457c-11 27-45   BL00232C 10.65 7.457c-11 27-45   BL00232C 10.65 7.457c-11 27-45   BL00232C 10.65 7.457c-11 27-45   BL00232C 10.65 7.457c-11 27-45   BL00232C 10.65 7.457c-11 27-45   BL00232C 10.65 7.457c-11 27-45   BL00232C 10.65 7.457c-11 27-45   BL0023C 10.65 7.457c-11 27-45   BL0023C 10.65 7.457c-11 27-45   BL0023C 10.65 7.457c-11 27-45   BL0026C 11 27-45   BL0026C 11 27-45   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-27   BL0026C 11 27-28   BL0026C 11 27-28   BL0026C 11 27-28   BL0026C 11 27-28   BL0026C 11 27-28   BL0026C 11 27-28   BL0026C 11 27-28   BL0026C 11 27-28   BL0026C 11 27-28   BL0026C 11 27-28   BL0026C 11	SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
9.384e-15 463-511	ONG ID NO:		DESCRIPTION	
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12 244-262 BL00232C			1	
10.65 4.326e-11 356- 374 BL00232C 10.65 7.457e- 11 27-45   11 27-45   11 27-45   11 27-45   11 27-45     407				
April		1	1	
A07				
### BL00232C 10.65 7.457e.  ### 407   PF00426   Outer Capsid protein VP4 (Hemagglutinin).  ### 409   BL01160   Kinesin light chain repeat proteins.  ### 410   BL00741   Guanine-nuclectide diasociation stimulators CCC24 family sign.  ### 410   PF00646   F-box domain proteins.   DF00741B 14.27 2.731c-domain proteins.   O9 126-180    ### 412   BL00603   Thymidine kinase   BL00741B 14.27 2.731c-domain proteins.   DF00646A 14.37 6.344c-domain proteins.   DF00646A 14.37 6.344c-domain proteins.   DF00646A 14.37 8.500c-cellular-type proteins.   DF00646A 14.37 8.500c-cellular-type proteins.   DF00646A 14.37 8.500c-cellular-type proteins.   DF00646B 36.29 3.571c-synthase subdomain proteins.   DF00646B 36.29 3.571c-synthase subdomain proteins.   DF00646B 36.29 3.571c-synthase subdomain proteins.   DF00741B 28.49 7.555c-domain proteins.   DF00791B 28.49 7.555c-domain proteins.   DF00791B 28.49 7.555c-domain proteins.   DF00791B 28.49 7.555c-domain proteins.   DF00791B 28.49 7.555c-domain proteins.   DF00791B 28.49 7.818c-domain proteins.   DF00791B 28.49 7.818c-domain proteins.   DF00791B 28.49 7.818c-domain proteins.   DF00791B 28.49 7.818c-domain proteins.   DF00791B 28.49 7.818c-domain proteins.   DF00791B 28.49 7.818c-domain proteins.   DF00791B 28.49 7.818c-domain proteins.   DF00791B 28.49 7.818c-domain proteins.   DF00791B 28.49 7.818c-domain proteins.   DF00791B 28.49 7.818c-domain proteins.   DF00791B 28.49 7.818c-domain proteins.   DF00791B 28.49 7.818c-domain proteins.   DF00791B 28.49 7.818c-domain proteins.   DF00791B 28.49 7.818c-domain proteins.   DF00791B 28.49 7.818c-domain proteins.   DF00791B 28.49 7.818c-domain proteins.   DF00791B 28.49 7.818c-domain proteins.   DF00791B 28.49 7.818c-domain proteins.   DF00791B 28.49 7.818c-domain proteins.   DF00791B 28.49 7.818c-domain proteins.   DF00791B 28.49 7.818c-domain proteins.   DF00791B 28.49 7.818c-domain proteins.   DF00791B 28.49 7.818c-domain proteins.   DF00791B 28.49 7.818c-domain proteins.   DF00791B 28.49 7.818c-domain proteins.   DF00791B 28.49 7.8				
11 27-45				
More				
Glemagglutinin	7.5			
BL01160   Kinesin light chain   repeat proteins.   09 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 126-180   19 1	407	PF00426		
Repeat proteins.   09 126-180			(Hemagglutinin).	
BL00741   Guanine-nucleotide disocciation etimulators   CDC24 family sign.	409	BL01160	Kinesin light chain	
dissociation stimulators				
CDC24 family sign.	410	BL00741		
### STONS AND STANDARD PROOFS A PROOFS A PROOFS A PROOFS A PROOFS B PROOFS A PROOFS A PROOFS A PROOFS B PROOFS A PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS B PROOFS				09 252-275
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Calbular-type proteins.   09 542-557	<del> </del>			
BL00866   Carbamoyl-phosphate synthase subdomain proteins.   31 245-291 BL00866C   32.25 9.000e-25 331-365   32.45-291 BL00866C   32.25 9.000e-25 331-366   36.27 9.552-3156   36.25 9.000e-25 331-366   36.27 9.552-316   36.25 9.000e-25 331-366   36.27 9.550-602   36.25 9.000e-25 331-366   36.27 9.550-602   36.25 9.000e-25 9.000e-25 9.000e-25 9.000e-25 9.000e-25 9.000e-25 9.000e-26   36.26 9.000e-25 9.000e-25 9.000e-25 9.000e-25 9.000e-25 9.000e-25 9.000e-25 9.000e-25 9.000e-25 9.000e-25 9.000e-25 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.000e-26 9.0	412	BL00603		
### Synthase Subdomain proteins.  ### Synthase Subdomain proteins.  ### ADLLUSCAN RHODOPSIN C-				· I
### PRO0239 ### MOLLUSCAN RHODOPSIN C-TERMINAL TAIL SIGNATURE 09 590-602 ### PRO0239E 1.58 6.114e-09 590-602 ### PRO0239E 1.58 6.114e-09 590-602 ### PRO0239E 1.58 6.114e-09 590-602 ### PRO0239E 1.58 6.114e-09 590-602 ### PRO0239E 1.58 6.114e-09 590-602 ### PRO0239E 1.58 6.114e-09 590-602 ### PRO0239E 1.58 6.114e-09 590-602 ### PRO0239E 1.58 6.114e-09 590-602 ### PRO0239E 1.58 6.114e-09 590-602 ### PRO0239E 1.58 6.114e-09 590-602 ### PRO0239E 1.58 6.114e-09 590-602 ### PRO0239E 1.58 6.114e-09 590-602 ### PRO0239E 1.58 6.114e-09 590-602 ### PRO0239E 1.58 6.114e-09 590-602 ### PRO0239E 1.58 6.114e-09 590-602 ### PRO0239E 1.58 6.114e-09 590-602 ### PRO0239E 1.58 6.114e-09 590-602 ### PRO0239E 1.58 6.114e-09 590-602 ### PRO0239E 1.58 6.114e-09 590-602 ### PRO023B 1.24-1 56-111 ### PRO023B 1.58 6.114e-09 590-602 ### PRO023B 1.58 6.114e-09 590-903 ### PRO023B 1.58 6.114e-09 590-903 ### PRO023B 1.58 6.114e-09 590-903 ### PRO023B 1.58 6.114e-09 590-903 ### PRO023B 1.58 6.114e-09 590-903 ### PRO023B 1.58 6.114e-09 590-903-903-903 ### PRO023B 1.65 7.652e-12 169-185 ### PRO023B 1.65 7.652e-12 169-185 ### PRO023B 1.65 7.652e-12 169-185 ### PRO023B 1.65 7.652e-12 169-185 ### PRO023B 1.65 7.652e-12 169-185 ### PRO023B 1.65 7.652e-12 169-185 ### PRO023B 1.65 7.652e-12 169-185 ### PRO023B 1.65 7.652e-12 169-185 ### PRO023B 1.65 7.652e-12 169-185 ### PRO023B 1.65 7.652e-12 169-185 ### PRO023B 1.65 7.652e-12 169-185 ### PRO023B 1.65 7.652e-12 169-185 ### PRO023B 1.65 7.652e-12 169-185 ### PRO023B 1.65 7.652e-12 169-185 ### PRO023B 1.65 7.652e-12 169-185 ### PRO023B 1.65 7.652e-12 169-185 ### PRO023B 1.65 7.652e-12 169-185 ### PRO023B 1.65 7.652e-12 169-185 ### PRO023B 1.65 7.652e-12 169-185 ### PRO023B 1.65 7.652e-12 169-185 ### PRO023B 1.65 7.652e-12 169-185 ### PRO023B 1.65 7.652e-12 169-185 ### PRO023B 1.65 7.652e-12 169-185 ### PRO023B 1.65 7.652e-12 169-185 ### PRO023B 1.65 7.652e-12 169-185 ### PRO023B 1.65 7.652e-12 169-185 ### PRO023B 1.65 7.652e-12 169-185 ### PRO023B 1.65 7.652e-12 169-185 ### PRO023B 1.65 7.652e-12 169	415	BL00866		BL00866B 36.29 3.571e-
### MOLLUSCAN RHODOPSIN C- TERMINAL TAIL SIGNATURE  ### PR00239		1		
### PRO0239 MOLLUSCAN RHODOPSIN C- TERMINAL TAIL SIGNATURE  #### PF00791 Domain present in ZO-1 and Unc5-like netrin receptors.  #### PF00791 28.49 7.955e- 14 23-78 PF00791B 28.49 7.955e- 14 23-78 PF00791B 28.49 3.653e-12 273- 328 PF00791B 28.49 7.818e- 11 89-144 PF00791B 28.49 1.524e-10 56-111 PF00791C 20.98 3.559e- 09 37-76 PF00791C 20.98 5.235e-09 317- 209 PF00791C 20.98 5.235e-09 317-20 PF00791B 28.49 6.202e- 09 189-244 PF00791B 28.49 7.028e-09 435- 490 PF00791B 28.49 6.202e- 09 189-244 PF00791B 28.49 7.028e-09 435- 490 PF00791B 28.49 6.202e- 09 189-244 PF00791B 28.49 7.028e-09 435- 490 PF00791B 28.49 6.202e- 09 189-244 PF00791B 28.49 7.028e-09 435- 490 PF00791B 28.49 6.202e- 09 189-244 PF00791B 28.49 7.028e-09 435- 490 PF00791B 28.49 6.202e- 09 189-244 PF00791B 28.49 7.028e-09 435- 490 PF00791B 28.49 6.202e- 09 189-244 PF00791B 28.49 7.028e-09 435- 490 PF00791B 28.49 6.202e- 09 189-244 PF00791B 28.49 7.028e-09 435- 490 PF00791B 28.49 6.202e- 09 189-244 PF00791B 28.49 7.028e-09 435- 490 PF00791B 28.49 6.202e- 09 189-244 PF00791B 28.49 7.028e-09 435- 490 PF00791B 28.49 6.202e- 09 189-244 PF00791B 28.49 7.028e-09 435- 490 PF00791B 28.49 6.202e- 09 189-244 PF00791B 28.49 7.028e-09 435- 490 PF00791B 28.49 6.202e- 09 189-244 PF00791B 28.49 7.028e-09 435- 490 PF00791B 28.49 6.202e- 09 189-244 PF00791B 28.49 7.028e-09 435- 48.602e-09 9F00791B 28.49 6.202e- 09 189-244 PF00791B 28.49 7.028e-09 435- 490 PF00791B 28.49 6.202e- 09 189-244 PF00791B 28.49 7.028e-09 435- 490 PF00791B 28.49 6.202e- 09 189-244 PF00791B 28.49 7.028e-09 435- 490 PF00791B 28.49 6.202e- 09 189-244 PF00791B 28.49 7.028e-09 9F00791B 28.49 7.028e-09 9F00791B 28.49 7.028e-09 9F00791B 28.49 7.028e-09 9F00791B 28.49 7.028e-09 9F00791B 28.49 7.028e-09 9F00791B 28.49 7.028e-09 9F00791B 28.49 7.028e-09 9F00791B 28.49 7.028e-09 9F00791B 28.49 7.028e-09 9F00791B 28.49 7.028e-09 9F00791B 28.49 7.028e-09 9F00791B 28.49 7.028e-09 9F00791B 28.49 7.028e-09 9F00791B 28.49 7.028e-09 9F00791B 28.49 7.028e-09 9F00791B 28.49 7.028e-09 9F00791B 28.49 7.028e-09 9F007		1	proteins.	23.26 9.000e-25 331-
### TERMINAL TAIL SIGNATURE   09 590-602   49 7.9556   ### TERMINAL TAIL SIGNATURE   09 590-602   49 7.9556   ### TERMINAL TAIL SIGNATURE   120-1   23-48 PF00791B 28.49 7.9556   ### TERMINAL TAIL SIGNATURE   14 23-78 PF00791B 28.49   ### TERMINAL TAIL SIGNATURE   14 23-78 PF00791B 28.49 7.9556   ### TERMINAL TAIL SIGNATURE   14 23-78 PF00791B 28.49 7.9556   ### TERMINAL TAIL SIGNATURE   14 23-78 PF00791B 28.49 7.028-10 970791B 28.49 7.018-11 156-211   ### PF00791B 28.49 7.018-11 156-211   ### PF00791C 20.98 5.2356-09 381-420   ### PF00791C 20.98 5.2356-09 381-420   ### PF00791B 28.49 6.2026-09 189-244 PF00791B 28.49 6.6798-09 367-422   ### TERMINAL TAIL SIGNATURE   PR00109D 17.04 5.8816-1090   ### TERMINAL TAIL SIGNATURE   13 11-40   ### TERMINAL TAIL SIGNATURE   15 11 31-40   ### TERMINAL TAIL SIGNATURE   PR00109D 17.04 5.8816-1090   ### TERMINAL TAIL SIGNATURE   PR00109D 17.04 5.8816-1090   ### TERMINAL TAIL SIGNATURE   PR00109D 17.04 5.8816-1090   ### TERMINAL TAIL SIGNATURE   PR00109D 17.04 5.8816-1090   ### TERMINAL TAIL SIGNATURE   PR00109D 17.04 5.8816-1090   ### TERMINAL TAIL SIGNATURE   PR00109D 17.04 5.8816-1090   ### TERMINAL TAIL SIGNATURE   PR00109D 17.04 5.8816-1090   ### TERMINAL TAIL SIGNATURE   PR00109D 17.04 5.8816-1090   ### TERMINAL TAIL SIGNATURE   PR00109D 17.04 5.8816-1090   ### TERMINAL TAIL SIGNATURE   PR00109D 17.04 5.8816-1090   ### TERMINAL TAIL SIGNATURE   PR00109D 17.04 5.8816-1090   ### TERMINAL TAIL SIGNATURE   PR00109D 17.04 5.8816-1090   ### TERMINAL TAIL SIGNATURE   PR00109D 17.04 5.8816-1090   ### TERMINAL TAIL SIGNATURE   PR00109D 17.04 5.8816-1090   ### TERMINAL TAIL SIGNATURE   PR00109D 17.04 5.8816-1090   ### TERMINAL TAIL SIGNATURE   PR00109D 17.04 5.8816-1090   ### TERMINAL TAIL SIGNATURE   PR00109D 17.04 5.8816-1090   ### TERMINAL TAIL SIGNATURE   PR00109D 17.04 5.8816-1090   ### TERMINAL TAIL SIGNATURE   PR00109D 17.04 5.8816-1090   ### TERMINAL TAIL SIGNATURE   PR00109D 17.04 5.8816-1090   ### TERMINAL TAIL SIGNATURE   PR00109D 17.04 5.8816-1090   ### TERMINAL TAIL S				1
### PF00791 Domain present in ZO-1 and Unc5-like netrin receptors.  #### PF00791 PF00791B 28.49 7.955e-10	41.8	PR00239		
and Unc5-like netrin receptors.  28.49 3.653e-12 273-328 PF00791B 28.49 4.273e-11 156-211 PF00791B 28.49 7.818e-11 89-144 PF00791B 28.49 7.818e-11 89-144 PF00791B 28.49 7.818e-11 89-144 PF00791B 28.49 7.818e-11 89-144 PF00791B 28.49 7.526e-09 37-76 PF00791C 20.98 5.235e-09 370-76 PF00791C 20.98 5.235e-09 381-420 PF00791B 28.49 6.202e-09 189-244 PF00791B 28.49 6.202e-09 189-244 PF00791B 28.49 8.679e-09 367-422 PF00791B 28.49 8.679e-09 367-422 PF00791B 28.49 8.679e-09 367-422 PF00791B 28.49 8.679e-09 367-422 PF00791B 28.49 8.679e-09 367-422 PF00109 TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE PROTEINASE. DM00892C 23.55 7.207e-28 1645-1679 PF00109D 17.04 5.881e-10 228-251 PF00109D 17.04 5.881e-10 228-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.881e-10 288-251 PF00109D 17.04 5.			1	
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328 PF00791B 28.49				
### ### ##############################			receptors.	
PF00791B 28.49 7.818e- 11 89-144 PF00791B 28.49 1.524e-10 56-111 PF00791C 20.98 3.559e- 09 37-76 PF00791C 20.98 5.235e-09 170- 209 PF00791C 20.98 5.235e-09 381-420 PF00791B 28.49 6.202e- 09 189-244 PF00791B 28.49 7.028e-09 435- 490 PF00791B 28.49 6.202e- 09 189-244 PF00791B 28.49 7.028e-09 435- 490 PF00791B 28.49 424 DM00892 3 RETROVIRAL PROTEINASE. DM0892C 23.55 7.207e- 28 1645-1679 425 PR00109 TYROSINE KINASE PR00109D 17.04 5.881e- CATALYTIC DOMAIN SIGNATURE DM00892 Zinc finger, C3HC4 type (RING finger), proteins. 11 31-40 431 BL00039 DEAD-box subfamily ATP- dependent helicases proteins. 12 14.40 EL00039D 21.67 1.844e- dependent helicases proteins. 18.44 5.615e-19 205- 244 BL00039B 19.19 8.920e-16 251-277 BL00039C 15.63 5.781e- 15 333-357 432 PR00828 FORMIN SIGNATURE PR00452B 11.65 7.652e- 12 169-185 433 PR00828 FORMIN SIGNATURE PR0082BB 5.23 8.218e- 10 382-405 436 BL00415 Synapsins proteins. BL00415N 4.29 8.643e- 11 195-239 BL00415N 4.29 3.036e-09 809-853 443 PR00834 HTRA/DEGO PROTEASE PR00834F 10.91 6.040e-				
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### BL00518   Zinc finger, C3HC4 type (RING finger), proteins.   11 31-40   ### BL00039   DEAD-box subfamily ATP- dependent helicases   14 490-536 BL00039A   ### proteins.   18.44 5.615e-19 205-244 BL00039B 19.19   ### 8.920e-16 251-277   ### BL00039C 15.63 5.781e-15 333-357   ### BR000452   SH3 DOMAIN SIGNATURE   PR00452B 11.65 7.652e-12 169-185   ### 433   PR00828   FORMIN SIGNATURE   PR00828B 5.23 8.218e-10 382-405   ### 436   BL00415   Synapsins proteins.   BL00415N 4.29 8.643e-11 195-239 BL00415N 4.29 3.036e-09 809-853   ### 443   PR00834   HTRA/DEGQ PROTEASE   PR00834F 10.91 6.040e-14				10 228-251
(RING finger), proteins. 11 31-40  BL00039  DEAD-box subfamily ATP- dependent helicases proteins. 18.44 5.615e-19 205- 244 BL00039B 19.19 8.920e-16 251-277 BL00039C 15.63 5.781e- 15 333-357  PR00452  SH3 DOMAIN SIGNATURE PR00452B 11.65 7.652e- 12 169-185  433 PR00828 FORMIN SIGNATURE PR00828B 5.23 8.218e- 10 382-405  BL00415 Synapsins proteins. BL00415N 4.29 8.643e- 11 195-239 BL00415N 4.29 3.036e-09 809-853  443 PR00834 HTRA/DEGQ PROTEASE PR00834F 10.91 6.040e-	400	1 2 2 2 2 2 2		
### BL00039 DEAD-box subfamily ATP- dependent helicases   34 490-536 BL00039A     18.44 5.615e-19 205-244 BL00039E 19.19     8.920e-16 251-277     8.920e-16 251-277     8.920e-16 251-277     8.920e-16 251-277     8.920e-16 251-277     8.920e-16 251-277     8.920e-16 251-277     8.920e-16 251-277     8.920e-16 251-277     8.920e-16 251-277     8.920e-16 251-277     8.920e-16 251-277     8.920e-16 251-277     8.920e-16 251-277     8.920e-16 251-277     8.920e-16 251-277     8.920e-16 251-277     8.920e-16 251-277     8.920e-16 251-277     8.920e-16 251-277     8.920e-16 251-277     8.920e-16 251-277     8.920e-16 251-277     8.920e-16 251-277     8.920e-16 251-277     8.920e-16 251-277     8.920e-16 251-277     8.920e-16 251-277     8.920e-16 251-277     8.920e-16 251-277     8.920e-16 251-277     8.920e-16 251-277     8.920e-16 251-277     8.920e-16 251-277     8.920e-16 251-277     8.920e-16 251-277     8.920e-16 251-277     8.920e-16 251-277     8.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-16 251-277     9.920e-	429	BL00518		•
dependent helicases   34 490-536 BL00039A   18.44 5.615e-19 205-244 BL00039B 19.19   8.920e-16 251-277   BL00039C 15.63 5.781e-15 333-357   BL00039C 15.63 5.781e-15 333-357   BL000452B 11.65 7.652e-12 169-185   BL00415N SIGNATURE   PR00828B 5.23 8.218e-10 382-405   BL00415N 4.29 8.643e-11 195-239 BL00415N 4.29 3.036e-09 809-853   BL00415N 4.29 3.036e-09 809-853   A43   PR00834   HTRA/DEGQ PROTEASE   PR00834F 10.91 6.040e-11 221-234   BL00415N 4.29 8.643e-11 221-234   BL00415N 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.29 8.643e-11 4.2	43.1	1	(RING tinger), proteins.	
PRO0452 SH3 DOMAIN SIGNATURE PR00452B 11.65 7.652e- 12 169-185  433 PR00828 FORMIN SIGNATURE PR00828B 5.23 8.218e- 10 382-405  436 BL00415 Synapsins proteins. BL00415N 4.29 8.643e- 11 195-239 BL00415N 4.29 3.036e-09 809-853  443 PR00834 HTRA/DEGQ PROTEASE PR00834F 10.91 6.040e- FAMILY SIGNATURE 11 221-234	431	BP00039		
244 BL00039B 19.19 8.920e-16 251-277 BL00039C 15.63 5.781e- 15 333-357 432 PR00452 SH3 DOMAIN SIGNATURE PR00452B 11.65 7.652e- 12 169-185 433 PR00828 FORMIN SIGNATURE PR00828B 5.23 8.218e- 10 382-405 436 BL00415 Synapsins proteins. BL00415N 4.29 8.643e- 11 195-239 BL00415N 4.29 3.036e-09 809-853 443 PR00834 HTRA/DEGQ PROTEASE PR00834F 10.91 6.040e- FAMILY SIGNATURE 11 221-234				
8.920e-16 251-277 BL00039C 15.63 5.781e- 15 333-357  432 PR00452 SH3 DOMAIN SIGNATURE PR00452B 11.65 7.652e- 12 169-185  433 PR00828 FORMIN SIGNATURE PR00828B 5.23 8.218e- 10 382-405  436 BL00415 Synapsins proteins. BL00415N 4.29 8.643e- 11 195-239 BL00415N 4.29 3.036e-09 809-853  443 PR00834 HTRA/DEGQ PROTEASE PR00834F 10.91 6.040e- FAMILY SIGNATURE 11 221-234			proteins.	
### BL00039C 15.63 5.781e- ### 15 333-357  #### 15 333-357  #### 15 333-357  #### 16				
15 333-357  432 PR00452 SH3 DOMAIN SIGNATURE PR00452B 11.65 7.652e- 12 169-185  433 PR00828 FORMIN SIGNATURE PR00828B 5.23 8.218e- 10 382-405  436 BL00415 Synapsins proteins. BL00415N 4.29 8.643e- 11 195-239 BL00415N 4.29 3.036e-09 809-853  443 PR00834 HTRA/DEGQ PROTEASE PR00834F 10.91 6.040e- FAMILY SIGNATURE 11 221-234				
432 PR00452 SH3 DOMAIN SIGNATURE PR00452B 11.65 7.652e- 12 169-185 433 PR00828 FORMIN SIGNATURE PR00828B 5.23 8.218e- 10 382-405 436 BL00415 Synapsins proteins. BL00415N 4.29 8.643e- 11 195-239 BL00415N 4.29 3.036e-09 809-853 443 PR00834 HTRA/DEGQ PROTEASE PR00834F 10.91 6.040e- FAMILY SIGNATURE 11 221-234		1		-
12 169-185     12 169-185				
433 PR00828 FORMIN SIGNATURE PR00828B 5.23 8.218e- 10 382-405 436 BL00415 Synapsins proteins. BL00415N 4.29 8.643e- 11 195-239 BL00415N 4.29 3.036e-09 809-853 443 PR00834 HTRA/DEGQ PROTEASE PR00834F 10.91 6.040e- FAMILY SIGNATURE 11 221-234	432	PR00452	SH3 DOMAIN SIGNATURE	
10 382-405  436 BL00415 Synapsins proteins. BL00415N 4.29 8.643e- 11 195-239 BL00415N 4.29 3.036e-09 809-853  443 PR00834 HTRA/DEGQ PROTEASE PR00834F 10.91 6.040e- FAMILY SIGNATURE 11 221-234				
436 BL00415 Synapsins proteins. BL00415N 4.29 8.643e- 11 195-239 BL00415N 4.29 3.036e-09 809-853 443 PR00834 HTRA/DEGQ PROTEASE PR00834F 10.91 6.040e- FAMILY SIGNATURE 11 221-234	433	PR00828	FORMIN SIGNATURE	
11 195-239 BL00415N   4.29 3.036e-09 809-853   443   PR00834   HTRA/DEGQ PROTEASE   PR00834F 10.91 6.040e-   FAMILY SIGNATURE   11 221-234		<u>L</u>		10 382-405
11 195-239 BL00415N   4.29 3.036e-09 809-853   443   PR00834   HTRA/DEGQ PROTEASE   PR00834F 10.91 6.040e-   FAMILY SIGNATURE   11 221-234	436	BL00415	Synapsins proteins.	BL00415N 4.29 8.643e-
4.29 3.036e-09 809-853 443 PR00834 HTRA/DEGQ PROTEASE PR00834F 10.91 6.040e- FAMILY SIGNATURE 11 221-234				
443 PR00834 HTRA/DEGQ PROTEASE PR00834F 10.91 6.040e- FAMILY SIGNATURE 11 221-234				
FAMILY SIGNATURE 11 221-234	443	PR00834	HTRA/DEGQ PROTEASE	
				11 221-234
446 PF01140 Matrix protein (MA), PF01140D 15.54 9.663e-	446	PF01140		PF01140D 15.54 9.663e-

SEQ ID N	NO: ACCESSION NO.	DESCRIPTION	RESULTS*
		p15.	10 183-218 PF01140D 15.54 3.093e-09 246-
449	PR00568	DOPAMINE D3 RECEPTOR SIGNATURE	PRC0568G 13.95 5.551e- 09 39-53
451	PF00084	Sushi domain proteins (SCR repeat proteins.	PF00084B 9.45 3.813e-
452	BL00790	Receptor tyrosine kinase class V proteins.	BL00790I 20.01 2.821e- 09 618-649
456	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 1.000e- 25 77-99 PR00380D 9.93 1.000e-21 281-303 PR00380C 13.18 8.286e- 17 230-249 PR00380B 12.64 4.724e-16 194- 212
457	PR00253	GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE	PR00253A 9.15 9.143e- 24 246-267 PR00253B 13.47 2.000e-23 272- 294 PR00253C 13.85 7.000e-23 306-328 PR00253D 16.68 5.950e- 21 452-473
467	PR00849	GLYCOSYL HYDROLASE FAMILY 58 SIGNATURE	PR00849D 9.77 9.236e-
471	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 8.200e-12
472	BL00226	Intermediate filaments proteins.	BL00226B 23.86 3.721e- 09 282-330
473	BL00344	GATA-type zinc finger domain proteins.	BL00344 17.99 7.000e- 12 814-852
474	BL00481	Thiol-activated cytolysins proteins.	BL00481E 13.07 8.909e- 09 173-199
479	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319B 11.47 2.571e-
480	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 1.900e- 38 8-47
481	PR00405	HIV REV INTERACTING PROTEIN SIGNATURE	PR00405C 19.41 1.000e- 19 451-473 PR00405B 11.83 4.333e-18 430- 448 PR00405A 17.71 4.971e-18 411-431
482	PR30049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 9.286e- 10 959-974 PR00049D 0.00 9.857e-10 958-973 PR00049D 0.00 1.305e- 09 937-952 PR00049D 0.00 8.322e-09 939-954
186	PR00007	COMPLEMENT C1Q DOMAIN SIGNATURE	PR00007B 14.16 8.615e- 23 653-673 PR00007A 19.33 6.192e-22 626- 653 PR00007C 15.60 5.846e-19 698-720 PR00007D 9.64 3.647e- 13 732-743
187	PD00567	PROTEIN RNA-BINDING RNA REPEAT HYD.	PD00567B 18.23 2.853e- 09 200-214
188	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 4.569e- 12 3-21
189	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-	PD01066 19.43 4.882e- 27 30-69 PD01066
190	PR00049	BINDING NU. WILM'S TUMOUR PROTEIN SIGNATURE	19.43 3.430e-10 71-110 PR00049D 0.00 7.864e-
92	BL01128	Shikimate kinase proteins.	09 663-678 BL01128A 18.84 6.464e-
97	PF00429	ENV polyprotein (coat	17 58-92 PF00429 31.08 7.171e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		polyprotein).	15 21-71
498	BL00120	Lipases, serine proteins.	BL00120B 11.37 7.923e- 09 185-200
500	BL00030	Eukaryotic RNA-binding	BL00030A 14.39 7.353e-
501	BL01159	region RNP-1 proteins.	11 299-318
		WW/rsp5/WWP domain proteins.	BL01159 13.85 8.579e- 12 131-146
505	BL00021	Kringle domain proteins.	BL00021B 13.33 3.739e- 17 492-510
508	PR00120	H+TRANSPORTING ATPASE (PROTON PUMP) SIGNATURE	PR00120C 9.90 5.800e- 19 705-722
509	DM01417	6 kw INDUCING XPMC2 MUSHROOM SPAC22G7.04.	DM01417E 20.62 2.938e- 16 362-395 DM01417D 11.08 3.800e-13 322- 338
510	PF00534	Glycosyl transferases group 1.	PF00534B 14.47 6.625e- 09 346-370
511	PF00534	Glycosyl transferases	PF00534B 14.47 6.625e-
		group 1.	09 293-317
512	PF00534	Glycosyl transferases group 1.	PF00534B 14.47 6.625e- 09 366-390
513	PD01841	PHOSPHORYLASE KINASE ALPHA MUSCL.	PD01841A 21.71 1.000e- 40 110-160 PD01841B 14.35 1.000e-40 181- 222 PD01841D 17.87 1.000e-40 243-295 PD01841F 13.36 1.000e- 40 333-382 PD01841G 24.26 1.000e-40 386- 440 PD01841L 18.42 1.000e-40 968-1010 PD01841I 23.00 4.545e- 37 762-804 PD01841E 18.60 3.750e-36 295- 333 PD01841J 14.94 6.023e-35 851-888 PD01841H 21.30 2.909e- 33 490-527 PD01841K 14.81 7.088e-33 924- 954 PD01841C 13.78 9.386e-23 222-243 PD01841M 10.82 8.594e- 21 1054-1073 PD01841I 23.00 2.667e-13 549- 591
514	PR00153	CYCLOPHILIN PEPTIDYL- PROLYL CIS-TRANS ISOMERASE SIGNATURE	PR00153C 11.01 7.188e- 13 95-111 PR00153E 9.10 4.150e-12 122-138
515	BL00740	MAM domain proteins.	BL00740A 13.87 7.188e- 12 410-423
516	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 6.087e-
517	BL00242	Integrins alpha chain proteins.	BL00242C 16.86 8.320e-
523	DM00031	IMMUNOGLOBULIN V REGION.	09 12-42 DM00031A 16.80 3.750e- 39 20-68 DM00031B 15.41 1.000e-25 84-118
525	BL00319	Amyloidogenic glycoprotein extracellular domain proteins.	BL00319C 17.12 8.375e- 10 61-95
526	PF00789	Domain present in ubiquitin-regulatory proteins.	PF00789B 19.70 3.308e- 12 322-343 PF00789C 20.98 5.269e-09 367- 392
528	BL01162	Quinone oxidoreductase / zeta-crystallin proteins.	BL01162C 22.80 1.500e- 16 120-164

SEQ ID NO:	ACCESSION	DESCRIPTION	
102 25 270	NO.	DESCRIPTION	RESULTS*
529	PR00910	LUTEOVIRUS ORF6 PROTEIN	222222
	11100310	SIGNATURE	PR00910A 2.51 3.893e-
532	BL00215	Mitochondrial energy	BL00215A 15.82 4.000e-
	-200223	transfer proteins.	17 11-36 BL00215A
		ramonal proteins.	15.82 8.660e-11 123-
			148
533	BL00215	Mitochondrial energy	BL00215A 15.82 4.000e~
		transfer proteins.	17 11-36 BL00215A
			15.82 8.660e-11 97-122
534	BL00098	Thiolases acyl-enzyme	BL00098C 21.65 2.800e-
		intermediate proteins.	38 181-227 BL00098B
			32.59 5.345e-38 86-141
İ			BL0009BD 26.30 8.364e-
			35 245-288 BL00098E
			22.12 1.000e-34 314-
			352 BL00098F 10.18
			4.971e-22 365-386
		Į	BL00098A 10.60 6.455e-
			11 38-50
535	PR00370	FLAVIN-CONTAINING	PR00370E 11.96 7.429e-
	1	MONOOXYGENASE (FMO)	22 321-340 PR00370D
1	1	SIGNATURE	16.33 6.143e-21 185-
	1		204 PR00370F 17.75
			6.559e-21 376-396
			PR00370B 10.91 9.591e-
			21 27-46 PR00370C
	·		12.72 3.500e-20 140-
	ļ		157 PR00370A 3.35
536	BL00028	Zinc finger, C2H2 type,	6.442e-17 4-20
	2200020	domain proteins.	BL00028 16.07 7.429e- 16 285-302 BL00028
		donari processis.	16.07 6.294e-14 341-
		1	358 BL00028 16.07
	ĺ	1	1.346e-11 369-386
		1	BL00028 16.07 1.692e-
			11 397-414 BL0002B
		1	16.07 4.462e-11 453-
ĺ			470 BL00028 16.07
			7.231e-11 425-442
			BL00028 16.07 4.300e-
537			10 313-330
53 /	BL00762	WHEP-TRS domain	BL00762A 23.43 9.419e-
538	BL00762	proteins.	15 844-881
536	PT/// 165	WHEP-TRS domain	BL00762A 23.43 9.419e-
539	BL00762	Proteins. WHEP-TRS domain	15 819-856
	BB05762	proteins.	BL00762A 23.43 9.419e-
540	PR00985	LEUCYL-TRNA SYNTHETASE	15 822-859
· · · · ·		SIGNATURE	PR00985A 12.10 9.000e-
541	PD02102	SUBUNIT E V-ATPASE	10 357-375
		VACUOLAR ATP SYNTHASE	PD02102A 16.74 1.000e- 40 3-47 PD02102B
1		HYDROL.	18.28 4.375e-34 57-100
			PD02102D 21.69 1.923e-
[			30 179-218 PD02102C
			26.34 8.929e-26 100-
			146
543	EL00028	Zinc finger, C2H2 type,	BL00028 16.07 1.000e-
		domain proteins.	10 48-65 BL00028
			16.07 6.400e-10 193-
i			210 BL00028 16.07
		1	1.000e-09 343-360
1			BL00028 16.07 6.914e-
			09 78-95
545	BL00250	TGF-beta family	BL00250A 21.24 8.000e-
1		proteins.	31 293-329 BL00250B
į		1	27.37 5.286e-24 354-
			390
547	PR00319	BETA G-PROTEIN	,

SEQ ID N	O:   ACCESSION	DESCRIPTION	DDCW MO+
	NO.		RESULTS*
		(TRANSDUCIN) SIGNATURE	09 186-201 PR00319A 15.27 7.344e-09 210- 227
548	BL01204	NF-kappa-B/Rel/dorsal domain proteins.	BJ.01204A 17.74 1.000e- 40 8-56 BL01204D 16.42 1.000e-40 177- 221 BL01204E 13.83 7.652e-30 225-250 BL01204C 13.93 8.714e- 22 141-160 BL01204B 15.41 4.333e-16 102- 116
549	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 8.364e-
551	PF00632	HECT-domain (ubiquitin- transferase).	15 255-276 PF00632C 20.66 3.302e- 23 1569-1601 PF00632B 18.45 3.700e-21 1515- 1543
554	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290B 13.17 1.600e- 14 187-205 BL00290A 20.89 2.059e-14 130- 153
557	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 6.339e- 09 846-879
559	DM01111	1 kw PHOSPHATASE TRANSFORMING 61K PDF1.	DM01111L 11.93 3.762e- 09 7-35
562	PF00658	Poly-adenylate binding protein, unique domain proteins.	PF00658C 16.33 9.455e- 32 118-155
564	BL00141	Eukaryotic and viral aspartyl proteases proteins.	BL00141A 12.10 4.150e- 10 472-488
566	PF00855	PWWP domain proteins.	PF00855 13.75 5.667e-
567	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 4.977e- 13 229-268
569	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 7.000e- 19 118-149 BL00107B 13.31 5.500e-15 183- 199
570	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 7.000e- 19 118-149 BL00107B 13.31 5.500e-15 183-
572	PR00193	MYOSIN HEAVY CHAIN SIGNATURE	PR00193D 14.36 1.857e- 34 454-483 PR00193C 12.60 2.636e-31 223- 251 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.588e- 22 115-135 PR00193E 19.47 6.559e-19 508- 537
573	PR00193	MYOSIN HEAVY CHAIN SIGNATURE	PR00193D 14.36 1.857e- 34 470-499 PR00193C 12.60 2.636e-31 239- 267 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.588e- 22 115-135 PR00193E 19.47 6.559e-19 524- 553
575	BL00752	XPA protein.	BL00752B 19.17 9.703e- 10 885-929
577	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 7.000e- 09 276-295
	BL00116	DNA polymerase family B	BL00116A 12.81 5.737e-

SEQ ID N	O: ACCESSION NO.	DESCRIPTION	RESULTS*
	100.	proteins.	
		proceins.	13 864-877 BL00116B 11.82 1.529e-12 952- 965
578	BL00195	Glutaredoxin proteins.	BL00195B 15.31 7.158e-
579	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PRO0019B 11.36 9.000e- 11 217-231 PR00019B 11.36 1.360e-09 386- 400 PR00019A 11.19 3.333e-09 389-403
580	PR00253		PR00019B 11.36 8.920e- 09 363-377
		GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE	PR00253A 9.15 2.125e- 25 275-296 PR00253B 13.47 7.923e-24 301- 323 PR00253D 16.68 5.846e-23 444-465 PR00253C 13.85 2.241e- 20 335-357
583	PR00343	SELECTIN SUPERFAMILY COMPLEMENT-BINDING REPEAT SIGNATURE	PR00343C 16.85 2.286e- 11 1233-1252 PR00343C 16.85 5.500e-11 333- 352 PR00343C 16.85 5.500e-11 783-802 PR00343C 16.85 4.246e- 10 1491-1510 PR00343C 16.85 8.230e-10 1686- 1705
584	DM01537	kw SKI2W SKI2 NUCLEOLAR HELICASE.	DM01537B 21.63 1.878e- 37 79-126 DM01537B 21.63 9.491e-30 916- 963 DM01537A 15.14
586	PFC0013	KH domain proteins family of RNA binding proteins.	3.196e-11 784-804 PF00013 5.78 1.450e-09 124-136
587	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 4.409e-
589	BL00478	LIM domain proteins.	BL00478B 14.79 1.643e- 13 261-276 BL00478B 14.79 7.709e-09 321-
590	PF00855	PWWP domain proteins.	336 PF00855 13.75 8.000e- 15 931-948
591	PF00855	PWWP domain proteins.	PF00855 13.75 8.000e- 15 1062-1079
593	PF00628	PHD-finger.	PF00628 15.84 3.455e-
594	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 2.241e- 16 558-576 PR00205A 14.73 9.308e-13 542- 558 PR00205C 13.65 5.304e-12 594-609 PR00205B 11.39 4.273e-
596	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 4.789e-
98	PD01675	GLYCOPROTEIN MAJOR ENVELOPE PROBABLE U3.	18 307-338   PD01675C 19.89 2.330e-   10 55-89
500	BL00242	Integrins alpha chain proteins.	BL00242E 9.03 9.591e- 27 985-1014 BL00242C 16.86 4.115e-26 286- 316 BL00242D 13.57 4.150e-25 357-382 BL00242B 8.13 7.353e- 12 189-199 BL00242D 13.57 3.455e-11 421- 446 BL00242A 13.80

SEQ ID NO:	ACCESSION	DESCRIPTION	I DOOLL TO
	NO.		RESULTS*
[			5.000e-11 61-73
			BL00242D 13.57 4.986e-
601	750000		10 291-316
901	PR00320	G-PROTEIN BETA WD-40	PR00320A 16.74 5.610e-
602	7700000	REPEAT SIGNATURE	09 198-213
002	PR00278	PANCREATIC HORMONE	PR00278A 12.43 4.569e-
603	BL00479	SIGNATURE	10 331-348
000	1000479	Phorbol esters /	BL00479C 12.01 3.250e-
	1	diacylglycerol binding domain proteins.	12 170-183
604	BL00315	Dehydrins proteins.	
		Denyarins processs.	BL00315A 9.35 1.672e- 09 424-452
605	BL00415	Synapsins proteins.	BL00415N 4.29 9.794e-
	Į	1 mpanna process.	10 295-339
606	PR00926	MITOCHONDRIAL CARRIER	PR00926F 17.75 1.000e-
		PROTEIN SIGNATURE	13 335-358
608	PF00855	PWWP domain proteins.	PF00855 13.75 5.167e-
		)	15 265-282
609	PF00855	PWWP domain proteins.	PF00855 13.75 5.167e-
	1	_	15 211-228
612	DM01206	CORONAVIRUS NUCLEOCAPSID	
		PROTEIN.	10 877-897 DM01206B
			10.69 8.027e-10 861-
	1	1	881 DM01206B 10.69
			9.137e-10 873-893
	ļ		DM01206B 10:69 1.456e-
			09 859-879 DM01206B
			10.69 1.797e-09 879-
			899 DM01206B 10.69
			4.076e-09 865-885
			DM01206B 10.69 7.038e-
			09 898-918 DM01206B
			10.69 7.949e-09 871-
			891 DM01206B 10.69
615	PD02699		8.291e-09 767-787
1	FD02699	PROTEIN DNA-BINDING	PD02699A 8.91 2.023e-
		BINDING DNA.	28 129-158 PD02699C
İ		Í	24.84 1.000e-27 317-
			364 PD02699B 18.28
616	PR00380	KINESIN HEAVY CHAIN	1.000e-17 158-182 PR00380A 14.18 4.086e-
J		SIGNATURE	22 288-310 PR00380D
į			9.93 3.721e-17 486-508
		1	PR00380B 12.64 2.241e-
			16 410-428 PR00380C
1			13.18 2.976e-13 436-
			455
517	PR00380	KINESIN HEAVY CHAIN	PR00380A 14.18 4.086e-
ı		SIGNATURE	22 288-310 PR00380D
ŀ		· ·	9.93 3.721e-17 486-508
- 1		}	PR00380B 12.64 2.241e-
		•	16 410-428 PR00380C
		1	13.18 2.976e-13 436-
:10			455
518	DM01206	CORONAVIRUS NUCLEOCAPSID	DM01206B 10.69 5.143e-
		PROTEIN.	12 531-551 DM01206B
		1	10.69 2.603e-10 535-
21	DDAARAC		555
	PR00700	PROTEIN TYROSINE	PR00700B 16.80 3.160e-
22	77.0077.0	PHOSPHATASE SIGNATURE	21 561-582
	BL00239	Receptor tyrosine kinase	BL00239F 28.15 3.222e-
i		class II proteins.	10 647-692 BL00239C
,			
i			18.75 8.304e-10 543-
23			18.75 8.304e-10 543- 566
23	PR00407	EUKARYOTIC MOLYBDOPTERIN	
		DOMAIN SIGNATURE	566
	PR00407 BL00641		566 PR00407K 9.94 8.448e-

SEQ ID	NO: ACCESSION NO.	DESCRIPTION	RESULTS*
		subunit proteins.	24.37 1.000e-40 255- 308 BL00641F 33.12 1.000e-40 571-623 BL00641A 17.15 1.818e- 37 48-80 BL00641B 12.62 5.846e-34 113- 139 BL00641D 13.23
627	PR00103	CAMP-DEPENDENT PROTEIN KINASE SIGNATURE	9.308e-29 216-240  PR00103E 17.80 2.500e- 18 367-380 PR00103B 13.39 2.080e-14 297- 312 PR00103A 9.59 2.957e-14 282-297 PR00103D 10.83 3.077e- 12 346-358 PR00103C 15.68 1.000e-11 334- 344 PR00103B 13.39 1.450e-11 175-190 PR00103A 9.59 1.720e-
630	PR00081	GLUCOSE/RIBITOL DBHYDROGENASE FAMILY	10 160-175 PR00081A 10.53 6.211e- 16 4-22
631	PF00651	SIGNATURE BTB (also known as BR-	PF00651 15.00 8.500e-
632	DM01206	C/Ttk) domain proteins.  CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 2.233e- 10 1324-1344 DM01206B 10.69 4.822e-10 1276- 1296 DM01206B 10.69 7.658e-10 1328-1348 DM01206B 10.69 8.274e- 10 1280-1300 DM01206B 10.69 4.532e-09 1320- 1340 DM01206B 10.69
635	BL00107	Protein kinascs ATP- binding region proteins.	7.266e-09 1326-1346 BL00107A 18.39 7.600e- 23 145-176 BL00107B 13.31 2.636e-13 211-
536	BL00657	Fork head domain proteins.	227 BL00657A 19.39 1.545e- 30 101-143 BL00657B 22.27 7.750e-26 149-
37	BL00107	Protein kinases ATP-	192 BL00107B 13.31 1.000e-
43	BL00018	binding region proteins.  EF-hand calcium-binding	10 607-623 BL00018 7.41 4.913e-09
47	PF00628	domain proteins. PHD-finger.	199-212 PF00628 15.84 2.350e- 13 385-400 PF00628 15.84 3.455e-12 464- 479
48	BL01129	Hypothetical yabO/yceC/sfhB family proteins.	BL01129E 13.25 4.000e- 25 332-357 BL01129C 25.56 8.200e-23 236- 279 BL01129B 12.51
49	BL01228	Hypothetical cof family proteins.	6.118e-13 191-212 BL01228D 17.44 3.908e-
50	BL00027	'Homeobox' domain proteins.	10 455-480 BL00027 26.43 6.684e-
51	BL50002	Src homology 3 (SH3) domain proteins profile.	13 771-814 BL50002A 14.19 1.750e- 12 1026-1045
53	PR00253	GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE	PRO0253A 9.15 4.000e- 24 253-274 PRO0253C 13.85 8.800e-24 313- 335 PRO0253B 13.47 3.143e-22 279-301 PR00253D 16.68 7.652e-

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			20 422-443
654	PD01719	PRECURSOR GLYCOPROTEIN SIGNAL RE.	PD01719A 12.89 4.452e- 11 969-997 PD01719A 12.89 3.961e-10 128- 156 PD01719A 12.89 7.395e-10 1276-1304 PD01719A 12.89 1.222e- 09 1220-1248
657	BL00354	HMG-I and HMG-Y DNA- binding domain proteins (Ahook).	BL00354C 6.61 8.397e- 09 563-578
658	BL00354	HMG-I and HMG-Y DNA- binding domain proteins (Ahook).	BL00354C 6.61 8.397e- 09 580-595
659	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 2.174e- 13 539-572 DM00215 19.43 4.750e-12 549- 582 DM00215 19.43 9.824e-11 551-584 DM00215 19.43 2.929e- 10 548-581 DM00215 19.43 4.054e-1C 550- 583 DM00215 19.43 5.339e-10 552-585 DM00215 19.43 7.107e- 10 544-577
660	PR00688	XYLOSE ISOMERASE SIGNATURE	PR00688I 13.78 9.518e- 09 224-236
661	BL00027	'Homeobox' domain proteins.	BL00027 26.43 5.950e- 23 249-292
662	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.158e- 10 596-610
663	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.158e- 10 596-610
664	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.158e- 10 596-610
666	PR00819	CEXX/CFQX SUPERFAMILY SIGNATURE	PR00819B 10.83 8.988e- 10 704-720
667	BL50040	Elongation factor 1 gamma chain profile.	BL50040C 22.62 2.143e- 16 135-178
668	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 1.360e- 09 139-153 PR00019A 11.19 1.667e-09 94-108 PR00019B 11.36 4.600e- 09 163-177
670	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 3.250e-10 681-694 BL00018 7.41 6.400e-10 717-730
672	PD00131	ATP-BINDING TRANSPORT TRANSMEMBR.	FD00131B 34.97 1.000e- 34 356-410 PD00131C 19.59 1.346e-26 504- 542
673	PR00667	RETINAL PIGMENT EPITHELIUM-RETINAL GPCR SIGNATURE	PR00667G 15.33 7.557e- 10 106-123
674	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 4.857e- 13 593-608 PR00320B 12.19 4.115e-12 635- 650 PR00320C 13.01 8.435e-11 717-732 PR00320C 13.01 2.800e- 10 635-650 PR00320C 13.01 6.400e-10 593- 608 PR00320B 12.19 3.250e-09 593-608
675	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 4.857e- 13 572-587 PR00320B

SEQ ID N	O: ACCESSION	DESCRIPTION	RESULTS*
	NO.		
			629 PR00320C 13.01 8.435e-11 696-711 PR00320C 13.01 2.800e- 10 614-629 PR00320C 13.01 6.400e-10 572- 587 PR00320B 12.19
676	PR00019	LEUCINE-RICH REFEAT SIGNATURE	3.250e-09 572-587 PR00019A 11.19 9.667e-
679	PF00642	Zinc finger C-x8-C-x5-C- x3-H type (and similar).	16 225-236 PF00642 11.59 7.900e-12 187-
680	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308C 3.83 8.754e-
681	BL00019	Actinin-type actin- binding domain proteins.	10 286-296 BL00019D 15.33 4.200e-
682	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	19 227-257 PR00700D 12.47 4.000e- 09 99-118
687	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 8.500e-
689	BL01024	Protein phosphatase 2A regulatory subunit PR55 proteins.	BL01024A 10.26 1.000e- 40 22-69 BL01024B 8.91 1.000e-40 86-127 BL01024C 7.80 1.000e- 40 146-185 BL01024D 13.22 1.000e-40 185- 222 BL01024E 11.96 1.000e-40 222-266 BL01024F 9.42 1.000e- 40 266-317 BL01024G 11.09 1.000e-40 317- 349 BL01024H 13.88 1.000e-40 389-442
691	BL00027	'Homeobox' domain proteins.	BL00027 26.43 8.071e- 31 152-195
692	BL00211	ABC transporters family proteins.	BL00211A 12.23 5.050e- 09 45-57
693	BL00211	ABC transporters family proteins.	BL00211A 12.23 5.050e- 09 45-57
694	BL00211	ABC transporters family proteins.	BL00211A 12.23 5.050e- 09 58-70
696	BL00680	Methionine aminopeptidase subfamily l proteins.	BL00680 14.37 5.304e- 17 173-195
697	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 3.418e- 11 242-265
698	DM01930	2 kw FINGER SMCX SMCY YDR096W.	DM01930E 15.41 1.367e- 37 170-215 DM01930F 14.16 8.232e-28 267- 303 DM01930B 19.86 9.163e-10 37-71
700	PR00869	DNA-POLYMERASE FAMILY X SIGNATURE	PR00869A 12.80 1.281e-
701	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 2.174e- 10 77-91 PR00048A 10.52 6.870e-10 133- 147 PR00048A 10.52 8.826e-10 105-119 PR00048A 10.52 5.320e- 09 161-175
702	BL00523	Sulfatases proteins.	BL00523E 19.27 2.565e- 25 326-356 BL00523A 13.36 5.050e-16 38-55 BL00523B 8.64 5.909e- 15 86-98 BL00523C 12.64 5.500e-13 137-

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		
			148 BL00523D 9.89
		1	1.844e-11 290-302
			BL00523G 9.46 5.500e- 10 513-523 BL00523F
			10.85 6.351e-09 413-
		İ	424
703	PR00048	C2H2-TYPE ZINC FINGER	PR00048A 10.52 8.412e-
		SIGNATURE	12 376-390 PR00048B
			6.02 1.000e-10 334-344
1	Í		PR00048B 6.02 1.474e-
707	<u> </u>		09 364-374
/0/	PD00787	SYNTHASE BIOSYNTHESIS	PD00787A 14.84 8.941e-
708	PR00761	TRANSFERASE. BINDIN PRECURSOR	14 66-82
	2100761	SIGNATURE	PR00761E 14.32 8.500e- 10 822-841
712	DM01354	kw TRANSCRIPTASE REVERSE	DM01354Y 10.69 4.977e-
		II ORF2.	38 425-465 DM01354X
			13.86 7.300e-34 376-
			415 DM01354V 12.97
			4.923e-17 311-358
		į.	DM01354W 12.64 5.596e-
71.5	L 77 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		10 356-376
713	BL00039	DEAD-box subfamily ATP-	BL00039D 21.67 7.545e-
		dependent helicases proteins.	27 450-496 BL00039A
		proteins.	18.44 2.537e-18 147-
	ļ		186 BL00039C 15.63
	Ì		2.216e-14 280-304 BL00039B 19.19 1.947e-
	}	ļ	13 194-220
715	BL00383	Tyrosine specific	BL00383E 10.35 4.981e-
	ļ	protein phosphatases	10 150-161
		proteins.	
717	PF00777	Sialyltransferase	PF00777C 18.60 4.035e-
718	DM00031	family.  IMMUNOGLOBULIN V REGION.	21 106-161
	3.,00031	IMMONOGEOBULIN V REGION.	DM00031A 16.80 3.750e- 39 20-68 DM00031B
			15.41 2.688e-28 84-118
			DM00031C 12.79 1.300e-
			12 131-142
719	BL00243	Integrins beta chain	BL00243B 17.54 1.000e-
		cysteine-rich domain	40 131-172 BL00243C
		proteins.	16.42 1.000e-40 172-
			208 BL00243D 24.07 1.000e-40 222-274
			BL00243F 22.63 1.000e-
			40 314-358 BL00243I
			31.77 6.571e-39 607-
İ			650 BL00243E 16.70
ľ		1	3.077e-35 274-304.
		1	BL00243G 21.38 3.625e-
		<b>.</b>	34 358-400 BL00243H
			17.53 5.235e-29 567-
			593 BL00243A 17.61
			3.250e-21 63-84 BL00243H 17.53 7.167e-
		j	16 477-503 BL00243H
			17.53 2.304e-11 524-
}			550 BL00243H 17.53
İ		1	5.304e-11 606-632
1		1	BL00243I 31.77 1.380e-
720	BB00015		09 610-653
720	PR00217	43 KD POSTSYNAPTIC	PR00217C 10.91 8.022e-
722	PR00704	PROTEIN SIGNATURE	09 20-36
·~-	FRUU/U4	CALPAIN CYSTEINE	PR00704D 11.05 5.909e-
ļ		PROTEASE (C2) FAMILY SIGNATURE	34 135-161 PR00704F
		JUNIORS	13.61 7.000e-26 190- 218 PR00704E 12.55
		1	8.071e-26 165-189
		<del></del>	2.2.20 20 103-103

SEQ ID	NO: ACCESSION	DESCRIPTION	RESULTS*
	NO.		
			PR00704B 17.94 2.241e-
i			23 75-98 PR00704A 14.68 4.094e-19 30-54
1	j		PR00704C 11.88 1.871e-
			18 99-116
725	PR00194	TROPOMYOSIN SIGNATURE	PR00194A 7.86 7.652e-
726	PR00194	TROPOMYOGIN GIOVENIA	09 169-187
	1100194	TROPOMYOSIN SIGNATURE	PR00194A 7.86 7.652e- 09 169-187
727	PR00320	G-PROTEIN BETA WD-40	PR00320C 13.01 2.125e-
		REPEAT SIGNATURE	13 277-292 PR00320A
			16.74 1.310e-11 277-
			292 PR00320C 13.01
			4.522e-11 323-338 PR00320A 16.74 6.586e-
			11 323-338 PR00320B
			12.19 4.343e-10 323-
		•	338 PR00320B 12.19
731	PR00195	DYNAMIN SIGNATURE	6.914e-10 277-292 PR00195A 11.94 8.627e-
			16 288-307 PR00195E
733	77700610		9.82 3.912e-11 457-474
733	PF00642	Zinc finger C-x8-C-x5-C-	PF00642 11.59 9.082e-
738	BL00039	x3-H type (and similar). DEAD-box subfamily ATP-	10 787-798 BL00039A 18.44 2.565e-
		dependent helicases	28 26-65 BL00039D
		proteins.	21.67 2.105e-20 338-
			384 BL00039C 15.63
			9.100e-13 160-184
			BL00039B 19.19 9.617e-
739	BL01289	TSC-22 / dip / bun	BL01289A 12.18 8.909e-
		family proteins.	31 326-353 BL01289B
			10.45 9.571e-17 353-
742	BL01019	ADP-ribosylation factors	383 BL01019A 13.20 7.078e-
743		family proteins.	12 41-81
743	BL00965	Phosphomannose isomerase	BL00965C 23.78 1.000e-
		type I proteins.	40 256-305 BL00965B 17.77 1.600e-25 126-
		İ	153 BL00965A 10.57
747			6.400e-19 94-113
147	BL00021	Kringle domain proteins.	BL00021D 24.56 4.563e-
		· ·	25 231-273 BL00021B
748	BL00612	Osteonectin domain	13.33 5.345e-21 60-78 BL00612B 11.35 2.034e-
···		proteins.	11 93-126
749	PR00450	RECOVERIN FAMILY	PR00450C 12.22 6.880e-
752	BL00795	SIGNATURE Involucrin proteins.	10 135-157
		involucin proceins.	BL00795C 17.06 6.000e- 11 384-429 BL00795C
			17.06 9.444e-11 370-
754	DYCOCC		415
124	BL00051	Ribosomal protein L39e	BL00051 20.92 1.935e-
755	DM01970	proteins.   0 kw ZK632.12 YDR313C	16 4-50
		ENDOSOMAL III.	DM01970B 8.60 7.723e- 09 171-184
760	BL01020	SAR1 family proteins.	BL01020C 15.35 9.020e-
762	27.00042		12 99-150
	3L00046	Histone H2A proteins.	BL00046 12.95 1.000e-
163	PD02411	PROTEIN TRANSCRIPTION	40 33-88
		REGULATION NUCLEAR.	PD02411 21.89 9.137e- 10 206-240
64	BL00027	'Homeobox' domain	BL00027 26.43 8.800e-
67		proteins.	29 417-460 ·
0/	BL01208	VWFC domain proteins.	BL01208B 15.83 6.063e-
		1	10 309-324 BL01208B
		<u></u>	15.83 8.031e-10 165-

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		RESORIS
			180 BL01208B 15.83
770	- DV 3 4 4 4 4		4.162e-09 85-100
770	BL00031	Nuclear hormones	BL00031A 19.55 9.571e-
		receptors DNA-binding	32 208-241 BL00031B
		region proteins.	22.25 5.500e-27 242-
772	PRO0449	TRANSFORMING PROTEIN P21	274
	1.00115	RAS SIGNATURE	PR00449A 13.20 1.450e- 18 4-26 PR00449E
	İ		13.50 3.520e-14 142-
	}		165 PR00449C 17.27
			3.032e-13 44-67
	Ì		PR00449D 10.79 8.579e-
		ĺ	13 107-121 PR00449B
773	Dyosess		14.34 3.455e-11 27-44
113	BL00523	Sulfatases proteins.	BL00523E 19.27 9.333e-
			23 299-329 BL00523A
	1		13.36 2.200e-13 47-64
			BL00523B 8.64 2.607e- 13 91-103 BL00523D
			9.89 7.923e-12 224-236
	1		BL00523C 12.64 4.512e-
	ļ ·		10 141-152 BL00523F
			10.85 5.821e-10 373-
			384
775	BL00028	Zinc finger, C2H2 type,	BL00028 16.07 7.686e-
776		domain proteins.	09 568-585
//6	BL00028	Zinc finger, C2H2 type,	BL00028 16.07 7.686e-
777	BL00028	domain proteins.	09 621-638
	5500028	Zinc finger, C2H2 type,	BL00028 16.07 7.686e-
778	BL00030	domain proteins.  Eukaryotic RNA-binding	09 595-612
	2200030	region RNP-1 proteins.	BL00030A 14.39 8.412e-
		region Mir-1 processis.	11 322-341 BL00030A 14.39 7.000e-10 220-
			239
779	PR00079	GLUCOSE-6-PHOSPHATE	PR00079B 12.98 2.929e-
		DEHYDROGENASE SIGNATURE	26 193-222 PR00079E
			16.65 4.150e-23 348-
			375 PR00079C 8.68
1			6.351e-16 246-264
			PR00079D 13.51 7.070e-
			16.12 6.769e-13 169-
			183
781	BL00215	Mitochondrial energy	BL00215A 15.82 9.250e-
ĺ		transfer proteins.	17 10-35 BL00215A
.			15.82 6.000e-16 221-
			246 BL00215A 15.82
		1	7.857e-12 108-133
-			BL00215B 10.44 9.526e-
783	PD00289	PROTEIN SH3 DOMAIN	11 168-181 PD00289 9.97 6.276e-09
	<del>-</del>	REPEAT PRESYNA.	159-173
85	BL00690	DRAH-box subfamily ATP-	BL00690B 13.38 1.000e-
		dependent helicases	12 147-165 BL00690A
		proteins.	6.87 5.320e-10 114-124
j			BL00690C 7.51 3.189e-
100	DD0011		09 218-228
86	PR00449	TRANSFORMING PROTEIN P21	PR00449C 17.27 8.500e-
		RAS SIGNATURE	16 50-73 PR00449A
		}	13.20 5.235e-14 8-30
		]	PR00449E 13.50 2.853e-
ļ		1	11 150-173 PR00449D
		j l	10.79 1.545e-09 111-
1		<u> </u>	125
88	DM01206	CODOMALITATIC MILET PARAMETE	DWG100CD 10 CC
88	DM01206	CORONAVIRUS NUCLEOCAPSID	DM01206B 10.69 8.767e-
	DM01206 BL00915	PROTEIN.	10 1-21

SEQ ID NO		DESCRIPTION	RESULTS*
<u> </u>	NO.		
	1		22.78 5.050e-33 633- 671 BL00915D 27.02
	1		1.529e-21 795-831
	İ	1	BL00915A 10.09 1.000e-
			13 395-407
791	PR00208	GLIADIN AND LMW GLUTENIN	PR00208A 12.59 6.294e-
	İ	SUPERFAMILY SIGNATURE	10 120-138 PR00208A
			12.59 6.294e-10 121-
		1	139 PR00208A 12.59
[		1	6.294e-10 122-140
	İ		PR00208A 12.59 6.294e-
			10 123-141 PR00208A
			12.59 6.294e-10 124- 142 PR00208A 12.59
		İ	6.294e-10 125-143
			PR00208A 12.59 6.294e-
			10 126-144 PR00208A
,	•		12.59 6.294e-10 127-
			145 PR00208A 12.59
			6.294e-10 128-146
			PR00208A 12.59 6.294e-
			10 129-147 PR00208A
	/		12.59 7.411e-09 130-
		1	148 PR00208A 12.59
			7.658e-09 131-149 PR00208A 12.59 7.904e-
		ì	09 132-150 PR00208A
			12.59 8.274e-09 118-
			136 PR00208A 12.59
			8.274e-09 119-137
795	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 5.034e-
	İ		16 302-320 PR00205A
	ļ	· ·	14.73 1.257e-11 284-
		•	300 PR00205C 13.65
796	BL00412	Neuromodulin (GAP-43)	1.333e-11 337-352
		proteins.	BL00412D 16.54 4.000c 12 196-247 BL00412D
			16.54 5.705e-11 197-
			248 BL00412D 16.54
			7.848e-10 199-250
	1		BL00412D 16.54 1.827e-
			09 195-246 BL00412D
	1		16.54 1.918e-09 194-
	}	}	245 BL00412D 16.54
797	BL00021	Kringle domain proteins.	2.102e-09 201-252 BL00021B 13.33 6.339e-
		Arrigre domain processs.	13 40-58
799	BL01052	Calponin family repeat	BL01052C 18.51 1.000e-
		proteins.	40 87-127 BL01052A
		1	16.12 1.529e-32 3-35
•		· ·	BL01052B 15.31 1.257e-
			25 52-78 BL01052D
			10.26 5.737e-25 174-
800	BL00348	nc2 tumor actions	194
	2500346	p53 tumor antigen proteins.	BL00348F 23.19 3.714e-
801	BL00309	Vertebrate galactoside-	09 197-240
		binding lectin proteins.	BL00309C 18.65 1.621e- 09 62-87
802	PR00245	OLFACTORY RECEPTOR	PR00245D 10.47 5.224e-
		SIGNATURE	09 187-199
804	PF00774	Dihydropyridine	PF00774A 16.47 8.457e-
	1	sensitive L-type calcium	10 110-156
		channel (Beta subuni.	
808	PR00667	RETINAL PIGMENT	PR00667C 11.71 9.875e-
	ĺ	EPITHELIUM-RETINAL GPCR	09 12-28
910	DDOOR	SIGNATURE .	
810	PD02346	PHOTOSYSTEM II PROTEIN	PD02346F 12.89 4.340e-
		PRECURSOR	09 317-354

SEQ ID N	O: ACCESSION	DESCRIPTION	RESULTS*
	NO.		RESOUTS-
033		PHOTOSYNTHESIS.	
811	BL00685	CBF-A/NF-YB subunit	BL00685B 14.41 6.779e-
		proteins.	14 54-95 BL00685A 11.22 4.798e-13 5-54
812	PR00080	ALCOHOL DEHYDROGENASE	PR00080A 9.32 9.419e-
		SUPERFAMILY SIGNATURE	10 93-105
813	BL00357	Histone H2B proteins.	BL00357 7.74 1.988e-17 22-65
815	PD00066	PROTEIN ZINC-FINGER	PD00066 13.92 7.923e-
		METAL-BINDI.	15 158-171 PD00066
	- }		13.92 5.200e-14 46-59
			PD00066 13.92 7.000e-
			·14 18-31 PD00066
			13.92 7.000e-13 130- 143 PD00066 13.92
			7.500e-13 214-227
			PD00066 13.92 9.000e-
			13 102-115 PD00066
			13.92 4.429e-12 186-
			199 PD00066 13.92
			1.783e-11 74-87
816	BL01195	Peptidyl-tRNA hydrolase	BL01195C 20.12 3.348e-
020	- PT-00000	proteins.	20 100-139
820	BLC0520	Interleukin-10 family	BL00520A 6.21 6.471e-
822	BL00972	proteins.	09 1-14
022	BE00972	Ubiquitin carboxyl- terminal hydrolases	BL00972A 11.93 8.113e-
		family 2 proteins.	09 224-242
825	PR00876	NEMATODE METALLOTHIONEIN	PR00876B 7.66 2.268e-
		SIGNATURE	10 101-115
829	PD02855	FLAVOPROTEIN PROTEIN	PD02855A 18.37 4.732c-
		DNA/PANTOTHEN.	28 88-124 PD02855B
			8.36 6.478e-09 132-142
830	PR00405	HIV REV INTERACTING	PR00405B 11.83 7.000e-
		PROTEIN SIGNATURE	21 44-62 PR00405C
			19.41 1.000e-13 65-87 PR00405A 17.71 7.283e-
			13 25-45
831	⊋R00019	LEUCINE-RICH REPEAT	PR00019A 11.19 1.000e-
		SIGNATURE	09 47-61 PR00019B
			11.36 1.720e-09 136-
			150 PR00019B 11.36
832	PR00011	TYPE III EGF-LIKE	3.880e-09 44-58 PR00011B 13.08 3.438e-
	1100011	SIGNATURE	16 164-183 PR00011D
			14.03 6.850e-16 164-
	1		183 PR00011A 14.06
		1	8.364e-14 164-183
	1		PR00011C 24.25 5.415e-
			12 231-260 PR00011D
			14.03 9.852e-11 212-
834	PD00306	PROTEIN GLYCOPROTEIN	PD00306A 10.26 7.000e-
	1.2	PRECURSOR RE.	12 232-246
835	PD00306	PROTEIN GLYCOPROTEIN	PD00306A 10.26 4.000e-
		PRECURSOR RE.	10 290-304
836	PD00306	PROTEIN GLYCOPROTEIN	PD00306A 10.26 7.000e-
		PRECURSOR RE.	12 216-230
837	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 3.898e-
020	7700000		09 78-111
839	PD02784	PROTEIN NUCLEAR	PD02784B 26.46 8.302e-
840	DD00700	RIBONUCLEOPROTEIN.	09 73-116
040	PR00700	PROTEIN TYROSINE	PR00700B 16.80 5.091e-
		PHOSPHATASE SIGNATURE	22 369-390 PR00700D 12.47 5.765e-21 491-
			12.47 5.765e-21 491- 510 PR00700C 13.17
			4.750e-14 449-467
			PR00700F 11.18 8.500e-

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			11 538-549 PR00700E 17.57 3.100e-10 522- 538
841 .	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 5.404e- 13 134-153
844	PD02785	PROTEIN RIBOSOMAL 60S L22 RNA-BINDING HEP.	PD02785B 14.43 1.000e- 40 58-112 PD02785A 15.23 1.915e-28 8-57
845	BLC0826	MARCKS family proteins.	BL00826C 7.63 6.738e- 09 203-230
846	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 4.429e 10 15-24
849	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 1.000e- 08 340-349
850	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308A 5.90 6.506e- 09 12-27
851	PD02411	PROTEIN TRANSCRIPTION REGULATION NUCLEAR.	PD02411 21.89 7.000e- 16 246-280
	BL00420	Speract receptor repeat proteins domain proteins.	BL00420B 22.67 1.000e- 40 723-778 BL00420B 22.67 1.321e-38 933- 988 BL00420B 22.67 8.457e-28 482-537 BL00420B 22.67 4.500e- 27 587-642 BL00420B 22.67 9.625e-27 270- 325 BL00420B 22.67 4.205e-26 163-218 BL00420B 22.67 5.731e- 23 55-110 BL00420B 22.67 6.464e-20 377- 432 BL00420B 22.67 2.800e-15 830-885 BL00420C 11.90 1.900e- 13 355-366 BL00420C 11.90 1.900e-12 808- 819 BL00420C 11.90 3.550e-12 248-259 BL00420C 11.90 2.831e- 11 141-152 BL00420C 11.90 5.119e-11 1018- 1029 BL00420C 11.90 7.955e-10 567-578
853	BL00420	Speract receptor repeat proteins domain proteins.	BL00420B 22.67 1.000e- 40 756-811 BL00420B 22.67 1.321e-38 966- 1021 BL00420B 22.67 8.457e-28 482-537 BL00420B 22.67 4.500e- 27 620-675 BL00420B 22.67 9.625e-27 270- 325 BL00420B 22.67 4.205e-26 163-218 BL00420B 22.67 5.731e- 23 55-110 BL00420B 22.67 6.464e-20 377- 432 BL00420B 22.67 2.800e-15 863-918 BL00420C 11.90 1.900e- 13 355-366 BL00420C 11.90 1.900e-12 841- 852 BL00420C 11.90 3.550e-12 248-259 BL00420C 11.90 2.831e- 11 141-152 BL00420C 11.90 5.119e-11 1051- 1062 BL00420C 11.90

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		RESULIS-
662			7.955e-10 567-578
857	PR00388	3',5'-CYCLIC NUCLEOTIDE CLASS II PHOSPHODIESTERASE SIGNATURE	PR00388A 10.45 2.778e- 09 64-83
859	BF00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 2.929e- 13 37-56 BL00030B 7.03 1.900e-11 167-177 BL00030A 14.39 2.000e- 10 128-147
861	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 4.250e- 17 23-41 PR00988C 13.64 8.714e-16 107- 123 PR00988F 12.23 7.828e-15 198-212 PR00988E 8.27 9.769e- 12 176-188 PR00988D 5.95 8.250e-11 163-174 PR00988B 11.60 4.512e-
863	BL00215	Mitochondrial energy transfer proteins.	10 60-72 BL00215B 10.44 8.071e-
864	PR00775	90 KD HEAT SHOCK PROTEIN SIGNATURE	12 41-54  PR00775E 8.06 1.000e- 24 198-221 PR00775B 3.52 1.837e-23 107-130  PR00775D 8.91 4.884e- 17 171-189 PR00775A 9.90 8.342e-17 86-107  PR00775C 10.68 9.379e- 17 153-171 PR00775G 10.64 6.850e-15 267- 286 PR00775F 12.76
866	DM01688	2 POLY-IG RECEPTOR.	6.769e-14 249-267 DM01688G 16.45 9.460e-
867	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	09 89-121 PD01066 19.43 5.596e- 29 14-53
868	BL01287	RNA 3'-terminal phosphate cyclase proteins.	BL01287A 17.95 2.688e- 26 16-48
	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 6.464e- 10 304-337
	BL00046	Histone H2A proteins.	BL00046 12.95 1.000e- 40 30-85
874	BL00188	Biotin-requiring enzymes attachment site proteins.	BL00188 30.29 9.036e- 32 665-711
876	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.686e- 09 298-315
877	PD02102	SUBUNIT E V-ATPASE VACUOLAR ATP SYNTHASE HYDROL	PD02102A 16.74 4.176e- 10 97-141
879	BL01189	Ribosomal protein S12e proteins.	BL01189A 14.27 1.000e- 40 35-71 BL01189B 13.49 1.000e-40 71-125
882	BL00284	Serpins proteins.	BL00284C 28.56 6.400e- 25 62-104 BL00284B 17.99 6.182e-12 35-56
889	3L00216	Sugar transport proteins.	BL00216B 27.64 4.375e- 21 35-85
	PR00391	PHOSPHATIDYLINOSITOL TRANSFER PROTEIN SIGNATURE	PR00391E 12.50 7.785e- 15 211-231 PR00391B 8.39 1.000e-13 83-104 PR00391D 12.21 9.328e- 13 191-207 PR00391A 7.83 5.390e-11 16-36
897	R00327	ICE NUCLEATION PROTEIN	PR00327C 6.37 5.247e-

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		SIGNATURE	09 313-328
898	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039D 21.67 7.800e- 26 386-432 BL00039A 18.44 6.674e-16 113- 152 BL00039B 19.19 1.947e-13 153-179 BL00039C 15.63 9.460e- 11 236-260
901	PD00066	PROTEIN ZINC-FINGER METAL-BINDI,	PD00066 13.92 8.200e- 16 254-267 PD00066 13.92 8.200e-16 282- 295 PD00066 13.92 8.200e-16 310-323 PD00066 13.92 8.200e- 16 366-379 PD00066 13.92 8.200e-16 394- 407 PD00066 13.92
902	BI:01115	GTP-binding nuclear	8.200e-14 338-351 BL01115A 10.22 9.321e-
903	PR00806	Protein ran proteins. VINCULIN SIGNATURE	PR00806B 4.28 9.160e-
904	PR00381	KINESIN LIGHT CHAIN SIGNATURE	09 97-111  PR00381E 8.75 6.586e- 25 335-356 PR00381B 18.17 2.667e-24 204- 224 PR00381A 9.55 2.800e-24 107-125 PR00381C 12.48 4.522e- 24 226-245 PR00381D 13.94 1.084e-22 291- 309 PR00381F 9.13 3.288e-22 370-392 PR00381F 9.13 7.181e- 13 286-308 PR00381E 8.75 4.066e-11 251-272 PR00381E 8.75 7.033e- 11 293-314 PR00381E 8.75 8.364e-10 377-398 PR00381D 13.94 5.230e- 09 333-351 PR00381C 12.48 7.120e-09 310- 329
906	PR00345	STATHMIN FAMILY SIGNATURE	PR00345C 4.54 8.557e- 09 525-549
907	PRC0345	STATHMIN FAMILY SIGNATURE	PR00345C 4.54 8.557e- 09 513-537
908	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 9.308e-11 144-155
910	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 2.800e- 30 48-87
912	BL01104	Ribosomal protein Ll3e proteins.	BL01104C 15.14 6.000e- 09 364-392
922	3L00678	Trp-Asp (WD) repeat	BL00678 9.67 3.842e-09
923	PR00320	proteins proteins. G-PROTEIN BETA WD-40 REPEAT SIGNATURE	500-511 PR00320C 13.01 2.500e- 09 323-338 PR00320C 13.01 5.500e-09 187- 202
924	PD02181	PROTOCHLOROPHYLLIDE REDUCTASE PHOTOSYNT.	PD02181D 12.85 8.609e- 09 36-64
926	BL00678	Actinin-type actin- binding domain proteins.	BL00019C 14.66 7.453e- 25 108-144 BL00019B 13.34 6.510c-11 61-84 BL00019D 15.33 9.338e- 11 205-235 BL00019A 12.56 2.373e-10 34-45
740	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 9.308e-11

SEQ ID NO		DESCRIPTION	RESULTS*
	NO.		
		proteins proteins.	273-284 BL00678 9.67 1.600e-10 314-325 BL00678 9.67 7.600e-10 360-371 BL00678 9.67
929	BL00518	Zinc finger, C3HC4 type	8.579e-09 206-217 BL00518 12.23 1.857e-
930	BL01085	(RING finger), proteins. Ribulose-phosphate 3-	10 137-146 BL01085D 16.55 4.600e-
		epimerase family proteins.	24 134-165 BL01085B 10.15 5.680e-22 30-52 BL01085E 18.87 8.676e- 20 172-202 BL01085C 21.81 2.038e-14 66-97
931	BL01085	Ribulose-phosphate 3- epimerase family proteins.	BLC1085D 16.55 4.600e- 24 152-103 BL01085B 10.15 5.680e-22 30-52 BL01085E 18.87 8.676e- 20 190-220 BL01085C 21.81 2,038e-14 66-97
933	PD00301	PROTEIN REPEAT MUSCLE CALCIUM-BI.	PD00301A 10.24 6.400e- 09 160-171
936	PF00168	C2 domain proteins.	PF00168C 27.49 4,000e-
937	BL00415	Synapsins proteins.	BL00415N 4.29 9.519e-
940	PR00862	PROLYL OLIGOPEPTIDASE SERINE PROTEASE (S9A) SIGNATURE	PR00862D 16.17 4.086e- 09 63-84
945	BL01230	RNA methyltransferase trmA family proteins.	BL01230B 11.62 2.373e-
948	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 7.429e- 18 52-68 BL00479A 19.86 2.200e-13 26-49
949	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 1.474e-09
954	PD01311	PROTEIN OXIDOREDUCTASE NAD INTERGENIC RE.	PD01311A 30.23 5.909e- 10 66-111
955	PF00651	BTB (also known as BR- C/Ttk) domain proteins.	PF00651 15.00 3.250e-
956	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 3.250e-
957	BL00379	CDP-alcohol phosphatidyltransferases proteins.	BL00379 24.64 1.610e- 15 111-148
959	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 1.884e- 10 31-75
960	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 3.438e- 14 110-154
962	BL00061	Short-chain dehydrogenases/reductase s family proteins.	BL00061B 25.79 6.586e- 13 198-236
963	PR00502	MUTT DOMAIN SIGNATURE	PR00502A 15.06 8.200e- 11 210-225
966	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308A 5.90 7.035e-
967	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 1.286e- 12 104-124 DM01206B 10.69 5.299e-11 23-43 DM01206B 10.69 8.274e- 10 73-93 DM01206B 10.69 3.962e-09 108- 128 DM01206B 10.69 5.671e-09 38-58
969	PF01008	Initiation factor 2 subunit.	PF01008B 25.59 4.724e- 31 417-460 PF01008C 12.25 5.333e-18 506- 526 PF01008A 20.14 5.875e-15 369-390

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970	BL01277	Ribonuclease PH proteins.	BL01277C 10.18 7.648e- 10 112-143 BL01277A
975	BL01159		17.39 9.806e-10 40-78
3,3	PROTIZA	WW/rsp5/WWP domain proteins.	BL01159 13.85 3.605e-
		proceins.	12 130-145 BL01159 13.85 4.122e-10 171-
			186
977	PF00791	Domain present in ZO-1	PF00791C 20.98 2.235e-
		and Unc5-like netrin	09 55-94
700		receptors.	
978	BL01167	Ribosomal protein L17	BL01167B 20.66 B.258e-
979	BL00478	proteins.  LIM domain proteins.	19 88-127
	2200476	dim domain process.	BL00478B 14.79 9.357e-
			13 33-48 BL00478B 14.79 7.250e-12 98-113
980	PR00312	CALSEQUESTRIN SIGNATURE	PR00312E 8.32 3.423e-
			36 169-199 PR00312I
			15.78 5.286e-35 332-
			361 PR00312F 15.06
			5.865e-35 199-229
			PR00312H 13.31 8.313e-
		1	35 263-291 PR00312J 13.73 5.688e-34 363-
	ì		392 PR00312D 9.43
			2.636e-33 128-158
			PR00312C 15.14 8.839e-
	1	İ	33 92-122 PR00312B
			15.08 8.941e-33 62-92
		į	PR00312G 11.11 6.657e- 32 230-258 PR00312A
			11.70 6.914e-27 35-59
981	PF00992	Troponin.	PF00992A 16.67 8.816e-
000			09 414-449
982	PR00299	ALPHA CRYSTALLIN	PR00299F 13.20 2.367e-
983	BL01150	Respiratory-chain NADH	09 127-149
	2201130	dehydrogenase 20 Kd	BL01150B 17.16 1.000e- 40 156-202 BL01150A
		subunit proteins.	14.10 8.200e-39 100-
			138
986	BL00795	Involucrin proteins.	BL00795C 17.06 7.211e-
			14 4-49 BL00795C
		•	17.06 1.778e-11 1-46
		}	BL00795C 17.06 3.407e-
		1	10 14-59 BL00795C 17.06 7.802e-10 2-47
			BL00795C 17.06 8.640e-
			10 19-64 BL00795C
			17.06 7.400e-09 11-56
			BL00795C 17.06 7.800e-
87	3L00939	Ribosomal protein Lle	09 3-48
		proteins.	BL00939F 17.27 5.393e- 09 810-840
88	PR00452	SH3 DOMAIN SIGNATURE	PR00452B 11.65 6.538e-
			11 525-541
89	PR00452	SH3 DOMAIN SIGNATURE	PR00452B 11.65 6.538e-
194	Dr. o con a		11 497-513
794	BL00027	'Homeobox' domain	BL00027 26.43 2.500e-
97	BL01304	proteins. ubiH/COQ6 monooxygenase	25 146-189
		family proteins.	BL01304A 8.05 3.893e-
98	DM01767	5 TRANSMITTER DOMAIN.	DM01767B 10.07 7.868e-
			09 22-39
000	PR00926	MITOCHONDRIAL CARRIER	PR00926C 16.07 1.750e-
	<b>\</b>	PROTEIN SIGNATURE	24 73-94 PR00926D
			10.53 3.250e-23 126-
	l l		145 PR00926F 17.75
			6.211e-23 217-240 PR00926E 11.70 6.625e-

NO.	SEQ ID N	O: ACCESSION	DESCRIPTION	DECIT CO.
16.07 2.125e-18 24-39     PRO0326A 1.0.1 2.000c.     PRO0326A 1.0.1 2.000c.     PRO0326A 1.0.1 2.000c.     PRO0326A 1.0.1 2.000c.     PRO0326F 1.7.5 5.5558-09 120-113				RESULTS*
PRO0326A 10.4: 1.000e-		1		20 174-193 PR00926B
15 11-25 PR00326F   17.75 5.5658-09 120-103				16.07 2.125e-18 24-39
17.75 5.5656-09 120-143		İ		15 11-25 PR00926F
143   BL00406   Actins proteins.   BL004068 S.47 1.000e-40   417-202   81.004066   4.75   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   1.000e-40   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   417-202   41				
BLOO4068	1006			
	1002	BL00406	Actins proteins.	
BL00406   12.58 3.700e- 40 270-325 BL00406   8.44 7.375e-38 327-37; BL00406   8.95 3.348e- 29 11-46   BL00406   Actins pxoteins.   BL00406   8.47 1.000e- 40 88-143 BL00406   6.75 1.000e-40 147-202   BL004068 8.44 1.000e- 35 248-298 BL00406   35 248-298 BL004068   8.47 1.000e- 40 88-143 BL00406   6.75 1.000e-40 147-202   8.69 4.667e-20 81-114   8.714e- 40 PRO10304   TAILLESS COMPLEX   PRO304D 11.04 8.714e- 40 PRO10304   PRO10304   PRO10304A   9.20 3.382e-16 46-63   PRO304B 11.60 7.5716   9.20 3.382e-16 46-63   PRO304B 11.60 7.5716   9.20 3.382e-16 46-63   PRO304B 11.60 7.5716   9.20 3.382e-16 46-63   PRO304B 11.60 7.5716   9.20 3.382e-16 46-63   PRO304B 11.60 7.5716   9.20 3.382e-16 46-63   PRO304B 11.60 7.5716   9.20 3.382e-16 46-63   PRO304B 11.60 7.5716   9.20 3.382e-16 46-63   PRO304B 11.60 7.5716   9.20 3.382e-16 46-63   PRO304B 11.60 7.5716   9.20 3.382e-16 46-63   PRO304B 11.60 7.5716   9.20 3.382e-16 46-63   PRO304B 11.60 7.5716   9.20 3.382e-16 46-63   PRO304B 11.60 7.5716   9.20 3.382e-16 46-63   PRO304B 11.60 7.5716   9.20 3.382e-16 46-63   PRO304B 11.60 7.5716   9.20 3.382e-16 46-63   PRO306B 19.43 2.929e-21NC-FINGER METAL-BINDING NU.   9.20 3.382e-16 46-63   PRO306B 19.43 2.929e-21NC-FINGER METAL-BINDING NU.   9.20 4.882e-10   9.20 3.382e-16 46-63   9.20 3.382e-16 46-63   9.20 3.382e-16 46-63   9.20 3.382e-16 46-63   9.20 3.382e-16 46-63   9.20 3.382e-16 46-63   9.20 3.382e-16 46-63   9.20 3.382e-16 46-63   9.20 3.382e-16 46-63   9.20 3.382e-16 46-63   9.20 3.382e-16 46-63   9.20 3.382e-16 46-63   9.20 3.382e-16 46-63   9.20 3.382e-16 46-63   9.20 3.382e-16 46-63   9.20 3.382e-16 46-63   9.20 3.282e-10   9.20 3.282e-10   9.20 3.282e-10   9.20 3.282e-10   9.20 3.282e-10   9.20 3.282e-10   9.20 3.282e-10   9.20 3.282e-10   9.20 3.282e-10   9.20 3.282e-10   9.20 3.282e-10   9.20 3.282e-10   9.20 3.282e-10   9.20 3.282e-10   9.20 3.282e-10   9.20 3.282e-10   9.20 3.282e-10   9.20 3.282e-10   9.20 3.282e-10   9.20 3.282e-10   9.20 3.282e-10   9.20 3.282e-10   9.20 3.282e-10   9.20 3.282e-10   9.20 3.28				
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(CHAPERONE) SIGNATURE  8.69 4.667e-20 98-118 PRO0304B 11.60 7.577e- 19 68-87 PR00304B 9.20 3.382e-16 46-63 PR00304E 7.79 6.870e- 13 418-431 13 418-431 1011 PD01066 PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.  PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.  PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.  PD01066 PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.  PD01068 PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.  PD01068 PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.  PD01068 PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.  PD01068 PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.  PD01068 PROTEIN GENCH RING FINGEY, C3HC4 type (RING Finger), proteins.  PD01068 PROTEIN GENCH RING FINGEY PP01068 PROTEIN GENCH RING FINGEY PP00930 PROTEIN GENCH RING FINGER PP00930 PROTEIN GENCH RING FINGER PP00930 PROTEIN GENCH RING FINGER PP00930 PROTEIN GENCH RING FINGER PP00930 PP00930 PROTEIN GENCH RING FINGER PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00930 PP00	100.7	PR00304		PR00304D 11.04 8.714e-
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ZINC-FINGER METAL-    32 58-107   BINDING NU.   Zinc finger, C3HC4 type (RING finger), proteins.   10 64-73   10 64-73   10 64-73   10 64-73   10 64-73   10 64-73   10 64-73   10 64-73   10 64-73   10 64-73   10 64-73   10 64-73   11 174-194   11 174-194   11 174-194   11 174-194   11 174-194   11 174-194   11 174-194   11 174-194   11 174-194   12 08 1.000e-100   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10 690   10	1011	PD01066		PD01066 :0 43 7 000
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PROTEIN ALANYL.  PROTEIN ALANYL.  PROTEIN GTPASE DOMAIN ACTIVATION.  PROSPHOGLY PROSPONDATION ACTIVATION.  PROSPHOGLY PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOOL PROSPHOO	1016	PD01168	SYNTHETASE LIGAGE	
PD00930   PROTEIN GTPASE DOMAIN   ACTIVATION.   32 261-302 PD00930A   25.62 9.550e-22 157-			· · · · · · · · · · · · · · · · · · ·	
ACTIVATION.  32 261-302 PD00930A 25.62 9.550e-22 157- 183  Phosphoglycerate mutase family phosphohistidine proteins.  14-3-3 PROTEIN ZETA SIGNATURE  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO0353  DELO035	1018	PD00930	PROTEIN GTPASE DOMAIN	
BL00175   Phosphoglycerate mutase   family phosphohistidine   12 6-26 BL00175C   12 6-26 BL00175C   23.75 8.062e-10 79-111   12 6-26 BL00175C   23.75 8.062e-10 79-111   14-3-3 PROTEIN ZETA   PR00305D 16.34 1.439e-   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-1			ACTIVATION.	32 261-302 PD00930A
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family phosphohistidine proteins. 22 6-26 BL00175C 23.75'8.062e-10 79-111 23.75'8.062e-10 79-111 PR00305 14-3-3 PROTEIN ZETA PR00305D 16.34 1.439e-10 158-185	1022	BL00175	Phograposito	
PRO0305   14-3-3 PROTEIN ZETA   PRO0305D 16.34 1.439e-   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185   10 158-185			family phosphohistidine	
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BL00353B 11.47 2.436e- 18 238-288 BL00353C 14.83 8.844e-11 288- 335   BL00183   Ubiquitin-conjugating enzymes proteins.   BL00183 28.97 1.310e- 33 43-91   Strong proteins   BL00183 28.97 1.310e- 33 43-91   Strong proteins   PF00580A 13.37 4.720e- 09 111-133   PF00413   HALOACID   PF00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171   PR00413E 15.78 3.429e- 09 154-171	1026	77.000		10 158-185
14.83 8.844e-11 288-335	1020	BT:00323	HMG1/2 proteins.	
028   BL00183   Ubiquitin-conjugating enzymes proteins.   335     033   2F00580   UvrD/REP helicase.   PF00580A 13.37 4.720e-				18 238-288 BL00353C
BL00183   Ubiquitin-conjugating enzymes proteins.   33 43-91   33 43-91   33 43-91   33 43-91   33 43-91   33 43-91   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-1   34 39-				
enzymes proteins.   33 43-91	1028	BL00183	Ubiquitin-conjugating	
PF00580   UvrD/REP helicase.   PF00580A 13.37 4.720e-   09 111-133   PR00413   HALOACID   PR00413E 15.78 3.429e-   DEHALOGENASE/EPOXIDE   HYDROLASE FAMILY   SIGNATURE   PD01066 19.43 9.657e-   ZINC-FINGER METAL-   O9 5-44     D101796   PROTEIN TRANSMEMBRANE   PD01796 15.01 4.259e-   COBALT ZINC CADMIU.   11 55-82     D101796   D101796   D101796   D101796   D101796   D101796   D101796     D101796   PR00970   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D101796   D10	A 3 3		enzymes proteins.	
09 111-133	1033	PF00580		
DEHALOGENASE/EPOXIDE HYDROLASE FAMILY SIGNATURE  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 154-171  09 15	034	7700412		09 111-133
HYDROLASE FAMILY   SIGNATURE   PD01066 19.43 9.657e-   ZINC-FINGER METAL-   09 5-44   BINDING NU.   D01796   PROTEIN TRANSMEMBRANE   PD01796 15.01 4.259e-   COBALT ZINC CADMIU.   11 55-82   D1796   PR00970   PR00970   ARGININE ADP-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.143e-   PR00970A 17.73 6.1448e-   PR00970A 17.73 6.1448e-   PR00970A 17.73 6.1448e-   PR00970A 17.73 6.1448e-   PR00970A 17.73 6.1448e-   PR00970A 17.73 6.1448e-   PR00970A 17.73 6.1448E-   PR00970A 17.73 6.1448E-   PR00970A 17.73 6.1448E-   PR00970A 17.73 6.1448E-		FR00413		PR00413E 15.78 3.429e-
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PD01066   PROTEIN ZINC FINGER   PD01066 19.43 9.657e-				
ZINC-FINGER METAL- BINDING NU.  PROTEIN TRANSMEMBRANE COBALT ZINC CADMIU.  BL00299 BL00299 Ubiquitin domain proteins.  PR00970  PR00970  PR00970  PR00970  PR00970  PR00970A 17.73 6.143e-	037	PD01066		PD01066 19 63 9 6570
BINDING NU.  PROTEIN TRANSMEMBRANE PD01796 15.01 4.259e- COBALT ZINC CADMIU. 11 55-82  D39 BL00299 Ubiquitin domain BL00299 28.84 9.036e- proteins. 09 17-69  PR00970 ARGININE ADP- PR00970A 17.73 6.143e-		1		09 5-44
COBALT ZINC CADMIU. 11 55-82  D39 BL00299 Ubiquitin domain BL00299 28.84 9.036e- proteins. 09 17-69  PR00970 ARGININE ADP- PR00970A 17.73 6.143e-	000			
COBALT ZINC CADMIU. 11 55-82  Ubiquitin domain BL00299 28.84 9.036e- proteins. 09 17-69  PR00970 ARGININE ADP- PR00970A 17.73 6.143e-	038	PD01796		PD01796 15.01 4.259e-
proteins. 09 17-69  ARGININE ADP- PR00970A 17.73 6.143e-	039	DI 00000		11 55-82
PR00970 ARGININE ADP- PR00970A 17.73 6.143e-		BL00299		BL00299 28.84 9.036e-
PRO09/0A 17.73 6.143e-	040	PR00970		
20 36-78 PR00970B				
			RIBOSYLTRANSFERASE	

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
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	}	SIGNATURE	9.96 2.154e-18 154-171 PR00970F 12.30 1.000e-
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	1		PR00970B 16.37 1.290e-
	1		13 86-105 PR00970C
			11.05 1.643e-11 115-
	1		130 PR00970E 11.23
			9.820e-11 202-218
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1043	PR00048	C2H2-TYPE 2INC FINGER	PR00048A 10.52 6.786e-
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	•		10.52 1.000e-09 172-
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1046	BL01092	Adenylate cyclases	331
2010	1 0000002	class-I proteins.	BL01092N 13.54 8.924e-
1047	BL01216	ATP-citrate lyase /	10 3-40 BL01216D 21.75 4.316e-
	3301210	succinyl-CoA ligases	28 314-344 BL01216A
		family proteins.	13.91 1.000e-10 97-112
1049	DM00031	IMMUNOGLOBULIN V REGION.	DM00031B 15.41 7.618e-
		The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s	12 102-136
1050	BL01073	Ribosomal protein L24e	BL01073 24.30 1.000e-
		proteins.	40 12-62
1054	BL00571	Amidases proteins.	BL00571 25.69 5.875e-
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	J		7.03 4.316e-09 137-147
1058	BL00223	Annexins repeat proteins	BL00223C 24.79 8.754e-
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1060	BL00027	'Homeobox' domain	11 118-152
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1064	BL00455	Putative AMP-binding	BL00455 13.31 6.211e-
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1065	PR00019	LEUCINE-RICH REPEAT	PR00019A 11.19 2.000e-
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1066	PR00326	GTP1/OBG GTP-BINDING	PR00326A 8.75 4.600e-
j		PROTEIN FAMILY SIGNATURE	16 151-172 PR00326C
Ì			9.79 1.290e-14 200-216
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			19.09 1.257e-13 217-
1071	B9886		236
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1075	BL01009	Extracellular proteins	BL01009D 14.19 4.300e-
		SCP/Tpx-1/Ag5/PR-1/Sc7	20 127-148 BL01009A
l		proteins.	13.75 6.586e-13 57-75
İ			BL01009E 13.50 1.439e-
1077	PR00724	CARRAVARRATINACE	11 159-175
	* ****	CARBOXYPEPTIDASE C SERINE PROTEASE (S10)	PR00724A 10.91 1.000e-
İ		FAMILY SIGNATURE	08 366-379
1078	BL00215	Mitochondrial energy	PV 0001F2 1E 00 1 000
		transfer proteins.	BL00215A 15.82 1.000e-
J		cranster proteins.	12 170-195 BL00215A
1079	BL00678	Trp-Asp (WD) repeat	15.82 7.529e-10 79-104
		Typh-wah /uni rehear	BL00678 9.67 4.316e-09

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		proteins proteins.	298-309
1081	BL00326	Tropomyosins proteins.	BL00326A 14.01 7.398e- 10 23-57
1094	B1.00460	Glutathione peroxidases selenocysteine proteins.	BL00460A 28.67 3.204e- 18 57-92 BL00460B 9.73 6.400e-13 100-118 BL00460D 16.89 9.143e- 12 162-182 BL00460C 14.35 5.500e-09 133- 156
1095	PD02811	PROTEIN PEPTIDE REDUCTASE MG448 PILB FIMBRIA TRAN.	PD02811A 20.67 3.017e- 22 67-105 PD02811B 17.07 2.263e-21 118- 151 PD02811C 13.25 5.696e-13 154-167
1096	PD02811	PROTEIN PEPTIDE REDUCTASE MG448 PILB FIMBRIA TRAN.	PD02811A 20.67 3.017e- 22 60-98 PD02811B 17.07 2.263e-21 111- 144 PD02811C 13.25 5.696e-13 147-160
1097	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 6.143e- 09 200-216
1105	PF00881	Nitroreductase family.	PF00881A 27.15 9.229e-
1109	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 3.077e- 10 15-37 PR00449E 13.50 1.857e-09 185- 208 PR00449D 10.79 8.364e-09 131-145
1115	PR00405	HIV REV INTERACTING PROTEIN SIGNATURE	PRO0405B 11.83 5.737e- 20 42-60 PRO0405A 17.71 2.703e-17 23-43 PR00405C 19.41 6.902e- 10 63-85
1116	BL00355	HMG14 and HMG17 proteins.	BL00355 5.97 2.528e-25
1117	BL00355	HMG14 and HMG17	BL00355 5.97 2.528e-25 20-51
1120	BL00107	Protein kinases ATP- binding region proteins.	BL00107B 13.31 4.857e- 10 290-306
1123	PR00412	EPOXIDE HYDROLASE SIGNATURE	PR00412F 18.76 9.526e-
1125	PR00186	HEMERYTHRIN SIGNATURE	PR00186A 13.62 2.800e- 09 87-101
1129	BL00170	Cyclophilin-type peptidyl-prolyl cis- trans isomerase signatur.	BL00170C 18.49 3.077e- 33 84-129 BL00170B 20.97 6.838e-25 37-77 BL00170A 17.08 3.455e- 15 10-37
1131	BL00636	Nt-dnaJ domain proteins.	BL00636A 8.07 5.304e- 15 29-46 BL00636B
1132	BL00678	Trp-Asp (WD) repeat proteins proteins.	15.11 1.360e-14 59-80 BL00678 9.67 6.211e-09 29-40
1133	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 6.211e-09 29-40
1136	BL00990	Clathrin adaptor complexes medium chain proteins.	BL00990C 18.78 4.176e- 38 235-269 BL00990A 21.44 4.316e-36 94-132 BL00990B 20.15 2.125e- 27 157-187 BL00990D 16.13 5.320e-18 403- 422
1137	PR00314	CLATHRIN COAT ASSEMBLY PROTEIN SIGNATURE	PR00314B 15.68 8.000e- 34 100-128 PR00314D 9.66 3.531e-33 233-261 PR00314C 16.05 8.909e-

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	NO.	DESCRIPTION	RESULTS*
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	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 6.364e- 13 13-57
1141	BL00107	Protein kinases ATP-	BL00107A 18.39 4.00Ce-
		binding region proteins.	19 451-482 BL00107B
			13.31 3.077e-12 519-
·		_	535
1148	PR00685	TRANSCRIPTION INITIATION	PR00685A 13.62 4.676e-
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1155	PD01652	RECEPTOR CELL NK	PD01652B 8.50 9.396e-
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1157	PD02894	HYDROLASE N4- PRECURSOR	PD02894A 21.96 7.873e-
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1159	BL00623	GMC oxidoreductases	BL00623E 15.00 3.531e-
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8854			176
1161	PD01937	DNA PROTEIN POLYMERASE	PD01937A 6.68 3.475e-
11.60		ENDONUCLEASE DNA	09 330-341
1162	PD01937	DNA PROTEIN POLYMERASE	PD01937A 6.68 3.475e-
1163	770000	ENDONUCLEASE DNA	09 221-232
1163	PR00624	HISTONE H5 SIGNATURE	PR00624D 11.94 7.455e-
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1167	BL00226		337
110/	RT00556	Intermediate filaments	BL00226B 23.86 7.384e-
1177	BL01032	proteins.	09 302-350
	PD01035	Protein phosphatase 2C	BL01032G 8.33 1.422e-
1178	PR00320	proteins.	10 34-48
2270	PRV0320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 1.794e-
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1180	PR00454	ETS DOMAIN SIGNATURE	PR00454D 10.89 4.150e-
Ì			19 765-784
1181	BL00291	Prion protein.	BL00291A 4.49 8.962e-
			11 152-187
1184	BL00720	Guanine-nucleotide	BL00720B 16.57 4.103e-
		dissociation stimulators	18 1089-1113
		CDC25 family sign.	20 2005-1113
1185	BL00215	Mitochondrial energy	BL00215A 15.82 4.553e-
		transfer proteins.	13 204-229 BL00215A
		-	15.82 1.429e-12 11-36
1			BL00215A 15.82 9.809e-
			11 104-129
187	BL00983	Ly-6 / u-PAR domain	BL00983C 12.69 2.761e-
		proteins.	10 77-93
.188	BL00878	Orn/DAP/Arg	BL00878B 10.95 6.000e-
i		decarboxylases family 2	16 189-204 BL00878C
		pyridoxal-P attachment	17.74 8.435e-15 225-
1		si.	245 BL00878F 19.67
			3.625e-13 379-402
j		1	BL00878D 16.56 1.621e-
		<u> </u>	09 270-289
191	PD02939	PROTEIN GLUTATHIONE	PD02939B 10.10 2.723e-
ļ		SYNTHETASE SY.	12 203-220 PD02939C
}			20.01 1.000e-11 224-
		1	252
103	22222	<del></del>	
193	PR00345	STATHMIN FAMILY SIGNATURE	PR00345B 7.12 2.800e-

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
DEQ 25 NO.	NO.	DESCRIPTION	
			8.54 7.652e-28 149-174
			PR00345C 4.54 9.100e-
1	1		28 101-125 PR00345D
1			10.97 1.964e-24 125-
i	<b>}</b>		149 PR00345A 13.46
		į	5.645e-16 43-62
1194	PR00345	STATHMIN FAMILY	PR00345B 7.12 2.800e-
	-1100525	SIGNATURE	28 108-137 PR00345E
		DIGARITORE	8.54 7.652e-28 185-210
1			PR00345C 4.54 9.100e-
			28 137-161 PR00345D
ł			10.97 1.954e-24 161-
ì			185 PR00345A 13.46
			5.645e-16 79-98
1195	PF00995	Secl family.	PF00995B 17.37 1.120e-
L			13 224-264
1196	BL00982	Bacterial-type phytoene	BL00982A 18.41 6.738e-
		dehydrogenase proteins.	11 15-47
1197	BL01298	Dihydrodipicolinate	BL01298A 13.90 5.959c-
	-202250	reductase proteins.	09 51-73
1203	PERANCE		.]
1203	BL00061	Short-chain	BL00061B 25.79 1.000e-
1		dehydrogenases/reductase	14 152-190
		s family proteins.	
1204	PR00118	BETA-LACTAMASE CLASS A	PR00118F 16.42 9.386e-
	1	SIGNATURE	09 213-229
1206	BL01183	ubiE/CO05	BL01183B 21.31 1.429e-
ł		methyltransferase family	37 184-229 BL01183D
ĺ	1	proteins.	27.71 8.535e-27 264-
		process.	307 BL01183A 13.25
		į –	3.250e-23 51-73
			- · · •
			BL01183C 10.77 5.295e-
1000	<b>***</b>		09 246-258
1208	BL00979	G-protein coupled	BL00979L 20.63 2.485e-
		receptors family 3	09 105-146
		proteins.	
1209	PFC0023	Ank repeat proteins.	PF00023A 16.03 4.857e-
			11 49-65 PF00023B
			14.20 1.818e-09 45-55
1212	PR00048	C2H2-TYPE ZINC FINGER	PR00048A 10.52 7.750e-
		SIGNATURE	14 227-241 PR00048A
	ļ		10.52 4.316e-11 199-
	ľ		213
1213	PR00450	RECOVERIN FAMILY	
_ <del></del>	-100430	SIGNATURE	PR00450C 12.22 1.720e-
		JIGHATURE	10 20-42 PR00450C
		1	12.22 3.506e-09 56-78
		}	PR00450D 16.58 6.769e-
4046			09 44-64
1216	BL00412	Neuromodulin (GAP-43)	BL00412D 16.54 5.598e-
		proteins.	10 179-230
1219	PR00456	RIBOSOMAL PROTEIN P2	PR00456E 3.06 5.348e-
		SIGNATURE	11 249-264
1222	PD00066	PROTEIN ZINC-FINGER	PD00066 13.92 7.231e-
		METAL-BINDI.	15 295-308 PD00066
		ŀ	13.92 7.231e-15 406-
			419 PD00066 13.92
			2.286e-12 378-391
			PD00066 13.92 7.857e-
		1	12 434-447 PD00066
		1	13.92 3.348e-11 350-
1		1	363
1223	BL50058	G-protein gamma subunit	BL50058 27.23 1.000e-
		profile.	40 13-61
1226	BL00412	(	
	DUUUNIZ	Neuromodulin (GAP-43)	BL00412D 16.54 8.439e-
1000		proteins.	09 279-330
1227	BL00437	Catalase proximal heme-	BL00437A 18.82 1.000e-
		ligand proteins.	40 49-101 BL00437B
			16.28 1.000e-40 114-
j		· I	168 BL00437C 21.86

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	NO.		1.000e-40 190-239
	ľ		BL00437D 25.72 1.000e-
į	<u> </u>		40 248-301 BL00437E
			23.95 1.000e-40 327-
1230			379
1230	BL01160	Kinesin light chain	BL01160B 19.54 8.297e-
1231	PR00735	repeat proteins. GLYCOSYL HYDROLASE	10 5-60 PR00735A 11.19 6.857e-
1201	FR00/33	FAMILY 8 SIGNATURE	09 391-405
1232	PR00497	NEUTROPHIL CYTOSOL	PR00497A 6.92 5.553e-
	1	FACTOR P40 SIGNATURE	10 158-176
1233	PR00497	NEUTROPHIL CYTOSOL	PR00497A 6.92 5.553e-
		FACTOR P40 SIGNATURE	10 158-176
1235	BL00866	Carbamoyl-phosphate	BL00866B 36.29 2.776e-
		synthase subdomain	09 75-121
		proteins.	
1237	BL00027	'Homeobox' domain	BL00027 26.43 1.818e-
1243	2200103	proteins.	21 36-79
1643	PR00403	WW DOMAIN SIGNATURE	PR00403B 12.19 1.184e-
1246	PD01168	SYNTHETASE LIGASE	11 10-25 PD01168L 9.47 2.837e-
	-201100	PROTEIN ALANYL.	10 31-46 PD01168L
			9.47 4.490e-10 174-189
			PD01168L 9.47 7.612e-
			10 183-198
1249	BL00018	EF-hand calcium-binding	BL00018 7.41 2.800e-10
1254	D. 00. 22	domain proteins.	183-196
1234	BL00183	Ubiquitin-conjugating enzymes proteins.	BL00183 28.97 2.440e- 36 96-144
1255	BL01115	GTP-binding nuclear	BL01115A 10.22 5.670e-
		protein ran proteins.	11 8-52
1256	BL00373	Phosphoribosylglycinamid	BL00373C 10.35 3.348e-
	1	e formyltransferase	12 143-156
·		proteins.	
1258	PR00011	TYPE III EGF-LIKE	PR00011B 13.08 3.217e-
1259	BL00518	Zinc finger, C3HC4 type	10 174-193 BL00518 12.23 8.286e-
1233	D100318	(RING finger), proteins.	10 31-40
1261	PR00070	DIHYDROFOLATE REDUCTASE	PR00070D 11.63 1.000e-
		SIGNATURE	15 112-127 PR00070C
			13.09 9.500e-15 51-63
			PR00070A 12.92 5.500e-
1000			12 16-27
1262	BL00462	Gamma-	BL00462A 20.89 6.438e-
		glutamyltranspeptidase proteins.	24 140-183 BL00462B
		procerns.	17.88 5.500e-20 230- 267 BL00462C 27.41
			2.023e-11 292-347
1263	BL00038	Myc-type, helix-loop-	BL00038B 16.97 9.455e-
		helix' dimerization	11 62-83
		domain proteins.	
1264	BL01115	GTP-binding nuclear	BL01115A 10.22 5.670e-
1266	DD00027	protein ran proteins.	11 17-61
4600	PR00837	ALLERGEN V5/TPX-1 FAMILY SIGNATURE	PR00837C 17.21 2.714e-
		SIGNATURE	18 165-182 PR00837A 14.77 4.512e-12 86-105
		Ì	PR00837D 11.12 7.577e-
			12 201-215
1269	PR00449	TRANSFORMING PROTEIN P21	PR00449C 17.27 9.308e-
		RAS SIGNATURE	22 40-63 PR00449E
	:		13.50 1.000e-16 137-
			160 PR00449D 10.79
1270	BL00276	Champal Samuel and Champal	3.520e-11 102-116
	-1002/B	Channel forming colicins proteins.	BL00276A 8.87 1.500e- 09 17-29
1275	PD02327	GLYCOPROTEIN ANTIGEN	PD02327C 15.47 9.769e-
	·	PRECURSOR IMMUNOGLO.	09 228-243
1276	PR00412	EPOXIDE HYDROLASE	PR00412B 12.59 7.894e-
		·	

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		
}		SIGNATURE	12 119-135 PR00412C
			11.30 1.857e-11 165- 179 PR00412A 13.23
		*	3.400e-11 100-119
1277	PF00756	Putative esterase.	PF00756C 14.12 9.538e-
			10 127-157
1279	BL00134	Serine proteases,	BL00134A 11.96 9.325e-
	į	trypsin family, histidine proteins.	13 128-145
1280	BL01220	Phosphatidylethanolamine	BL01220C 14.75 9.348e-
		-binding protein family	15 248-276
		proteins.	
1285	BL00518	Zinc finger, C3HC4 type	BL00518 12.23 2.286e-
1287	PF00791	(RING finger), proteins.  Domain present in ZO-1	10 33-42
1207	PE00791	and Unc5-like netrin	PF00791B 28.49 7.182e-
	1	receptors.	11 200-343
1292	PR00802	SERUM ALBUMIN FAMILY	PR00802B 16.51 1.610e-
		SIGNATURE	10 81-105
1297	PR00716	M-PHASE INDUCER	PR00716C 17.65 5.696e-
1000		PHOSPHATASE SIGNATURE	09 23-44
1298	BL00478	LIM domain proteins.	BL00478B 14.79 6.478e- 14 268-283
1301	BL00127	Pancreatic ribonuclease	BL00127C 31.49 3.571e-
		family proteins.	28 82-126 BL00127B
	1		26.57 8.800e-28 23-68
1302	PR00637	TYPE 3 BOMBESIN RECEPTOR	PR00637E 11.27 4.250e-
1200		SIGNATURE	09 290-306
1307	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 5.500e-
		cransier processs.	17 13-38 BL00215A 15.82 1.000e-16 226-
			251 BL00215A 15.82
	<u> </u>		2.658e-13 107-132
1308	PRC0898	VASOPRESSIN V2 RECEPTOR	PR00898H 11.34 4.682e-
1309	PD00301	SIGNATURE PROTEIN REPEAT MUSCLE	09 552-572 PD00301B 5.49 2.731e-
		CALCIUM-BI.	09 390-401
1310	BL00983	Ly-6 / u-PAR domain	BL00983C 12.69 9.654e-
		proteins.	13 73-89 BL00983B
1313	BL00194	Thioredoxin family	8.19 3.132e-09 12-22
1010	BEOOTS	proteins.	BL00194 12.16 1.900e-
1314	BL00594	Aromatic amino acids	BL00594A 16.75 8.969e-
		permeases proteins.	10 53-97
1316	BL00134	Serine proteases,	BL00134A 11.96 9.325e-
		trypsin family, histidine proteins.	13 128-145
1320	BL00783	Ribosomal protein L13	BL00783C 22.43 6.559e-
		proteins.	24 87-117 BL00783A
			14.55 1.600e-19 8-33
			BL00783B 12.76 3.500e-
1327	PF00514	Armadillo/beta-catenin-	12 74-86
	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	like repeat proteins.	PF00514A 31.30 7.268e- 11 82-120
1329	BL00030	Eukaryotic RNA-binding	BL00030A 14.39 6.294e-
		region RNP-1 proteins.	11 129-148 BL00030B
			7.03 4.789e-09 168-178
1331	PR00497	NEUTROPHIL CYTOSOL	PR00497A 6.92 7.239e-
1332	PR00161	FACTOR P40 SIGNATURE NICKEL-DEPENDENT	09 25-43
-JJ4	-KOOTOI	HYDROGENASE/B-TYPE	PR00161C 9.51 4.930e- 09 317-337
1	1	CYTOCHROME SIGNATURE	V 311-331
1333	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 6.769e-
		ZINC-FINGER METAL-	33 10-49
1236	DD00700	BINDING NU.	
1336	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PR00700D 12.47 2.200e- 09 262-281
1337	PR00700	PROTEIN TYROSINE	PR00700D 12.47 2.200e-
		1	

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	NO.		RESULIS-
		PHOSPHATASE SIGNATURE	09 211-230
1340	PR00860	VERTEBRATE METALLOTHIONEIN SIGNATURE	PR00860A 5.46 5.034e- 13 5-18
1341	BL00893	mutT domain proteins.	BL00893 18.99 6.750e-
1343	BL01282	BIR repeat proteins.	BL01282B 30.49 5.974e- 21 383-422
1344	DM00099	4 kw A55R REDUCTASE TERMINAL DIHYDROPTERIDINE.	DM00099B 14.73 8.313e- 09 417-427
1345	BL00923	Aspartate and glutamate racemases proteins.	BL00923B 11.41 5.935e- 10 135-146
1348	PF00651	BTB (also known as BR- C/Ttk) domain proteins.	PF00651 15.00 7.231e-
1350	PR00193	MYOSIN HEAVY CHAIN SIGNATURE	PR00193D 14.36 3.571e- 32 416-445 PR00193C 12.60 6.318e-31 179- 207 PR00193B 11.69 3.571e-24 133-159 PR00193E 19.47 9.069e- 22 470-499 PR00193A
1352	PR00447	NATURAL RESISTANCE- ASSOCIATED MACROPHAGE PROTEIN SIGNATURE	15.41 1.783e-20 77-97 PR00447E 9.73 1.554e- 15 299-319 PR00447D 13.54 3.408e-15 200- 224 PR00447A 12.73 6.357e-11 97-124 PR00447G 6.69 9.877e-
<b>1353</b>	BL00303	S-100/ICaBP type calcium binding protein.	10 353-373 BL00303A 21.77 6.667e- 26 45-82 BL00303B 26.15 1.000e-24 93-130
1355	BL00039	DEAD-box subfamily ATP- dependent helicases proteins.	BL00039D 21.67 5.950e- 29 375-421 BL00039A 18.44 7.136e-29 99-138 BL00039C 15.63 4.000e- 18 225-249 BL00039B 19.19 3.182e-14 141- 167
1357	PF00615	Regulator of G protein signalling domain proteins.	PF00615B 16.25 2.216e- 12 84-101 PF00615C 10.05 8.412e-12 162-
1360	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	176 PD01066 19.43 9.234e- 29 10-49
1361	PR00925	NONHISTONE CHROMOSOMAL PROTEIN HMG17 FAMILY SIGNATURE	PR00925A 5.47 5.091e- 18 14-29 PR00925B 3.73 6.143e-14 29-42 PR00925C 5.57 4.789e- 12 53-64 PR00925D 6.56 1.857e-10 76-87
	BL01272	Glucokinase regulatory protein family proteins.	BL01272B 19.61 6.870e- 30 136-171 BL01272C 11.68 3.314e-25 249- 274 BL01272A 6.49 1.231e-18 99-117
	BL01272	Glucokinase regulatory protein family proteins.	BL01272B 19.61 6.870e- 30 113-148 BL01272C 11.68 3.314e-25 226- 251 BL01272A 6.49 1.231e-18 76-94
1364	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 5.304e- 09 167-177
1368	PR00169	POTASSIUM CHANNEL SIGNATURE	PR00169A 16.77 1.592e- 09 76-96

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332 23 110.	NO.	BBSCRIPTION	RESOURS.
			10 1-19
1371	BL00242	Integrins alpha chain proteins.	BL00242B B.13 8.615e- 09 469-479
1372	PR00625	DNAJ PROTEIN FAMILY SIGNATURE	PR00625B 13.48 7.353e- 19 46-67 PR00625A 12.84 1.391e-16 14-34
1373	BL00434	HSF-type DNA-binding domain proteins.	BL00434C 23.85 3.778e- 09 90-130
1374	PR00962	LETHAL(2) GIANT LARVAE PROTEIN SIGNATURE	PR00962C 8.00 6.337e-
1375	PD02475	MUCIN EPITHELIAL TUMOR- ASSOCIATE.	PD02475A 23.18 8.552e- 10 1111-1150
1376	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 9.571e- 32 24-63
1380	BL00194	Thioredoxin family proteins.	BL00194 12.16 8.333e- 12 48-61
1381	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 1.458e- 15 1123-1136
1383	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 7.600e-10
1384	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 7.600e-10
1385	BP00303	S-100/ICaBP type calcium binding protein.	BL00303B 26.15 6.203e-
1386	BL01160	Kinesin light chain	10 95-132 BL01160B 19.54 5.042e- 09 1574-1628
1387	BL00518	repeat proteins.  Zinc finger, C3HC4 type (RING finger), proteins.	09 1574~1628   BL00518 12.23 1.000e-   11 52-61
1389	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-	PD01066 19.43 3.600e- 30 10-49
1390	PD01066	BINDING NU. PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 3.512e- 31 32-71
1392	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308C 3.83 9.723e- 10 127-137
1393	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 9.625e- 25 88-110 PR00380D 9.93 2.406e-20 304-326 PR00380B 12.64 4.414e- 16 208-226 PR00380C 13:18 6.538e-16 243- 262
1394	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 3.400e- 14 462-475 PD00066 13.92 8.800e-14 348- 361 PD00066 13.92 9.571e-12 405-418 - PD00066 13.92 6.087e- 11 490-503 PD00066 13.92 8.043e-11 320- 333
1398	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 6.786c- 32 10-49
1400	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 7.038e- 09 270-290
1406	PD00930	PROTEIN GTPASE DOMAIN ACTIVATION.	PD00930A 25.62 7.324e- 15 363-389
1407	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 7.500e- 10 457-476
1408	PR00019 .	LEUCINE-RICH REPEAT SIGNATURE	PRO0019A 11.19 9.550e- 11 179-193 PRO0019A 11.19 8.826e-10 228- 242 PR00019B 11.36 1.360e-09 199-213 PR00019B 11.36 4.960e-

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			09 176-190
1409	PR00510	NEBULIN SIGNATURE	PRO0510A 9.09 4.150e- 12 182-202 PR00510B 12.96 8.767e-12 210- 230 PR00510F 9.88 8.172e-10 58-75 PR00510D 9.21 2.367e- 09 251-267
1410	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 5.696e- 09 31-44
1412	BL00358	Ribosomal protein L5 proteins.	BL00358B 22.76 1.00Ce- 40 57-103 BL00358C 13.75 6.087e-14 122- 136 BL00358D 14.26 5.500e-13 143-158 BL00358A 13.06 1.931e- 11 33-44
1414	BL00282	Kazal serine protease inhibitors family proteins.	BL00282 16.88 7.338e- 10 511-534
1415	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 4.300e- 29 40-77
1417	PR00681	RIBOSOMAL PROTEIN S1 SIGNATURE	PR00681G 12.54 2.149e- 09 38-60
1418	DM00973	3 kw RESISTANCE BENOMYL YLL028W CYCLOHEXIMIDE.	DM00973A 21.17 1.462e-
1419	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319B 11.47 1.571e- 09 428-443
1420	PD01941	TRANSMEMBRANE COTRANSPORTER SYMP.	PD01941A 14.81 1.000e- 40 142-196 PD01941B 15.02 7.049e-30 400- 447 PD01941E 15.92 2.475e-20 817-864 PD01941C 19.96 3.118e- 19 488-543 PD01941D 27.18 9.614e-18 641- 690 PD01941F 28.52 5.382e-15 1038-1093
1422	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 8.043e- 12 199-217
1423	PR00209	ALPHA/BETA GLIADIN FAMILY SIGNATURE	PR00209B 4.88 6.318e- 11 1009-1028
1424	BL50002	Src homology 3 (SH3) domain proteins profile.	BL50002A 14.19 8.200e- 14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e- 09 244-258
1425	PF00628	PHD-finger.	PF00628 15.84 3.045e- 12 330-345
1426	PF00628	PHD-finger.	PF00628 15.84 3.045e- 12 377-392
1427	PR00405	HIV REV INTERACTING PROTEIN SIGNATURE	PR00405B 11.83 5.114e- 16 281-299 PR00405A 17.71 4.306e-14 262- 282
1428	BL00039	DEAD-box subfamily ATP- dependent helicases proteins.	BL00039D 21.67 5.219e- 34 147-193
1429	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 8.920e- 10 577-592
1430	PR00378	INOSITOL PHOSPHATASE SIGNATURE	PR00378D 16.86 7.563e- 12 295-314 PR00378B 13.80 8.650e-10 166- 186
1431	PR00928	GRAVES DISEASE CARRIER	PR00928B 13.53 3.769e-

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	NO.	PROTEIN SIGNATURE	10 103-124
1433	BL01113	Clq domain proteins.	BL01113B 18.26 7.049e-
		Tag domest processes.	15 14-50 BL01113C
			13.18 7.000e-12 82-102
1434	PR00319	BETA G-PROTEIN	PR00319B 11.47 7.983e-
		(TRANSDUCIN) SIGNATURE	10 135-150
1436	BL00030	Eukaryotic RNA-binding	BL00030A 14.39 1.000e-
		region RNP-1 proteins.	12 84-103
1438	BL00290	Immunoglobulins and	BL00290B 13.17 2.500e-
		major histocompatibility	09 250-268 BL00290A
i		complex proteins.	20.89 4.000e-09 188-
			211
1440	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 4.960e-
			09 38-52
1441	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 4.960e-
			09 88-102
1444	BL00422	Granins proteins.	BL00422D 19.48 1.000e-
	<u> </u>		08 114-138
1445	PD01841	PHOSPHORYLASE KINASE	PD01841A 21.71 1.000e-
		ALPHA MUSCL.	40 73-123 PD01841B
			14.35 1.000e-40 144-
			185 PD01841D 17.87
	ļ		1.000e-40 206-258
	1		PD01841F 13.36 1.000e-
			40 296-345 PD01841G
			24.26 1.000e-40 349-
			403 PD01841I 23.00
			1.000e-40 494-536
	i		PD01841J 14.94 1.000e-
	l .	1	40 895-932 PD01841L
			18.42 1.000e-40 1083-
	Ì		1125 PD01841E 18.60
			9.719e-38 258-296
			PD01841K 14.81 1.000e-
			35 1041-1071 PD01841H 21.30 3.189e-31 435-
			472 PD01841C 13.78
			1,000e-25 185-206
	į	<b> </b>	PD01841M 10.82 1.250e-
	1		20 1175-1194
1446	PF00816	H-NS histone family.	PF00816B 13.84 8.875e-
			09 190-220
1447	PR00048	C2H2-TYPE ZINC FINGER	PR00048A 10.52 2.080e-
		SIGNATURE	09 402-416
1448	DM00315	072 RIBONUCLEASE	DM00315D 18.40 7.393e-
	]	INHIBITOR.	09 23-67
1451	BL00030	Eukaryotic RNA-binding	BL00030B 7.03 2.800e-
		region RNP-1 proteins.	10 94-104
1454	DM01688	2 POLY-IG RECEPTOR.	DM01688D 13.44 7.146e-
			09 382-405
1455	PF00777	Sialyltransferase	PF00777C 18.60 2.929e-
		family.	22 4-59
1457	BL00927	Trehalase proteins.	BL00927C 10.83 8.085e-
		1	09 42-53
1460	BL00545	Aldose 1-epimerase	BL00545C 11.28 7.353e-
		proteins.	17 169-182 BL00545A
			10.20 2.071e-15 73-89
			BL00545B 13.10 3.942e-
			09 140-153
1466	PR00097	ANTHRANILATE SYNTHASE	PR00097C 9.42 9.069e-
		COMPONENT II SIGNATURE	09 233-245
1472	BL01129	Hypothetical	BL01129E 13.25 5.250e-
		yabO/yceC/sfhB family	22 170-195 BL01129C
		proteins.	25.56 9.526e-18 63-106
1473	BL00790	Receptor tyrosine kinase	BL00790I 20.01 2.821e-
		class V proteins.	09 2114-2145
1475	PF00686	Starch binding domain	PF00686A 13.45 9.100e-
		proteins.	09 267-277
		<del></del>	

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1477	PF00566	Probable rabGAP domain proteins.	PF00566A 12.64 7.333e- 10 466-476
1478	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030B 7.03 9.400e- 10 43-53
1479	DM00406	GLIADIN.	DM00406 7.73 8.541e-10 292-305
1480	BL00290	Immunoglobulins and major histocompatibility	BL00290B 13.17 2.385e- 15 69-87 BL00290A
1481	PR00150	complex proteins.  PHOSPHOENOLPYRUVATE CARBOXYLASE SIGNATURE	20.89 5.091e-11 12-35 PR00150F 10.45 9.039e- 09 21-51
1482	PF00780	Domain found in NIX1- like kinases, mouse	PF007801 14.69 4.825e- 09 107-137
1483	BL01160	citron and yeast ROM.  Kinesin light chain repeat proteins.	BL01160B 19.54 1.153e-
1485	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 5.909e- 25 17-56
1486	BL00107	Protein kinases ATP- binding region proteins.	BL00107B 13.31 1.529e-
1488	BL00039	DEAD-box subfamily ATP- dependent helicases proteins.	BL00039D 21.67 9.586e- 10 116-162
1490	BL00166	Enoyl-CoA hydratase/isomerase proteins.	BL00166D 22.87 2.607e- 24 190-226 BL00166C 18.93 5.500e-14 140- 167 BL00166B 16.92 9.357e-11 93-115
1491	BL00452	Guanylate cyclases proteins.	BL00452D 28.59 3.700e- 31 63-106 BL00452E 11.92 3.045e-13 115- 131
1492	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PRO0019A 11.19 3.667e- 09 532-546
1497	BL00107	Protein kinases ATP- binding region proteins.	BL00107B 13.31 1.000e- 11 384-400 BL00107A 18.39 5.345e-11 322- 353
1500	PF00876	Ogre family.	PF00876E 7.99 1.947e- 10 107-117
1502	BL00027	'Homeobox' domain proteins.	BL00027 26.43 4.789e- 24 112-155
1503	BL00027	'Homeobox' domain proteins.	BL00027 26.43 4.789e- 24 112-155
1505	BL01177	Anaphylatoxin domain proteins.	BL01177B 20.64 5.800e- 24 448-475 BL01177C 17.39 5.333e-19 402- 421 BL01177B 13.61 7.840e-16 155-171 BL01177D 17.50 1.900e- 15 427-445
1506	BL00972	Ubiquitin carboxyl- terminal hydrolases family 2 proteins.	BL00972D 22.55 5.500e- 14 311-336 BL00972A 11.93 7.429e-14 48-66 BL00972E 20.72 8.759e- 10 341-363
1512	BL00523	Sulfatases proteins.	BL00523E 19.27 4.536e- 22 76-106 BL00523D 9.89 1.563e-11 40-52 BL00523F 10.85 4.162e- 09 159-170 BL00523G 9.46 5.333e-09 256-266
1516	BL00914	Syntaxin / epimorphin family proteins.	BL00914 24.91 7.045e- 14 168-218
1518	BL00600	Aminotransferases class- III pyridoxal-phosphate attachment si.	BL00600A 17.98 6.143e- 19 98-122 BL00600E 16.43 1.771e-17 302-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			331 BL006C0G 12.43 9.625e-17 377-396 BL006C0B 19.60 5.091e- 15 160-186 BL006C0C 16.18 6.04Ce-12 190-
			206 BL006C0F 8.77 1.000e-11 343-356 BL006C0D 8.71 1.000e- 10 281-295
1523	PD00930	PROTEIN GTPASE DOMAIN ACTIVATION.	PD00930B 33.72 9.600e-
1528	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320B 12.19 4.774e- 11 192-207 PR00320B 12.19 8.839e-11 272- 287 PR00320B 12.19 9.743e-10 106-121
		,	PR00320A 16.74 1.878e- 09 192-207 PR00320A 16.74 2.317e-09 106- 121 PR00320A 16.74 8.683e-09 272-287 PR00320C 13.01 8.800e-
1538	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	09 106-121 DM01970B 8.60 4.508e- 15 171-184
1539	PF00781	Diacylglycerol kinase catalytic domain proteins (presumed).	PF00781D 11.11 7.593e- 10 103-127
1540	PR00965	OCULAR ALBINISM TYPE 1 PROTEIN SIGNATURE	PR00965H 10.73 1.231e- 29 312-334 PR00965E 12.93 5.846e-29 172- 195 PR00965F 5.98 1.123e-28 209-231 PR00965C 15.04 1.000e- 27 131-151 PR00965D 5.84 1.000e-27 150-170 PR00965G 8.52 2.440e- 27 258-279 PR00965B 4.80 8.650e-26 88-109 PR00965A 12.52 1.000e- 25 35-55 PR00965I 3.91 6.442e-25 385-406
1541	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 9.719e- 17 163-207
1543	PD02699	PROTEIN DNA-BINDING BINDING DNA.	PD02699C 24.84 1.000e- 40 599-646 PD02699A 8.91 2.286e-34 219-248 PD02699B 18.28 6.143e- 21 485-509
1544	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 7.857e- 10 182-197 PR00049D 0.00 7.102e-09 67-82
1547	BL00951	ER lumen protein retaining receptor proteins.	BL00951C 19.35 1.000e- 40 93-142 BL00951D 13.94 8.714e-40 142- 177 BL00951A 15.10 1.000e-38 2-38 . BL00951B 14.23 6.250e- 33 38-69
1548	BL00536	Ubiquitin-activating enzyme proteins.	30 279-318 BL00536D 22.91 5.737e-24 21-65 BL00536E 16.94 4.696e- 18 248-279
1549	PR00139	ASPARAGINASE/GLUTAMINASE FAMILY SIGNATURE	PR00139C 11.72 9.679e- 09 550-569
1553	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 5.119e- 09 58-73
1549	PR00139	enzyme proteins.  ASPARAGINASE/GLUTAMINASE FAMILY SIGNATURE	33 38-69 BL00536F 13.65 8.920e- 30 279-318 BL00536D 22.91 5.737e-24 21-65 BL00536B 16.94 4.696e- 18 248-279 PR00139C 11.72 9.679e- 09 550-569

Short-chain   dehydrogenases/reductase   afmily proteins.   157-105   BL01228   Hypothetical cof family   12 107-132   12 107-132   1588   BL01228   Hypothetical cof family   12 107-132   108-1328   Hypothetical cof family   12 107-132   108-1328   17.44 8.105e-12 107-132   108-1328   17.44 8.105e-12 107-132   108-1328   17.44 8.105e-12 107-132   108-1328   17.44 8.105e-12 107-132   108-1328   17.44 8.105e-12 107-132   108-1328   17.44 8.105e-12 107-132   108-1328   17.44 8.105e-12 107-132   108-1328   12 107-132   108-1328   12 107-132   108-1328   12 107-132   108-1328   12 107-132   108-1328   12 107-132   108-1328   12 107-132   108-1328   12 107-132   108-1328   12 107-132   12 107-132   108-1328   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 107-132   12 10	SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
B.01228   Byothetical cof family proteins.   12 107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-13	1556			
BL01228   Byroteins			s family proteins.	13 67-105
1558   BL01228   Hypothetical cof family proteins   BL01228   T.44 8.1050-1 2.107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-132   107-13	1557	BL01228		
1559   BL01228   Hypothetical cof family proteins.   BL01228   17.44   8.1056-1   12.107-132   107-132   107-132   107-132   108-10522   12.107-132   108-10522   12.107-132   108-10522   12.107-132   108-10522   12.107-132   108-10522   12.108-10522   12.108-10522   12.108-10522   12.108-10522   12.108-10522   12.108-10522   12.108-10522   12.108-10522   12.108-10522   12.108-10522   12.108-10522   12.108-10522   12.108-10522   12.108-1052   12.108-10522   12.108-10522   12.108-10522   12.108-10522   12.108-10522   12.108-10522   12.108-10522   12.108-10522   12.108-10522   12.108-10522   12.108-10522   12.108-10522   12.108-10522   12.108-10522   12.108-10522   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   12.108-1052   1	1558	BL01228	Hypothetical cof family	BL01228D 17.44 8.105e-
DNA polymerase family X   BL00522C 11.90 6.600e-proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Proteins.   Prot	1559	BL01228		
Proteins   18 412-436 BL00522B   27.30   1.738e-16 364-4   10 BL00522B   25.60   6.000e-16 279-326   BL00522E   19.63 6.123e-14   590-2332 BL00522F   14.590-2332 BL00522F   14.590-2332 BL00522F   14.590-2332 BL00522F   14.590-23385e-13 551-575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575   575	1562	B1.00522		1
Alio BLOOS22A 25.52	-502	5200522		18 412-436 BL00522B
BL00522E 19.63 6.123e-14 502-532 BL00522F 14.90 2.385e-13 551- 575				
14 502-532 BL00522F   14.90 2.385e-13 551-575   1563   PF00651   BTB (also known as BR-C/Ttk) domain proteins.   11 46-59   11 46-59   11 46-59   10 19 19 19 19 19 19 19 19 19 19 19 19 19	1			
S75	,			14 502-532 BL00522F
C/Tkk   domain proteins	ł			
1564   BL00299   Ubiquitin domain   BL00299 28.84 2.823e   proteins   10 324-376	1563	PF00651	1	1 1
1566   BL01013   Oxysterol-binding proteins   17 184-228   BL01013C   26.81 8.594e-	1564	BL00299	Ubiquitin domain	BL00299 28.84 2.823e-
Protein family proteins	1566	BL01013	1 -	1
Trp-Asp (WD) repeat proteins   BL00678 9.67 3.400e-10   378-389 BL00678 9.67   5.800e-10   418-429   8100678 9.67 8.800e-10   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306   295-306		-2		17 184-228 BL01013C
S.800e-10 418-429	1567	BL00678	Trp-Asp (WD) repeat	
BL00479   Phorbol esters / Second   BL00479B   12.57 5.235e-   diacylglycerol binding   domain proteins.   BL00479B   12.57 5.235e-   17.297-313 BL00479A   19.86 6.625e-15 271-   294 BL00479A   19.86 6.625e-15 271-   294 BL00479A   19.86 6.625e-15 271-   294 BL00479A   19.86 6.6625e-15 271-   294 BL00479A   19.86 6.6625e-15 271-   294 BL00479A   19.86 6.6625e-15 271-   294 BL00479A   19.86 6.6625e-15 271-   294 BL00479A   19.86 6.6625e-15 2173-189   PR00665E   23.64-384 PR00665D   9.93 1.200e-22 138-155   PR00665F 11.73 4.000e-   22.337-354 PR00665C   5.89 1.000e-20 65-80   PR00665B 5.29 4.337e-   19.24-39 PR00665E   5.60 2.929e-15 246-260   PR00665A 5.99 5.622e-   15.11-25   PR00605A 5.99 5.622e-   15.11-25   PR00605A 5.99 5.622e-   15.11-25   PR00605A 5.99 5.622e-   15.11-25   PR00605A 5.99 5.622e-   15.12-25   PR00605A 5.99 5.622e-   15.12-25   PR00605A 5.99 5.622e-   15.12-25   PR00605A 5.99 5.622e-   15.12-25   PR00605A 5.99 5.622e-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-   15.202-	ļ		proteins proteins.	
BL00479				BL00678 9.67 8.800e-10
Description	1570	BL00479	Phorbol esters /	l
294 BL00479A 19.86   2.667e-14 147-170   BL00479B 12.57 6.294e-12 173-189   PR00665   OXYTOCIN RECEPTOR   PR00665G 12.36 4.673e-12 173-189   PR00665D   9.93 1.200e-22 138-155   PR00665F 11.73 4.000e-22 337-354 PR00665C   5.89 1.000e-20 65-80   PR00665E 5.60 2.939e-15 246-260   PR00665E 5.60 2.939e-15 246-260   PR00665E 5.60 2.939e-15 246-260   PR00665E 5.60 2.939e-15 246-260   PR00665E 5.60 2.939e-15 246-260   PR00665E 5.60 2.939e-15 246-260   PR00665A 5.99 5.622e-15 11-25   PR00605A 5.99 5.622e-15 11-25   PR00605A 5.99 5.622e-15 11-25   PR00605A 5.99 5.622e-15 11-25   PR00605A 5.99 5.622e-15 11-25   PR00605A 5.99 5.622e-15 11-25   PR00605A 5.99 5.622e-15 11-25   PR00605A 5.99 5.622e-15 11-25   PR00605A 5.99 5.622e-15 11-25   PR00605A 5.99 5.622e-15 11-25   PR00605A 5.99 5.622e-15 11-25   PR00605A 5.99 5.622e-15 11-25   PR00605A 5.99 5.622e-15 11-25   PR00605A 5.99 5.622e-15 11-25   PR00605A 5.99 5.622e-15 11-25   PR00605A 5.99 5.622e-15 11-25   PR00605A 5.99 5.622e-15 11-25   PR00605A 5.99 5.622e-15 11-25   PR00605A 5.99 5.622e-15 11-25   PR00605A 5.99 5.622e-15 11-25   PR00605A 5.99 5.622e-15 11-25   PR00605A 5.99 5.622e-15 11-25   PR00605A 5.99 5.622e-15 11-25   PR00605A 5.99 5.622e-15 11-25   PR00605A 5.99 5.622e-15   PR00605A 5.99 5.622e-15   PR00605A 5.99 5.622e-15   PR00605A 5.99 5.622e-15   PR00605A 5.99 5.622e-15   PR00605A 5.99 5.622e-15   PR00605A 5.99 5.622e-15   PR00605A 5.99 5.622e-15   PR00605A 5.99 5.622e-15   PR00605A 5.99 5.622e-15   PR00605A 5.99 5.622e-15   PR00605A 5.99 5.622e-15   PR00605A 5.99 5.622e-15   PR00605A 5.99 5.622e-15   PR00605A 5.99 5.622e-15   PR00605A 5.99 5.622e-15   PR00605A 5.99 5.622e-15   PR00605A 5.99 5.622e-15   PR00605A 5.99 5.622e-15   PR00605A 5.99 5.622e-15   PR00605A 5.99 5.622e-15   PR00605A 5.99 5.622e-15   PR00605A 5.99 5.622e-15   PR00605A 5.99 5.622e-15   PR00605A 5.99 5.622e-15   PR00605A 5.99 5.622e-15   PR00605A 5.99 5.622e-15   PR00605A 5.99 5.622e-15   PR00605A 5.99 5.99 5.622e-15   PR00605A 5.99 5.99 5.622e-15   PR00605A 5.99 5.99 5.622e-15   PR00605				
BL00479B 12.57 6.294e- 12 173-189	j	1	domain proteins.	294 BL00479A 19.86
12 173-189				
SIGNATURE   24 364-384 PR00665D   9.93 1.200e-22 138-155   PR00665F 11.73 4.000e-22 337-354 PR00665C   5.89 1.000e-20 65-80   PR00665E 5.29 4.337e-19 24-39 PR00665E   5.60 2.929e-15 246-260   PR00665A 5.99 5.622e-15 11-25   DM00099	1576	DDAAGGE	AVVMACTN DECEDORAD	•
PRO0665F 11.73 4.000e- 22 337-354 PR00665C 5.89 1.000e-20 65-80 PR00665B 5.29 4.337e- 19 24-39 PR00665E 5.60 2.929e-15 246-260 PR00665A 5.99 5.622e- 15 11-25  1577 DM00099	1576	PROUGES		24 364-384 PR00665D
22 337-354 PR00665C   5.89 1.000e-20 65-80   PR00665B 5.29 4.337e-19 24-39 PR00665E   5.60 2.929e-15 246-260   PR00665A 5.99 5.622e-15 11-25   DM00099				
PR00665B 5.29 4.337e-   19 24-39				22 337-354 PR00665C `
S.60 2.929e-15 246-260				
PR00665A 5.99 5.622e-   15 11-25				
DM00099				PR00665A 5.99 5.622e-
DIHYDROPTERIDINE.	1577	DM00099	4 kw A55R REDUCTASE	
BL00524   Somatomedin B domain   BL00524A 9.65 6.776e-proteins.   14 52-73   1580   PD02894   HYDROLASE N4- PRECURSOR   PD02894B 13.93 6.959e-PROTEIN SIGNAL BE.   16 182-215 PD02894A 21.96 2.125e-10 57-103   1581   BL00411   Kinesin motor domain   BL00411C 15.04 5.292e-proteins.   12 32-54 BL00411H   15.66 4.441e-11 245-276   1582   PR00604   CLASS IA AND IB   PR00604A 11.13 2.440e-CYTOCHROME C SIGNATURE   09 79-87   1584   PF00651   BTB (also known as BR-C/Ttk) domain proteins.   10 225-238   1585   DM01551   kw OSTEOINDUCTIVE YOPM   DM01551C 14.62 9.455e-MEMBRANE OUTER.   11 125-145   1586   DM01354   kw TRANSCRIPTASE REVERSE   DM01354S 11.61 7.750e-			TERMINAL	
PD02894	1579	BL00524	Somatomedin B domain	
PROTEIN SIGNAL BE. 16 182-215 PD02894A 21.96 2.125e-10 57-103  1581 BL00411 Kinesin motor domain BL00411C 15.04 5.292e- 12 32-54 BL00411H 15.66 4.441e-11 245- 276  1582 PR00604 CLASS IA AND IB PR00604A 11.13 2.440e- 09 79-87  1584 PF00651 BTB (also known as BR- C/Ttk) domain proteins. 10 225-238  1585 DM01551 kw 0STEOINDUCTIVE YOPM DM01551C 14.62 9.455e- MEMBRANE OUTER. 11 125-145  1586 DM01354 kw TRANSCRIPTASE REVERSE DM01354S 11.61 7.750e-	1580	PD02894 ·		
BL00411   Kinesin motor domain   BL00411C 15.04 5.292e-   12 32-54 BL00411H   15.66 4.441e-11 245-   276		•		16 182-215 PD02894A
15.66 4.441e-11 245-276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   276   27	1581	BL00411	Kinesin motor domain	
276			proteins.	
CYTOCHROME C SIGNATURE 09 79-87  1584 PF00651 BTB (also known as BR- PF00651 15.00 1.000e- C/Ttk) domain proteins. 10 225-238  1585 DM01551 kw OSTEOINDUCTIVE YOPM DM01551C 14.62 9.455e- MEMBRANE OUTER. 11 125-145  1586 DM01354 kw TRANSCRIPTASE REVERSE DM01354S 11.61 7.750e-				276
DM01551   BTB (also known as BR-   PF00551 15.00 1.000e-   C/Ttk) domain proteins.   10 225-238     1585   DM01551   kw OSTEOINDUCTIVE YOPM   DM01551C 14.62 9.455e-   MEMBRANE OUTER.   11 125-145     1586   DM01354   kw TRANSCRIPTASE REVERSE   DM01354S 11.61 7.750e-	1582	PR00604		
1585 DM015S1 kw OSTEOINDUCTIVE YOPM DM01551C 14.62 9.455e- MEMBRANE OUTER. 11 125-145 1586 DM01354 kw TRANSCRIPTASE REVERSE DM01354S 11.61 7.750e-	1584	PF00651	BTB (also known as BR-	PF00651 15.00 1.000e-
1586 DM01354 kw TRANSCRIPTASE REVERSE DM01354S 11.61 7.750e-	1585	DM01551		
	1586	DM01354		

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1507	PR00072	MALIC ENZYME SIGNATURE	PR00072B 13.77 7.955e- 33 180-210 PR00072A 12.75 6.040e-25 120- 145 PR00072C 11.42 2.286e-24 216-239 PR00072D 10.77 3.400e- 22 276-295 PR00072E 10.54 1.360e-19 301- 318 PR00072G 10.45 5.304e-19 433-450 PR00072F 8.87 5.935e- 15 332-349
1589	BL00191	Cytochrome b5 family, heme-binding domain proteins.	BL00191H 15.64 1.537e- 22 61-113 BL00191K 17.38 9.027e-12 398- 442
1590	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 7.716e- 13 211-224 DM01970B 8.60 2.157e-12 94-107
1591	DM00517	5 kw NUCLEAR 60.7 NUP1 CHROMOSOME.	DM00517B 10.96 6.625e- 16 1175-1193 DM00517A 8.21 1.000e-11 1015- 1026
1592	BL00037	Myb DNA-binding domain proteins repeat proteins proteins.	BL00037B 15.92 3.250e- 27 116-142 BL00037A 16.68 2.500e-24 83-107 BL00037A 16.68 3.250e- 12 31-55 BL00037B 15.92 3.526e-11 64-90 BL00037C 16.86 9.654e- 10 146-164
1595	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 1.514e- 09 110-127
1598	PF00628	PHD-finger.	PF00628 15.84 3.250e- 11 1667-1682
1599	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE	PR00014D 12.04 5.500e- 09 980-995
1600	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 6.571e- 10 30-39
1602	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 5.402e- 10 136-187
1605	PF00651	BTB (also known as BR- C/Ttk) domain proteins.	PF00651 15.00 3.571e- 10 44-57
1607	BL00252	Interferon alpha, beta and delta family proteins.	BL00252A 18.49 6.657e- 23 20-57 BL00252B 19.78 9.125e-16 58-109
1610	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 1.000e- 08 61-94
1611	BL00904	Protein prenyltransferases alpha subunit repeat proteins proteins.	BL00904C 8.98 7.353e- 10 91-125 BL00904D 1.47 6.018e-09 127-168
1612	PF00168-	C2 domain proteins.	PF00168C 27.49 3.250e- 09 365-391
1613	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 6.051e- 09 932-983 BL00412D 16.54 7.153e-09 933- 984
1614	BL00559	Eukaryotic molybdopterin oxidoreductases proteins.	BL00559I 13.63 3.531e- 25 54-83 BL00559K 13.17 2.957e-18 197- 224 BL00559J 19.63 6.870e-16 124-176 BL00559L 13.60 9.000e- 16 266-284
1615	PD01427	TRANSFERASE METHYLTRANSFERASE BI.	PD01427B 22.45 3.025e- 22 500-541 PD01427A 19.94 8.773e-18 439-

NO.	SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
BL00115		•	DESCRIPTION	RESUDIS-
Delymerase II   09 153-201 BL0011   heptapeptide repeat proteins   3.12 9.603e-09 145   proteins   S-100/IGABP type calcium   S-100303B 26.15 7.7   hinding protein.   BL00303B 26.15 7.7   hinding protein.   BL00303B 26.15 7.7   hinding proteins   BL01254   Fetuin family proteins   BL01254 Fetuin family proteins   BL01254 Fetuin family proteins   BL01254 Fetuin family proteins   BL01254 Fetuin family proteins   BL01254 Fetuin family proteins   BL01254 Fetuin family proteins   PRO188B 25.10 1.0   09 137-147   1619   PRO188B PEPTIDE REDUCTASE   PD0188B 25.10 1.0   155 PD0188B 25.10 1.0   1629   FROTEIN METHI.   40 47-97 PD0188C 21.56 7.000e-30 12   155 PD0188B 12.8   3.455   155 PD0188B 12.8   3.455   155 PD0188B 12.8   3.455   155 PD0188B 12.8   3.455   155 PD0188B 12.8   3.455   156 PD0188B 12.8   3.455   156 PD0188B 12.8   3.455   156 PD0188B 12.8   3.455   156 PD0188B 12.8   3.455   156 PD0188B 1.58   4.580   09 702-714 PR00239   1.58 4.580   09 702-714 PR00239   1.58 4.580   09 702-714 PR00239   1.58 4.580   09 702-714 PR00239   1.58 4.580   09 702-714 PR00239   1.58 4.580   09 702-714 PR00239   1.58 4.580   09 702-714 PR00239   1.58 5.193   09 702-714 PR00239   1.58 5.14 47 18 10 18 18 18 18 18 18 18 18 18 18 18 18 18		T		472
Polymerase II   13.12 9.603e-09 145   1617   BL00303   S-1007/GaBP type calcium   3.12 9.603e-09 145   1618   BL00303   S-1007/GaBP type calcium   BL00303B 26.15 7.7   1618   BL00254   Fetuin family protein.   32 51-88 BL00303A 21.77 1.947e-31 4-8   1618   BL001254   Fetuin family proteins.   BL01254F 10.02 8.7   09 137-147   1619   PD01888   PEPTIDE REDUCTASE   PD01888B 25.10 1.0   155 PD01888A 12.8   8.800e-15 7-23   FROTEIN METHI.   40 47-97 PD01888C 21.56 7.000e-30 12: 155 PD01888A 12.8   8.800e-15 7-23   FRO0239E 1.58 3.455   PD01888A 12.8   8.800e-15 7-23   FRO0239E 1.58 3.455   PD01888A 12.8   8.800e-15 7-23   FRO0239E 1.58 3.455   PD01888A 12.8   8.800e-15 7-23   FRO0239E 1.58 4.58   PR00239E 1.58 4.58   PR00239E 1.58 4.58   PR00239E 1.58 4.58   PR00239E 1.58 4.58   PR00239E 1.58 4.58   PR00239E 1.58 4.58   PR00239E 1.58 4.58   PR00239E 1.58 4.58   PR00239E 1.58 4.58   PR00239E 1.58 4.58   PR00239E 1.58 4.58   PR00239E 1.58 4.58   PR00239E 1.58 4.58   PR00239E 1.58 4.58   PR00860B 7.04 1.900   SIGNATURE   PR00860B 7.04 1.900   SIGNATURE   PR00860B 5.46 1.720   14 5-18   PR00860B 5.46 1.720   14 5-18   PR00860B 5.46 1.720   14 5-18   PR00860B 5.46 1.720   PR00239E 1.58 1.000e-40 13 182   PR00239E 1.58 1.000e-40 13 182   PR00239E 1.58 1.000e-40 13 182   PR00239E 1.58 1.000e-40 13 182   PR00239E 1.58 1.4 7.88 36 286-33 1 EL00064E 11.4 19 6.50 31 192-212   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   PR00239E   P	1616	BL00115	Eukaryotic RNA	BL00115Z 3.12 7.485e-
heptapeptide repeat proteins   3.12 9.603e-09 145 proteins   S-1007ICaBP type calcium binding protein.   32 51-88 BL00303B 26.15 7.7   32 51-88 BL00303B 26.15 7.7   32 51-88 BL00303B 26.15 7.7   32 51-88 BL00303B 26.15 7.7   32 51-88 BL00303B 26.15 7.7   32 51-88 BL00303B 26.15 7.7   32 51-88 BL00303B 26.15 7.7   32 51-88 BL00303B 26.15 7.7   32 51-88 BL0032B 27.77   1947e-31 4   21.77   1947e-31 4   21.77   1947e-31 4   21.77   1947e-31 4   21.77   1947e-31 4   21.77   1947e-31 4   21.77   1947e-31 4   21.77   1947e-31 4   21.57   19.00e-30   12.57   19.00e-30   12.57   19.00e-30   12.57   19.00e-30   12.57   19.00e-30   12.57   19.00e-30   12.57   19.00e-30   12.57   19.00e-30   12.57   19.00e-30   12.57   19.00e-30   12.57   19.00e-30   12.57   19.00e-30   19.00e-30   19.00e-30   19.00e-30   19.00e-30   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19.00e-40   19				09 152-201 BL00115Z
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BL00303   S-100/ICaBP type calcium   binding protein.   32 51-88 BL003030   26.15 7.7   32 51-88 BL003030   26.15 7.7   32 51-88 BL003030   26.15 7.7   32 51-88 BL003030   26.15 7.7   32 51-88 BL003030   26.15 7.7   32 51-88 BL003030   26.15 7.7   32 51-88 BL003030   26.15 7.7   32 51-88 BL003030   26.15 7.7   26.77   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.17   26.1			proteins.	
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1618   BL01254   Fetuin family proteins   BL01254F 10.02 8.7			The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s	1
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1621   PR00239   MOLLUSCAN RHODOPSIN C- TERMINAL TAIL SIGNATURE   PR00239E 1.58 3.45   1.58 4.580e-09 697-704 PR00239E 1.58 4.580e-09 697-704 PR00239E 1.58 4.580e-09 697-7000239E 1.58 4.580e-09 697-7000239E 1.58 4.580e-09 697-7000239E 1.58 4.580e-09 697-7000239E 1.58 4.580e-09 697-7000239E 1.58 4.580e-09 703-1.58 4.580e-09 703-1.58 4.580e-09 703-1.58 4.580e-09 703-1.58 4.580e-09 703-1.58 4.580e-09 703-1.58 4.580e-09 703-1.58 4.580e-09 703-1.58 4.580e-09 703-1.58 4.580e-09 703-1.58 4.580e-09 703-1.58 4.580e-09 703-1.58 4.590e-09 703-1.58 4.590e-09 703-1.58 4.590e-09 703-1.58 4.590e-09 703-1.58 4.590e-09 703-1.58 4.590e-09 703-1.58 4.590e-09 703-1.58 4.590e-09 703-1.58 4.590e-09 703-1.58 4.590e-09 703-1.58 4.590e-09 703-1.58 4.590e-09 703-1.58 4.590e-09 703-1.58 4.590e-09 703-1.58 4.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-09 703-1.590e-0				
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PR00239E 1.58 4.58			TERMINAL TAIL SIGNATURE	09 692-704 PR00239E
1622   PR00860   VERTEBRATE   PR00860B 7.04 1.900     METALLOTHIONEIN   18 27-41 PR00860C   9.61 1.474e-14 41-1     PR00860A 5.46 1.720   14 5-18     1624   PR00784   MITOCHONDRIAL BROWN FAT UNCOUPLING PROTEIN SIGNATURE   11 77-95     1626   BL00325   Actin-depolymerizing proteins.   24.83 6.786e-23 61-20     1631   BL00064   L-lactate dehydrogenase proteins.   BL000325B 21.66 1.00     17.28 1.000e-40 137-182   182 BL00064F 25.14 7.88     36 286-331 BL00064   21.16 1.000e-30 22-275     1632   PR00063   RIBOSOMAL PROTEIN L27   PR00063B 15.24 9.70     1634   PR00239   MOLLUSCAN RHODOPSIN C- TERMINAL TAIL SIGNATURE   PR00239D 0.00 1.105     1636   BL01210   Caveolins proteins.   BL001210B 13.92 9.53     1637   BL00982   Bacterial-type phytoene dehydrogenase proteins.   BL00183B 21.31 8.14     1639   BL01183   UbiE/CQQ5   BL01183B 21.31 8.14     1639   BL01183   UbiE/CQQ5   BL01183B 21.31 8.14     1639   BL01183   UbiE/CQQ5   BL01183B 21.31 8.14     1639   BL01183   UbiE/CQQ5   BL01183B 21.31 8.14     1639   PR00239   MULUSCAN PROTEIN L27   PR00239C 1.31 8.24 1.33     1639   BL01183   UbiE/CQQ5   BL01183B 21.31 8.14     1639   BL01183   UbiE/CQQ5   BL01183B 21.31 8.14     1639   BL01183   UbiE/CQQ5   BL01183B 21.31 8.14     1639   PR00239   PR00239C   PR00239C 1.31 8.14     1639   BL01183   UbiE/CQQ5   BL01183B 21.31 8.14     1639   BL01183   UbiE/CQQ5   BL01183B 21.31 8.14     1639   PR00239   PR00239C   PR00239C 1.31 8.14     1639   PR00239   PR00239C   PR00239C 1.31 8.14     1639   BL01183   UbiE/CQQ5   BL01183B 21.31 8.14     1639   BL01183   UbiE/CQQ5   BL01183B 21.31 8.14     1639   PR00239   PR00239C   PR00239C 1.31 8.14     1639   PR00239   PR00239C   PR00239C 1.31 8.14     1639   BL01183   UbiE/CQQ5   BL01183B 21.31 8.14     1639   PR00239   PR00239C 1.31 8.14     1639   PR00239   PR00239C 1.31 8.14     1639   PR00239   PR00239C 1.31 8.14     1639   PR00239   PR00239C 1.31 8.14     1639   PR00239   PR00239C 1.31 8.14     1639   PR00239   PR00239C 1.31 8.14     1639   PR00239   PR00239C 1.31 8.14     1639				1.58 4.580e-09 697-709
1622   PR00860   VERTEBRATE   PR00860B 7.04 1.900     METALLOTHIONEIN   18 27-41 PR00860C   9.61 1.474e-14 41-1     PR00860A 5.46 1.720   14 5-18     1624   PR00784   MITOCHONDRIAL BROWN FAT UNCOUPLING PROTEIN SIGNATURE   11 77-95     1626   BL00325   Actin-depolymerizing proteins.   24.83 6.786e-23 61-20     1631   BL00064   L-lactate dehydrogenase proteins.   BL000325B 21.66 1.00     17.28 1.000e-40 137-182   182 BL00064F 25.14 7.88     36 286-331 BL00064   21.16 1.000e-30 22-275     1632   PR00063   RIBOSOMAL PROTEIN L27   PR00063B 15.24 9.70     1634   PR00239   MOLLUSCAN RHODOPSIN C- TERMINAL TAIL SIGNATURE   PR00239D 0.00 1.105     1636   BL01210   Caveolins proteins.   BL001210B 13.92 9.53     1637   BL00982   Bacterial-type phytoene dehydrogenase proteins.   BL00183B 21.31 8.14     1639   BL01183   UbiE/CQQ5   BL01183B 21.31 8.14     1639   BL01183   UbiE/CQQ5   BL01183B 21.31 8.14     1639   BL01183   UbiE/CQQ5   BL01183B 21.31 8.14     1639   BL01183   UbiE/CQQ5   BL01183B 21.31 8.14     1639   PR00239   MULUSCAN PROTEIN L27   PR00239C 1.31 8.24 1.33     1639   BL01183   UbiE/CQQ5   BL01183B 21.31 8.14     1639   BL01183   UbiE/CQQ5   BL01183B 21.31 8.14     1639   BL01183   UbiE/CQQ5   BL01183B 21.31 8.14     1639   PR00239   PR00239C   PR00239C 1.31 8.14     1639   BL01183   UbiE/CQQ5   BL01183B 21.31 8.14     1639   BL01183   UbiE/CQQ5   BL01183B 21.31 8.14     1639   PR00239   PR00239C   PR00239C 1.31 8.14     1639   PR00239   PR00239C   PR00239C 1.31 8.14     1639   BL01183   UbiE/CQQ5   BL01183B 21.31 8.14     1639   BL01183   UbiE/CQQ5   BL01183B 21.31 8.14     1639   PR00239   PR00239C   PR00239C 1.31 8.14     1639   PR00239   PR00239C   PR00239C 1.31 8.14     1639   BL01183   UbiE/CQQ5   BL01183B 21.31 8.14     1639   PR00239   PR00239C 1.31 8.14     1639   PR00239   PR00239C 1.31 8.14     1639   PR00239   PR00239C 1.31 8.14     1639   PR00239   PR00239C 1.31 8.14     1639   PR00239   PR00239C 1.31 8.14     1639   PR00239   PR00239C 1.31 8.14     1639   PR00239   PR00239C 1.31 8.14     1639			1	PR00239E 1.58 4.580e-
PR00860   VERTEBRATE   PR00860E 7.04 1.906   18 27-41 PR00860E				09 702-714 PR00239E
PR00860   VERTEBRATE   PR00860E 7.04 1.906   18 27-41 PR00860E		1		1.58 5.193e-09 703-715
METALLOTHIONEIN SIGNATURE 9.61 1.474e-14 41-1 PRO0860A 5.46 1.72 14 5-18  1624 PR00784 MITOCHONDRIAL BROWN FAT UNCOUPLING PROTEIN SIGNATURE  1626 BL00325 Actin-depolymerizing BL00325E 21.66 1.00 proteins. 40 93-139 BL00325E 24.83 6.786e-23 61-24.83 6.786e-23 61-24.83 6.786e-23 61-24.83 6.786e-23 61-24.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 61-28.83 6.786e-23 6	1622	PR00860	VERTEBRATE	PR00860B 7.04 1.900e-
SIGNATURE   9.61 1.474e-14 41-5   PR00860A 5.46 1.720   14 5-18   PR00784				
PR00860A 5.46 1.720				
14 5-18	ļ			
1624   PR00784   MITOCHONDRIAL BROWN FAT UNCOUPLING PROTEIN   11 77-95   11 77-95   11 77-95   11 77-95   11 77-95   11 77-95   11 77-95   11 77-95   11 77-95   11 77-95   11 77-95   11 77-95   11 77-95   11 77-95   11 77-95   11 77-95   12 78-20   12 78-20   12 78-20   13 8 L003258   21.66   1.00   24.83   6.786e-23   61-24.83   6.786e-23   61-24.83   6.786e-23   61-24   17.28   1.000e-40   13.78   1.000e-40   13.78   1.000e-40   13.78   1.000e-40   13.78   1.000e-40   12.78   1.000e-40   12.78   1.000e-40   12.78   1.000e-40   12.78   1.000e-40   12.79   1.000e-40   12.79   1.000e-40   12.79   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1.000e-40   1				
UNCOUPLING PROTEIN SIGNATURE  Actin-depolymerizing Proteins.  L-lactate dehydrogenase Proteins.  BL00064  L-lactate dehydrogenase Proteins.  BL00064B 23.57 1.00 40 82-130 BL00064C 17.28 1.000e-40 13.31 182 BL00064E 27.20 1.000e-40 223-275 BL00064F 25.14 7.88 36 286-331 BL00064 21.16 1.000e-33 22- BL00064D 14.19 6.50 31 182-212  PR00063  RIBOSOMAL PROTEIN L27 SIGNATURE PR00239  MOLLUSCAN RHODOPSIN C- TERMINAL TAIL SIGNATURE 11 36-49 PR00239C 3.51 2.538e-09 37-4  1636  BL01210  Caveolins proteins.  BL01210B 13.92 9.53 1637  BL00982 Bacterial-type phytoene dehydrogenase proteins. 11 11-43 1639  BL01183  UbiE/COQ5  BL01183B 21.31 8.14	1624	PR00784	MITOCHONDETAL BROWN FAT	
SIGNATURE   BL00325   Actin-depolymerizing proteins.   Actin-depolymerizing proteins.   Actin-depolymerizing proteins.   Actin-depolymerizing proteins.   Actin-depolymerizing proteins.   Actin-depolymerizing proteins.   Actin-depolymerizing proteins.   BL00064B 23.57 1.00		1200701		
BL00325   Actin-depolymerizing   BL00325B 21.66 1.00				11 //-95
Decimin	1626	97.003.26		DV 00305B 01 65 1 000
24.83 6.786e-23 61-    1631   BL00064   L-lactate dehydrogenase   BL00064B 23.57 1.00     40 82-130	1020	DE00323		
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proteins.  40 82-130 3L000640 17.28 1.000e-40 137 182 BL00064E 27.20 1.000e-40 223-275 BL00064F 25.14 7.88 36 286-331 BL00064 21.16 1.000e-33 22- BL00064D 14.19 6.50 31 182-212  PRO0063 RIBOSOMAL PROTEIN L27 PRO0063B 15.24 9.70 21 59-84 PRO0063A 11.71 1.614e-09 34- 11.71 1.614e-09 34- 21.634 PRO0239 MOLLUSCAN RHODOPSIN C- TERMINAL TAIL SIGNATURE 11 36-49 PR00239C 3.51 2.538e-09 37-4 21 59-84 PR00239C 3.51 2.538e-09 37-4 21 59-84 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 22 3.51 2.538e-09 37-4 23 3.51 2.538e-09 37-4 24 3.51 2.538e-09 37-4 35 3.51 2.538e-09 37-4 36 39 BL01210 Caveolins proteins. BL00282A 18.41 5.38 36 286-331 BL00064E 27.20 31 182-212 31 13-43 32 31 182-212 33 182-212 34 36 286-331 BL00064 32 1.61 1.000e-30 22- 31 182-212 31 13-18 31 11-43 31 11-43 31 11-43 31 11-43 31 11-43 31 11-43 31 11-43 31 11-43 31 11-43 31 11-43 31 11-43 31 11-43 31 11-43 31 11-43 31 11-43 31 11-43 31 11-43 31 11-43	1.631	DY 00054		
17.28 1.000e-40 137 182 BL00064E 27.20 1.000e-40 223-275 BL00064F 25.14 7.88 36 286-331 BL00064 21.16 1.000e-33 22- BL00064D 14.19 6.50 31 182-212  PR00063 RIBOSOMAL PROTEIN L27 PR00063B 15.24 9.70 21 59-84 PR00063A 11.71 1.614e-09 34- 21.634 PR00239 MOLLUSCAN RHODOFSIN C- TERMINAL TAIL SIGNATURE 11 36-49 PR00239C 3.51 2.538e-09 37-4 21 59-84 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00239C 3.51 2.538e-09 37-4 21 36-49 PR00280C 3.51 2.538e-09 37-4	1031	BD00064		
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1.000e-40 223-275 BL00064F 25.14 7.88 36 286-331 BL00064 21.16 1.000e-33 22- BL00064D 14.19 6.50 31 182-212  1632 PR00063 RIBOSOMAL PROTEIN L27 PR00063B 15.24 9.70 SIGNATURE 11.59-84 PR00063A 11.71 1.614e-09 34- 1634 PR00239 MOLLUSCAN RHODOPSIN C- TERMINAL TAIL SIGNATURE 11 36-49 PR00239C 3.51 2.538e-09 37-4 1636 BL01210 Caveolins proteins. BL01210B 13.92 9.53 1637 BL00982 Bacterial-type phytoene dehydrogenase proteins. 11 11-43 1639 BL01183 UbiE/COQ5 BL01183B 21.31 8.14				1
BL00064F 25.14 7.88 36 286-331 BL00064 21.16 1.000e-33 22- BL00064D 14.19 6.50 31 182-212  1632 PR00063 RIBOSOMAL PROTEIN L27 PR00063B 15.24 9.70 SIGNATURE 11.59-84 PR00063A 11.71 1.614e-09 34- 1634 PR00239 MOLLUSCAN RHODOPSIN C- TERMINAL TAIL SIGNATURE 11 36-49 PR00239C 3.51 2.538e-09 37-4  1636 BL01210 Caveolins proteins. BL01210B 13.92 9.53 1637 BL00982 Bacterial-type phytoene dehydrogenase proteins. 11 11-43 1639 BL01183 UbiE/COQ5 BL01183B 21.31 8.14				
36 286-331 BL00064   21.16 1.000e-33 22-8   BL00064D 14.19 6.50   31 182-212   PR00063D 15.24 9.70   SIGNATURE				
21.16 1.000e-33 22- BL00064D 14.19 6.50 31 182-212  PR00063 RIBOSOMAL PROTEIN L27 PR00063B 15.24 9.70 SIGNATURE 12.59-84 PR00063A 11.71 1.614e-09 34- 1634 PR00239 MOLLUSCAN RHODOPSIN C- TERMINAL TAIL SIGNATURE 11 36-49 PR00239C 3.51 2.538e-09 37-4  1636 BL01210 Caveolins proteins. BL01210B 13.92 9.53 10 133-183  BL00982 Bacterial-type phytoene dehydrogenase proteins. 11 11-43  1639 BL01183 UbiE/COQ5 BL01183B 21.31 8.14				BL00064F 25.14 7.882e-
BL00064D 14.19 6.50   31 182-212   1632   PR00063   RIBOSOMAL PROTEIN L27   PR00063B 15.24 9.70   11 59-84 PR00063B   11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1.614e-09 34-11.71 1			1	36 286-331 BL00064A
31 182-212			1	21.16 1.000e-33 22-50
PR00063   RIBOSOMAL PROTEIN L27   PR00063B 15.24 9.70				BL00064D 14.19 6.500e-
SIGNATURE 11 59-84 PRO0063A 11.71 1.614e-09 34-  1634 PR00239 MOLLUSCAN RHODOPSIN C- TERMINAL TAIL SIGNATURE 11 36-49 PR00239C 3.51 2.538e-09 37-4  1636 BL01210 Caveolins proteins. BL01210B 13.92 9.53 10 133-183  1637 BL00982 Bacterial-type phytoene dehydrogenase proteins. 11 11-43  1639 BL01183 UbiE/COQ5 BL01183B 21.31 8.14				31 182-212
11.71 1.614e-09 34-  1634 PR00239 MOLLUSCAN RHODOPSIN C- TERMINAL TAIL SIGNATURE 11 36-49 PR00239C 3.51 2.538e-09 37-4  1636 BL01210 Caveolins proteins. BL01210B 13.92 9.53 10 133-183  1637 BL00982 Bacterial-type phytoene dehydrogenase proteins. 11 11-43  1639 BL01183 ubiE/COQ5 BL01183B 21.31 8.14	1632	PR00063	RIBOSOMAL PROTEIN L27	PR00063B 15.24 9.700e-
11.71 1.614e-09 34-  1634 PR00239 MOLLUSCAN RHODOPSIN C- TERMINAL TAIL SIGNATURE 11 36-49 PR00239C 3.51 2.538e-09 37-4  1636 BL01210 Caveolins proteins. BL01210B 13.92 9.53 10 133-183  1637 BL00982 Bacterial-type phytoene dehydrogenase proteins. 11 11-43  1639 BL01183 ubiE/COQ5 BL01183B 21.31 8.14			SIGNATURE	
MOLLUSCAN RHODOPSIN C- TERMINAL TAIL SIGNATURE   11 36-49 PR00239C   3.51 2.538e-09 37-4   1636   BL01210   Caveolins proteins.   BL01210B 13.92 9.53   10 133-183   BL00982   Bacterial-type phytoene   BL00982A 18.41 5.38   dehydrogenase proteins.   11 11-43   1639   BL01183   UbiE/COQ5   BL01183B 21.31 8.14	ŀ			11.71 1.614e-09 34-59
TERMINAL TAIL SIGNATURE 11 36-49 PR00239C 3.51 2.538e-09 37-4 1636 BL01210 Caveolins proteins. BL01210B 13.92 9.53 10 133-183 1637 BL00982 Bacterial-type phytoene BL00982A 18.41 5.38 dehydrogenase proteins. 11 11-43 1639 BL01183 UbiE/CQQ5 BL01183B 21.31 8.14	1634	PR00239	MOLLUSCAN RHODOPSIN C-	PR00239D 0.00 1.105e-
3.51 2.538e-09 37-4  1636 BL01210 Caveolins proteins. BL01210B 13.92 9.53 10 133-183  1637 BL00982 Bacterial-type phytoene dehydrogenase proteins. 11 11-43  1639 BL01183 ubiE/COQ5 BL01183B 21.31 8.14				
1636         BL01210         Caveolins proteins.         BL01210B 13.92 9.53 10 133-183           1637         BL00982         Bacterial-type phytoene dehydrogenase proteins.         BL00982A 18.41 5.38 11 11-43           1639         BL01183         ubiE/COQS         BL01183B 21.31 8.14				
10 133-183   1637   BL00982   Bacterial-type phytoene   BL00982A 18.41 5.38   dehydrogenase proteins   11 11-43   1639   BL01183   ubiE/COQ5   BL01183B 21.31 8.14	1636	BL01210	Caveolins proteins	
1637 BL00982 Bacterial-type phytoene dehydrogenase proteins. 11 11-43 1639 BL01183 ubiE/COQ5 BL01183B 21.31 8.14				
dehydrogenase proteins. 11 11-43  1639 BL01183 ubiE/COQ5 BL01183B 21.31 8.14	1637	BI-00982	Bacterial styme whistones	
1639 BL01183 ubiE/COQ5 BL01183B 21.31 8.14				
	1639	D7.03103		
metnyltransferase family   12 132-177	-0-0-	かいいエエロコ		
	ļ			12 132-177
proteins.	1540	222222		•
	1040	FK00015	1 1	PR00015B 9.84 8.468e-
SURFACE PROTEIN ANCHOR 10 128-149	}			10 128-149
SIGNATURE				
1641 PR00320 G-PROTEIN BETA WD-40 PR00320B 12.19 5.93	L641	PR00320	G-PROTEIN BETA WD-40	PR00320B 12.19 5.935e-
			REPEAT SIGNATURE	11 364-379 PR00320A
			1	16.74 7.828e-11 364-
				379 PR00320C 13.01
2.800e-10 279-294	Į.		1	
	ł		1	PR00320C 13.01 2.800e-
	į			10 364-379 PRD0320B
	1		]	
	1		1	12.19 5.114e-10 279-
294 PR00320A 16.74	1		1	
1.659e-09 279-294				1.659e-09 279-294

SEQ ID N	O: ACCESSION NO.	DESCRIPTION	RESULTS*
			PR00320A 16.74 2.098e-
1642	PF00023	Ank repeat proteins.	09 229-244 PF00023A 16.03 6.464e-
1643	PR00169	POTASSIUM CHANNEL	09 114-130 PR00169A 16.77 1.806e-
1644		SIGNATURE	11 74-94
1044	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 2.200e-10 109-120 BL00678 9.67 5.737e-09 528-539
1645	BL01108	Ribosomal protein L24 proteins.	BL01108A 20.33 7.366e-
1646	PR00380	KINESIN HEAVY CHAIN	PR00380A 14.18 9.270e-
		SIGNATURE	21 103-125 PR00380D 9.93 6.308e-18 386-408 PR00380C 13.18 7.923e- 16 332-351 PR00380B 12.64 6.657e-15 292- 310
1647	DM01242	3 THREONINETRNA	DM01242C 17.15 9.791e-
		LIGASE.	37 340-381 DM01242E 23.00 5.071e-31 463- 505 DM01242D 23.29 3.925e-30 420-463 DM01242B 23.57 8.054e- 18 265-314 DM01242F 10.61 7.618e-14 526- 540
1649	PD00126	PROTEIN REPEAT DOMAIN TPR NUCLEA.	PD00126A 22.53 5.500e-
1651	BL01160	Kinesin light chain	10 13-34 BL01160B 19.54 6.720e-
1652	BL00933	repeat proteins. FGGY family of	11 431-485
	3200333	carbohydrate kinases proteins.	BL00933A 17.50 4.673e- 12 11-35 BL00933E 13.80 9.217e-09 456- 472
1653	BL00795	Involucrin proteins.	BL00795C 17.06 2.988e-
1654	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 7.750e- 17 302-334
1655	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 7.750e- 17 282-314
1656	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 1.391e- 16 607-630
1657	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 7.938e-
1658	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 8.889e-
1659	В100972	Ubiquitin carboxyl- terminal hydrolases family 2 proteins.	BL00972D 22.55 4.140e- 12 376-401 BL00972E 20.72 5.629e-09 446- 468
1660	BL00406	Actins proteins.	BL00406D 12.58 8.767e- 15 188-243
1661	PR00105	CYTOSINE-SPECIFIC DNA METHYLTRANSFERASE SIGNATURE	PR00105A 10.36 4.900e- 13 1140-1157 PR00105B 12.32 2.800e-12 1259- 1274 PR00105C 10.86 1.000e-10 1305-1319
1662	BL00280	Pancreatic trypsin inhibitor (Kunitz) family proteins.	BL00280 24.61 3.172e- 33 3119-3163
	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319D 11.64 6.625e- 23 107-125 PR00319C 13.41 5.714e-20 89-105 PR00319A 15.27 5.286e- 19 51-68 PR00319B 11.47 8.200e-19 70-85

SEQ ID	NO:   ACCESSION	DESCRIPTION	DECIT MOA
L	NO.		RESULTS*
1664	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 5.050e-10
1667	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 8.500e-
		ZINC-FINGER METAL- BINDING NU.	38 7-46
1669	BL01153	NOL1/NOP2/sun family	BL01153D 19.69 1.188e-
		proteins.	17 115-141 BL01153C
			13.67 8.977e-15 66-80
	į		BL01153B 20.52 1.885e-
1671	PR00678	PI3 KINASE P85	PR00678H 9.13 3.100e-
		REGULATORY SUBUNIT SIGNATURE	10 1146-1169
1672	BL00598	Chromo domain proteins.	BL00598 14.45 8.500e-
1673	PR00326	GTP1/OBG GTP-BINDING	20 27-49 PR00326A 8.75 8.329e-
1674	DD00040	PROTEIN FAMILY SIGNATURE	09 686-707
10/4	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 7.580e-
		SIGNATURE	11 343-358 PR00049D 0.00 1.286e-10 342-357
1676	PR00747	GLYCOSYL HYDROLASE	PR00747H 12.76 8.636e-
		FAMILY 47 SIGNATURE	19 427-448 PR00747G
			14.50 2.286e-18 368-
			393 PR00747C 12.06 7.500e-18 112-131
		İ	PR00747A 14.05 4.600e-
			17 42-63 PR00747D
		1 .	15.23 8.759e-17 163-
			183 PR00747E 15.13 8.244e-15 254-272
		ļ	PR00747B 7.65 5.355e-
			13 75-90 PR00747F
			13.56 8.714e-10 311- 328
1677	PR00747	GLYCOSYL HYDROLASE	PR00747H 12.76 8.636e-
		FAMILY 47 SIGNATURE	19 309-330 PR00747G
	į		14.50 2.286e-18 250-
			275 PR00747C 12.06 7.500e-18 112-131
			PR00747A 14.05 4.600e-
			17 42-63 PR00747B
		İ	7.65 5.355e-13 75-90
			PR00747F 13.56 8.714e-
1680	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 4.600e-10
		proteins proteins.	406-417 BL00678 9.67
1681	BL00678	Trp-Asp (WD) repeat	6.684e-09 320-331
	2300070	proteins proteins.	BL00678 9.67 4.600e-10 329-340 BL00678 9.67
			6.684e-09 243-254
1683	PR00326	GTP1/OBG GTP-BINDING	PR00326A 8.75 1.346e-
1685	PR00646	PROTEIN FAMILY SIGNATURE RDC1 ORPHAN RECEPTOR	13 389-410
		SIGNATURE	PR00646H 6.32 4.188e- 09 755-771
1690	BL01160	Kinesin light chain	BL01160B 19.54 6.644e-
1691	PR00456	repeat proteins. RIBOSOMAL PROTEIN P2	09 75-129 PR00456E 3.06 7.281e-
		SIGNATURE	10 418-433 PR00456E
		1	3.06 7.281e-10 419-434
			PR00456E 3.06 8.125e-
1692	PR00456	RIBOSOMAL PROTEIN P2	10 420-435 PR00456E 3.06 7.281e-
		SIGNATURE	10 487-502 PR00456E
			3.06 7.281e-10 488-503
			PR00456E 3.06 8.125e-
1693	BL00674	AAA-protein family	10 489-504 PL006740 33 60 8 043-
		proteins.	BL00674C 22.60 8.043e- 24 274-317 BL00674B
		<del> </del>	3/4 31/ DD000/4D

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
<u></u>	NO.		1
	·		4.46 4.000e-23 241-263 BL00674D 23.41 8.560e- 18 338-385 BL00674E 15.24 1.720e-15 414- 434
1697	PR00409	PHTHALATE DIOXYGENASE REDUCTASE FAMILY SIGNATURE	PR00409F 12.70 4.388e- 10 427-447
1698	PR00466	CYTOCHROME B-245 HEAVY CHAIN SIGNATURE	PR00466C 10.17 3.443e- 13 187-208 PR00466B 5.03 5.500e-11 162-186 PR00466F 9.16 6.159e- 09 498-517
1699	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 9.217e- 12 283-300 BL00028 16.07 3.769e-11 255- 272 BL00028 16.07 5.154e-11 171-188 BL00028 16.07 5.500e- 11 227-244 BL00028 16.07 1.600e-10 199- 216
1700	BL01019	ADP-ribosylation factors family proteins.	BL01019A 13.20 3.348e- 15 62-102 BL01019B 19.49 4.000e-15 107-
1703	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	162 PD01066 19.43 2.484e- 12 200-239
1707	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 4.558e- 14 134-153
1710	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 2.565e- 10 116-130 PR00019B 11.36 4.600e-09 113- 127 PR00019B 11.36 7.120e-09 204-218
1711	BL01159	WW/rsp5/WWP domain proteins.	BL01159 13.85 6.523e- 11 232-247 BL01159 13.85 5.408e-10 613-
1712	PF00023	Ank repeat proteins.	628 PF00023A 16.03 7.000e- 10 187-203
1713	PF00642	Zinc finger C-x8-C-x5-C-x3-H type (and similar).	PF00642 11.59 9.550e- 11 230-241
1714	PF00642	Zinc finger C-x8-C-x5-C-x3-H type (and similar).	PF00642 11.59 9.550e- 11 230-241
1715	BL01115 .	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 7.129e- 09 7-51
	BL00353	HMG1/2 proteins.	BL00353C 14.83 6.018e- 10 136-183 BL00353B 11.47 8.866e-09 86-136
1719	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 5.408e- 09 432-483
1721	BL00038	Myc-type, 'helix-loop- helix' dimerization domain proteins.	BL00038B 16.97 8.448e- 12 79-100 BL00038A 13.61 4.000e-11 52-68
1723	PD00567	PROTBIN RNA-BINDING RNA REPEAT HYD.	PD00567C 9.17 8.500e- 09 418-428
1724	BL01279	Protein-L- isoaspartate(D- aspartate) O- methyltransferase signa.	BL01279A 24.27 5.663c- 12 233-281
1728	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 2.059e-11 73-86 BL00018 7.41
1730	BL00594	Aromatic amino acids permeases proteins.	4.176e-11 157-170 BL00594A 16.75 1.089e- 09 17-61

SEQ ID N	O: ACCESSION	DESCRIPTION	
	NO.		RESULTS*
1731	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 9.676e-
1732	BL01160	Kinesin light chain	10 296-350
		repeat proteins.	BL01160B 19.54 9.676e- 10 316-370
1733	PF00850	Histone deacetylase	PF00850F 15.70 4.349e-
		family.	22 246-279 PF00850D
			14.76 6.850e-20 177-
ļ	1		201 PF00850E 8.88
İ	1		8.691e-18 209-235
			PF00850G 22.75 4.098e-
1734	BL00354	VINO T - 3 VINO	14 281-323
	D000334	HMG-I and HMG-Y DNA- binding domain proteins	BL00354C 6.61 5.932e-
1		(Ahook)	09 292-307
1735	DM00179	w KINASE ALPHA ADHESION	DM00179 13.97 5.263e-
l		T-CELL.	10 492-502
1743	PR00449	TRANSFORMING PROTEIN P21	PR00449A 13.20 1.188e-
		RAS SIGNATURE	11 5-27 PR00449D
			10.79 2.241e-10 109-
		1	123 PR00449E 13.50
1744			9.289e-10 144-167
7.144	PR00449	TRANSFORMING PROTEIN P21	PR00449A 13.20 1.188e-
	1	RAS SIGNATURE	11 5-27 PR00449D
			10.79 2.241e-10 109-
			123 PR00449E 13.50
1745	BL00720	Guanine-nucleotide	9.289e-10 144-167 BL00720B 16.57 8.297e-
		dissociation stimulators	15 136-160
-		CDC25 family sign.	23 230-260
1746	PR00081	GLUCOSE/RIBITOL	PR00081B 10.38 6.727e-
		DEHYDROGENASE FAMILY	11 45-57 PR00081E
		SIGNATURE	17.54 3.935e-10 150-
1747	BL00439		168
	BD00439	Acyltransferases ChoActase / COT / CPT	BL00439H 18.24 8.435e-
		family proteins.	14 65-91 BL00439G
1749	PR00819	CBXX/CFQX SUPERFAMILY	13.40 2.895e-12 3-14 PR00819B 10.83 7.158e-
		SIGNATURE	11 4-20
1751	PD00066	PROTEIN ZINC-FINGER	PD00066 13.92 3.400e-
		METAL-BINDI.	14 33-46 PD00066
			13.92 1.000e-13 89-102
	1 .	)	PD00066 13.92 7.000e-
		•	13 61-74 PD00066
	}		13.92 6.571e-12 117-
1753	BL01013	Oxysterol-binding	130
		protein family proteins.	BL01013D 26.81 6.516e- 18 33-77
1754	BL00790	Receptor tyrosine kinase	BL00790I 20.01 2.393e-
		class V proteins.	09 490-521 BL007901
			20.01 2.821e-09 60-91
			BL00790I 20.01 6.357e-
1756	PDOTOGG		09 287-318
± / J0	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 9.750e-
		ZINC-FINGER METAL- BINDING NU.	35 10-49
1758	DM00406	GLIADIN.	DM00406 T TO TO
			DM00406 7.73 7.600e-09 653-666
1762	PD02929	ADHESION GLYCOPROTEIN	PD02929A 28.27 4.529e-
		PRECURSOR I.	09 224-278
1765	PR00326	GTP1/OBG GTP-BINDING	PR00326A 8.75 5.950e-
1776	777	PROTEIN FAMILY SIGNATURE	11 146-167
1775	PF00023	Ank repeat proteins.	PF00023A 16.03 3.077e-
1776	BL00942		14 523-539
	BB00347	glpT family of	BL00942F 15.07 4.343e-
		transporters proteins.	10 371-389 BL00942B
777	DM00215	PROLINE-RICH PROTEIN 3.	20.36 8.040e-09 94-137
		LACORING RICH PROTEIN 3.	DM00215 19.43 2.373e-
		<u> </u>	09 279-312

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1778	BL00084	Copper type II, ascorbate-dependent monooxygenases proteins.	BL00084D 25.11 3.700e- 20 169-224 BL00084B 24.26 8.134e-16 10-58 BL00084C 27.71 8.412e- 11 107-158
1779	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 3.758e- 18 611-655 BL01013A 25.14 2.881e-15 344- 380 BL01013C 9.97 6.308e-13 435-445 BL01013B 11.33 3.717e- 12 409-420
1783	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 8.138e- 13 492-515
1784	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 8.138e- 13 492-515

<sup>\*</sup> results include in order: accession number subtype; raw score; p-value; postion of signature in amino acid sequence.

TRADOCS:1416223.I(%CRJ0!!.DOC)

TABLE 4

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM
2	ig	Immunoglobulin domain	2.1e-32	109.5
3	pkinase	Eukaryotic protein kinase domain	1.3e-29	110.7
4	zf-C2H2	Zinc finger, C2H2 type	1.6e-21	84.9
5	fn3	Fibronectin type III domain	0	1097.1
6	fn3	Fibronectin type III domain	<del> </del> 0	1035.0
7	fn3	Fibronectin type III domain	-   0	
8	fn3	Fibronectin type III domain	<del>  0</del>	1090.4
9	TBC	TBC domain	4e-40	1097.1
10	p450	Cytochrome P450	9.5e-17	146.7
12	ank	Ank repeat	6e-20	62.0
14	ig	Immunoglobulin domain	1.7e-05	79.7
15	zf-MYND	MYND finger	1.7e-05	22.7
16	zf-MYND	MYND finger	1.3e-06	35.4
17	zf-C2H2	Zinc finger, C2H2 type		35.4
18	CAP GLY	CAP-Gly domain	1.7e-99	343.9
20	IMPDH C	IMP dehydrogenase / GMP	1.2e-25	98.7
		reductase C terminus	1.6e-119	410.5
21	IMPDH C	IMP dehydrogenase / GMP	1	
22	pkinase	reductase C terminus	4.3e-102	352.6
		Eukaryotic protein kinase domain	2.4e-79	277.0
23	pkinase	Eukaryotic protein kinase domain	8.4e-74	258.6
25	RNA_pol_A	RNA polymerase alpha subunit	<del>-</del>	1077.7
26	Clq	Clg domain	1.9e-10	44.4
27	Ribosomal_L2	Ribosomal protein L23	7.8e-32	111.2
28	Ribosomal_L2	Ribosomal protein L23	le-29	104.2
30	zf-A20	A20-like zinc finger	1.5e-10	48.5
31	zf-A20	A20-like zinc finger	1.5e-10	48.5
32	FMN_dh	FMN-dependent dehydrogenase	5.4e-179	608.1
34	PID	Phosphotyrosine interaction domain (PTB/PID)	3.8e-59	209.9
35	ig	Immunoglobulin domain	1.4e-13	48.8
36	ig	Immunoglobulin domain	1.4e-13	48.B
40	kinesin	Kinesin motor domain	6.7e-76	265.6
14	Ets	Ets-domain	1.4e-56	182.1
15	Ets	Ets-domain	1.4e-56	182.1
16	LRR	Leucine Rich Repeat	1.7e-13	58.3
18	zf-C2H2	Zinc finger, C2H2 type	2.3e-162	552.8
19	ITAM	Immunoreceptor tyrosine-based activation mot	1.4e-05	31.9
50	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	1.1e-26	102.0
1	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	1.1e-26	102.0
2	ras	Ras family		
3	PRK		8.5e-45	162.3
4	myb_DNA-	Phosphoribulokinase Myb-like DNA-binding domain	2.1e-65 0.096	230.7 15.2
5	binding voltage CLC			1
6		Voltage gated chloride channels	3.3e-186	631.9
7	sugar_tr TBC	Sugar (and other) transporter	0.00015	-64.3
8	ank	TBC domain	2.2e-37	137.6
9	ank	Ank repeat	5.9e-25	96.3
7		Ank repeat	5.9e-25	96.3
i	PMP22_Claudi n	PMP-22/EMP/MP20/Claudin family	7.9e-49	175.6
8	CZ	C2 domain	7.9e-54	192.2
9	C2	C2 domain	2.3e-54	194.0
0	Kelch	Kelch motif	9.4e-99	341.5
2	ig	Immunoglobulin domain	8.2e-28	94.7
3	pkinase	Eukaryotic protein kinase	8e-69	242.1

SEQ II	PEAM NAME	DESCRIPTION		
NO:		2200121 1201	p-value	PFAM SCORE
<u> </u>		domain	<del></del>	SCORE
74	pkinase	Eukaryotic protein kinase	2.8e-3B	140.6
1	.~	domain	2.06-30	140.6
76	zf-	Topoisomerase DNA binding C4	5.4e-54	192.8
L	C4_Topoisom	zinc fing	30 34	172.0
83	Peptidase_S9		4.3e-10	36.8
84	fn3	Fibronectin type III domain	4.1e-51	183.2
86	SH2	Src homology domain 2	3.1e-22	67.7
88	ig	Immunoqlobulin domain	0.0091	14.0
89	WD40	WD domain, G-beta repeat	2.1e-21	84.6
92	laminin_G	Laminin G domain	6.1e-27	98.5
93	AMP-binding	AMP-binding enzyme	2.4e-13	-37.2
95	pkinase	Eukaryotic protein kinase	1.4e-59	211.4
		domain	1	
96	pkinase	Eukaryotic protein kinase	2.6e-51	183.9
		domain		
97	adh_short	short chain dehydrogenase	2e-61	217.5
98	kinesin	Kinesin motor domain	2.2e-86	300.4
101	IRS	PTB domain (IRS-1 type)	5.4e-36	133.0
102	AAA	ATPases associated with various	6.8e-05	-5.2
		cellular act		
104	pkinase	Eukaryotic protein kinase	2.7e-73	256.9
		domain		
106	ras	Ras family	8.3e-24	92.5
107	FYVE	FYVE zinc finger	5.4e-27	100.7
108	Cyt_reductas	FAD/NAD-binding Cytochrome	7.7e-61	215.5
	е	reductase		
109	zf-C2H2	Zinc finger, C2H2 type	2.3e-122	420.0
113	pkinase	Eukaryotic protein kinase	4e-88	306.2
		domain		1
116	PH	PH domain	3.1e-11	45.2
117	lipocalin	Lipocalin / cytosolic fatty-	2.4e-14	53.5
110		acid binding pr		
118	pkinase	Eukaryotic protein kinase	4.5e-20	76.3
120	· WD40	domain		ł
121	WD40	WD domain, G-beta repeat	2.4e-14	61.1
123	IF5 eIF4 eIF	WD domain, G-beta repeat	2.4e-14	61.1
123	2	eIF4-gamma/eIF5/eIF2-epsilon	1e-32	122.2
124	ig			
127	mito carr	Immunoglobulin domain	6.5e-08	30.6
128	PP2C	Mitochondrial carrier proteins	3e-16	58.6
129	ATPIG1_PLM_M	Protein phosphatase 2C ATPIGI/PLM/MAT8 family	2.2e-71	250.6
	AT8	AIPIGI/PLM/MATE TAMILY	3.1e-20	80.6
130	pfkB	pfkB family carbohydrate kinase		
133	ACBP	Acyl CoA binding protein	4.5e-42	137.1
134	rrm	RNA recognition motif.	4.6e-22	86.7
135	IQ	IQ calmodulin-binding motif	1.2e-31	118.5
136	ATPIG1_PLM_M	ATPIGI/PLM/MATS family	2.6e-08	41.0
	AT8	worl frail with ramity	9.3e-22	85.7
139	WH2	Wiskott Aldrich syndrome	0.005=	-
		homology region 2	0.0067	23.1
140	zf-C2H2	Zinc finger, C2H2 type	2.5.00	
141	Peptidase S2	Signal peptidase I	1.7e-82	287.5
	6	3 hebitidase 1	5.7e-10	35.7
L43	arf	ADP-ribosylation factor family	1 0	
146	KRAB	KRAB box	1.2e-39	145.2
48	DUF6	Integral membrane protein DUF6	7.3e-30	112.6
		3'5'-cyclic nucleotide	0.096	8.0
	PDFase	( → → *CVCIIC BUCLĒĢĒIGĒ	3.8e-80	231.1
49	PDEase		J.00-00	1
.49		phosphodiesterase		
.51	S4	phosphodiesterase S4 domain	1.1e-08	42.3
.51 .53	S4 tRNA-synt_1d	phosphodiesterase S4 domain tRNA synthetases class I (R)	1.1e-08 3.8e-103	42.3 356.1
.51	S4 tRNA-synt_1d Cyt_reductas	phosphodiesterase S4 domain tRNA synthetases class I (R) FAD/NAD-binding Cytochrome	1.1e-08	42.3
.49 .51 .53	S4 tRNA-synt_1d Cyt_reductas e	phosphodiesterase S4 domain tRNA synthetases class I (R) FAD/NAD-binding Cytochrome reductase	1.1e-08 3.8e-103 7.8e-60	42.3 356.1 212.2
.49 .51 .53 .54	S4 tRNA-synt_1d Cyt_reductas	phosphodiesterase S4 domain tRNA synthetases class I (R) FAD/NAD-binding Cytochrome	1.1e-08 3.8e-103	42.3 356.1

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
158	Jacalin	Jacalin-like lectin domain	10.00	SCORE
160			0.09	-24.9
165	Zn_carbOpept pkinase	Zinc carboxypeptidase	5e-138	471.9
		Eukaryotic protein kinase domain	5.1e-67	236.1
167	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	5.3e-07	27.0
168	Ribosomal_S1	Ribosomal protein S15	1.1e-06	29.0
169	DEAD	DEAD/DEAH box helicase	le-48	157.0
171	DUF59	Domain of unknown function	0.07	-17.4
172	pkinase	DUF59 Eukaryotic protein kinase	3.7e-15	58.6
		domain	1	
173	globin	Globin	4.6e-18	67.4
174	WW	WW domain	7.3e-06	32.9
175	ras	Ras family	le-31	118.8
178	ATP1G1_PLM_M AT8	ATP1G1/PLM/MAT8 family	2.5e-17	71.0
179	zf-C2H2	Zinc finger, C2H2 type	1.5e-99	344.2
180	Clq	Clq domain	8.8e-72	251.9
190	Y_phosphatas e	Protein-tyrosine phosphatase	4.9e-287	967.0
191	efhand	EF hand	7.5e-16	66.1
193	pkinase	Eukaryotic protein kinase domain	6.5e-82	285.6
194	bromodomain	Bromodomain	5.8e-31	111.4
195	PALP	Pyridoxal-phosphate dependent enzyme	2.5e-64	227.1
197	DnaJ	DnaJ domain	1.6e-38	141.4
199	RrnaAD	Ribosomal RNA adenine dimethylases	0.00018	16.9
200	acid_phospha	Histidine acid phosphatase	2.5e-10	37.2
201	WH2	Wiskott Aldrich syndrome homology region 2	0.00048	26.9
204	vATP- synt AC39	ATP synthase (C/AC39) subunit	1.3e-159	543.7
205	vATP- synt_AC39	ATP synthase (C/AC39) subunit	1.6e-139	476.9
206	ldl_recept_a	Low-density lipoprotein receptor domain	2.4e-25	97.6
209	ank	Ank repeat	1.4e-19	78.4
210	Rhomboid	Rhomboid family	0.0035	1.2
211	Clq	Clq domain	1.6e-70	247.7
212	UO COD	Ubiquitin-conjugating enzyme	7.4e-74	258.8
213	UQ con	Ubiquitin-conjugating enzyme	1e-53	191.9
215	DEAD	DEAD/DEAH box helicase	1.8e-43	140.4
216	PMP22_Claudi	PMP-22/EMP/MP20/Claudin family	4.5e-21	83.4
218	Glycos_trans	Glycosyl transferases	4e-21	83.6
219	19	Immunoglobulin domain	0.092	10.7
	WD40	WD domain, G-beta repeat	7.4e-23	89.4
222				
	1	I'I'PR Domain	1 20-09	
224	TPR DnaJ_CXXCXGX	TPR Domain DnaJ central domain (4 repeats)	1.2e-08 1.5e-38	141.5
224 225	TPR DnaJ_CXXCXGX G DnaJ_CXXCXGX			
224 225 226	TPR DnaJ_CXXCXGX G DnaJ_CXXCXGX G	DnaJ central domain (4 repeats)  DnaJ central domain (4 repeats)	1.5e-38	141.5
224 225 226 229	TPR DnaJ_CXXCXGX G DnaJ_CXXCXGX G HSP70	DnaJ central domain (4 repeats)  DnaJ central domain (4 repeats)  Hsp70 protein	1.5e-38 1.5e-38 2.4e-54	141.5
224 225 226 229 230	TPR DnaJ_CXXCXGX G DnaJ_CXXCXGX G HSP70 GSHPx	DnaJ central domain (4 repeats)  DnaJ central domain (4 repeats)  Hsp70 protein  Glutathione peroxidases	1.5e-38 1.5e-38 2.4e-54 3.4e-47	141.5 141.5 194.0 170.2
224 225 226 229 230 231	TPR DnaJ_CXXCXGX G DnaJ_CXXCXGX G HSP70 GSHPx tsp_1	DnaJ central domain (4 repeats)  DnaJ central domain (4 repeats)  Hsp70 protein Glutathione peroxidases  Thrombospondin type 1 domain	1.5e-38 1.5e-38 2.4e-54 3.4e-47 0.0075	141.5 141.5 194.0 170.2 17.1
224 225 226 229 230 231 233	TPR DnaJ_CXXCXGX G DnaJ_CXXCXGX G HSP70 GSHPx tsp_1 cyclin	DnaJ central domain (4 repeats)  DnaJ central domain (4 repeats)  Hsp70 protein Glutathione peroxidases Thrombospondin type 1 domain Cyclin	1.5e-38 1.5e-38 2.4e-54 3.4e-47 0.0075 4.6e-144	141.5 141.5 194.0 170.2 17.1 492.0
224 225 226 229 230 231 233 234	TPR DnaJ_CXXCXGX G DnaJ_CXXCXGX G HSP70 GSHPx tsp_1 cyclin ras	DnaJ central domain (4 repeats)  DnaJ central domain (4 repeats)  Hsp70 protein  Glutathione peroxidases  Thrombospondin type 1 domain  Cyclin  Ras family	1.5e-38 1.5e-38 2.4e-54 3.4e-47 0.0075 4.6e-144 4.8e-50	141.5 141.5 194.0 170.2 17.1 492.0 179.7
224 225 226 229 230 231 233 234 235	TPR DnaJ_CXXCXGX G DnaJ_CXXCXGX G HSP70 GSHPx tsp_1 cyclin ras LRR	DnaJ central domain (4 repeats)  DnaJ central domain (4 repeats)  Hsp70 protein  Glutathione peroxidases  Thrombospondin type 1 domain  Cyclin  Ras family  Leucine Rich Repeat	1.5e-38 1.5e-38 2.4e-54 3.4e-47 0.0075 4.6e-144 4.8e-50 1.2e-30	141.5 141.5 194.0 170.2 17.1 492.0 179.7 115.3
222 224 225 226 229 230 231 233 234 235 235 2236	TPR DnaJ_CXXCXGX G DnaJ_CXXCXGX G HSP70 GSHPx tsp_1 cyclin ras	DnaJ central domain (4 repeats)  DnaJ central domain (4 repeats)  Hsp70 protein  Glutathione peroxidases  Thrombospondin type 1 domain  Cyclin  Ras family	1.5e-38 1.5e-38 2.4e-54 3.4e-47 0.0075 4.6e-144 4.8e-50	141.5 141.5 194.0 170.2 17.1 492.0 179.7

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:				SCORE
244	dCMP_cyt_dea	Cytidine and deoxycytidylate deaminase	2.5e-05	31.1
245	ig	Immunoglobulin domain	6.7e-08	30.5
248	wnt	wnt family of developmental signaling protei	9.1e-270	742.6
250	mito_carr	Mitochondrial carrier proteins	1.3e-55	193.6
254	adenylatekin ase	Adenylate kinase	1.8e-14	55.7
255	Cation_efflu	Cation efflux family	2.8e-33	124.0
256	SH3	SH3 domain	3.9e-14	60.4
257	Aa_trans	Transmembrane amino acid	2.5e-52	187.2
	] _	transporter protein		
258	adenylatekin ase	Adenylate kinase	2.1e-110	380.2
259	HIT	HIT family	8.2e-07	25.3
260	Bacterial_PQ	PQQ enzyme repeat	1.6e-15	65.0
262	proteasome	Proteasome A-type and B-type	6.5e-64	225.7
267	pkinase	Eukaryotic protein kinase domain	6.3e-27	101.0
270	filament	Intermediate filament proteins	3.2e-150	512.5
271	Choline_kina	Choline/ethanolamine kinase	2e-67	237.4
277	Ribosomal_S7	Ribosomal protein S7p/S5e	3.3e-20	80.6
279	pkinase	Eukaryotic protein kinase	3.3e-20	269.9
280	WD40	WD domain, G-beta repeat	7.8e-73	255.4
281	WD40	WD domain, G-beta repeat	7.8e-73	255.4
284	zf-DHHC	DHHC zinc finger domain	4.6e-24	93.4
287	Exonuclease	Exonuclease	1.4e-67	238.0
291	SAM	SAM domain (Sterile alpha motif)	0.034	11.2
292	SAM	SAM domain (Sterile alpha motif)	0.034	11.2
294	zf-C2H2	Zinc finger, C2H2 type	1.4e-29	111.7
295	zf-C2H2	Zinc finger, C2H2 type	2.2e-125	430.0
296	mito_carr	Mitochondrial carrier proteins	4.1e-59	205.5
297	HMG_box	HMG (high mobility group) box	6.7e-29	109.4
302	Glycos_trans f_4	Glycosyl transferase	5e-87	302.5
304	tRNA-synt_2	tRNA synthetases class II (D, K and N)		294.8
305	KRAB	KRAB box	2e-44	161.0
306 308	rxm	RNA recognition motif.	2.7e-44	160.6
	7tm_1	7 transmembrane receptor (rhodopsin family)	5.2e-39	126.1
309	DNA_polymera	DNA polymerase X family	2.4e-64	227.2
	F-box	F-box domain.	9.5e-08	39.2
312	ig	Immunoglobulin domain	6.8e-19	65.9
313	Ets	Ets-domain	8.1e-60	192.3
315 317	Kelch	Kelch motif	1.3e-106	367.6
	arf	ADP-ribosylation factor family	3.2e-35	130.4
318 320	sugar_tr	Sugar (and other) transporter	0.0003	-73.1
	pkinase	Eukaryotic protein kinase domain	8.1e-83	288.6
322	pkinase	Eukaryotic protein kinase domain	4.9e-81	282.6
324	Xlink	Extracellular link domain	4.5e-143	331.5
126	ARID	ARID DNA binding domain	5.1e-37	136.4
327	HMG_box	HMG (high mobility group) box	6.7e-29	109.4
328	cadherin	Cadherin domain	8.1e-81	281.9
331	chromo	'chromo' (CHRromatin Organization MOdifier)	4e-18	66.7
133	Peptidase M2	Glycoprotease family	1.2e-136	467.4

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
335	vwa			SCORE
		von Willebrand factor type A domain	2.3e-07	37.9
339	ras	Ras family	7.8e-07	~59.1
340	zf-C2H2	Zinc finger, C2H2 type	8.2e-64	225.4
342	zf-C2H2	Zinc finger, C2H2 type	2.4e-85	297.0
343	ig	Immunoglobulin domain	0.0005	18.0
346	pkinase	Eukaryotic protein kinase domain	6.5e-65	229.1
347	pkinase	Eukaryotic protein kinase domain	6.5e-65	229.1
351	EGF	EGF-like domain	8.5e-20	79.2
352	ank	Ank repeat	2.5e-101	350.0
354	TBC	TBC domain	5.1e-15	63.3
355	PHD	PHD-finger	3.2e-07	37.4
358	DUF6	Integral membrane protein DUF6		
359	zf-C2H2	Zinc finger, C2H2 type	0.033	15.8
361	ank		7.4e-20	79.4
362	ArfGap	Ank repeat	6.6e-34	126.1
	-	Putative GTP-ase activating protein for Arf	4.7e-53	189.7
363	efhand	EF hand	5.4e-10	46.6
367	LRR	Leucine Rich Repeat	8.8e-44	158.9
368	laminin_G	Laminin G domain	1.5e-33	121.7
369	PP2C	Protein phosphatase 2C	5.3e-20	73.9
372	LIM	LIM domain containing proteins	9.9e-15	57.1
373	KRAB	KRAB box	4.8e-23	90.0 .
376	ion_trans	Ion transport protein	2.9e-09	-4.2
377	Beach	Beige/BEACH domain	4.9e-208	704.5
380	pkinase	Eukaryotic protein kinase domain	1.6e-94	327.5
381	AMP-binding	AMP-binding enzyme	1.4e-07	-140.3
382	HECT	HECT-domain (ubiquitin-	1.3e-07	-13.5
		transferase).		
384	ank .	Ank repeat	2.5e-101	350.0
386	ig	Immunoglobulin domain	9.5e-06	23.6
388	zf-C2H2	Zinc finger, C2H2 type	1.7e-42	154.6
389	ig	Immunoglobulin domain	2.8e-15	54.3
390	mito_carr	Mitochondrial carrier proteins	3.5e-67	233.2
392	TPR	TPR Domain	6.1e-17	69.7
393	SH3	SH3 domain	3.5e-09	43.9
394	AAA	ATPases associated with various cellular act	4.le-21	83.6
396	spectrin	Spectrin repeat	2.1e-67	237.3
397	zf-C2H2	Zinc finger, C2H2 type	0.0066	23.1
399	fn3	Pibronectin type III domain	4.1e-102	352.6
400	WD40	WD domain, G-beta repeat	0.00049	26.8
401	El_dehydrog	Dehydrogenase El component	3e-119	409.6
402	£n3	Fibronectin type III domain	0	1719.6
404	LRR	Leucine Rich Repeat	2.1e-10	48.0
405	cadherin	Cadherin domain	8.1e-81	281.9
406	zf-CXXC	CXXC zinc finger	5e-15	63.4
410	RhoGEF	RhoGEF domain	1.1e-23	92.1
411	F-box	F-box domain.	4.2e-06	33.7
412	SNF2_N	SNF2 and others N-terminal	5.8e-16	61.6
		domain		
415	CPSase_L_cha	Carbamoyl-phosphate synthase	1.5e-172	586.6
	in	(CPsase)	1.5e-172	586.6
418	in LRR	(CPSase) Leucine Rich Repeat	1.5e-172 3.8e-24	93.6
418 419	in LRR DENN	(CPsase)	_	
418 419 420	in LRR DENN RasGEF	(CPSase) Leucine Rich Repeat	3.8e-24	93.6
418 419 420 421	in LRR DENN	(CPSase) Leucine Rich Repeat DENN (AEX-3) domain	3.8e-24 2e-58	93.6
418 419 420 421 424	in LRR DENN RasGEF	(CPSase) Leucine Rich Repeat DENN (AEX-3) domain RasGEF domain	3.8e-24 2e-58 8.1e-43 1.4e-153	93.6 207.5 155.7 523.7
418 419 420 421	in LRR DENN RasGEF ank	(CPSase) Leucine Rich Repeat DENN (AEX-3) domain RasGEF domain Ank repeat	3.8e-24 2e-58 8.1e-43	93.6 207.5 155.7 523.7 78.9
418 419 420 421 424 425	in LRR DENN RASGEF ank G-patch pkinase	(CPSase) Leucine Rich Repeat DENN (AEX-3) domain RasGEF domain Ank repeat G-patch domain Eukaryotic protein kinase domain	3.8e-24 2e-58 8.1e-43 1.4e-153 1e-19 2.2e-31	93.6 207.5 155.7 523.7 78.9 117.1
418 419 420 421 424	in LRR DENN RasGEF ank G-patch	(CPSase) Leucine Rich Repeat DENN (AEX-3) domain RasGEF domain Ank repeat G-patch domain Eukaryotic protein kinase	3.8e-24 2e-58 8.1e-43 1.4e-153 1e-19	93.6 207.5 155.7 523.7 78.9

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:			1	SCORE
	t		- <del> </del>	
429	zf-C3HC4	Zinc finger, C3HC4 type (RING	8.6e-11	39.2
43.0		finger)	<u> </u>	ļ
431 432	DEAD	DEAD/DEAH box helicase	1e-66	214.0
432	SH3	SH3 domain	3.4e-16	67.2
436	GTP_CDC	Cell division protein	2.1e-114	393.5
436	Collagen	Collagen triple helix repeat (20 copies)	4.6e-194	658.1
438	Ricin B lect	Similarity to lectin domain of		
130	in	ricin b	0.0085	10.5
441	Alpha adapti	Alpha adaptin carboxyl-terminal	1.2e-256	1055 0
	n C	domai	1.26-236	866.0
442	Alpha adapti	Alpha adaptin carboxyl-terminal	1.8e-235	795.7
	n_C	domai	2.00.200	,,,,,
443	PDZ	PDZ domain (Also known as DHR	1.9e-65	230.9
		or GLGF).		230.3
445	LON	ATP-dependent protease La (LON)	0.00012	-17.1
_		domain		
446	ig	Immunoglobulin domain	0.00011	20.1
<b>,451</b>	sushi	Sushi domain (SCR repeat)	1.4e-18	75.2
452	fn3	Fibronectin type III domain	1.5e-06	35.2
454	pyridoxal_de	Pyridoxal-dependent	8.3e-14	50.3
	C	decarboxylase conse	1	1
456	kinesin	Kinesin motor domain	4.9e-217	734.4
457	neur_chan	Neurotransmitter-gated ion-	1e-175	597.1
450		channel		
458	Josephin   bZIP	Josephin	0.0002	18.7
468 470		bZIP transcription factor	1.7e-07	31.8
470	NTP_transfer	Nucleotidyl transferase	6.3e-06	-26.3
471	WD40		1	
473	LIM	WD domain, G-beta repeat	2e-28	107.9
477	zf-RanBP	LIM domain containing proteins Zn-finger in Ran binding	0.00021	20.7
411	ZI-Kanbr	protein and others.	0.028	21.0
479	WD40	WD domain, G-beta repeat		-
480	KRAB	KRAB box	6.5e-18 le-31	73.0
481	ArfGap	Putative GTP-ase activating	8.4e-66	232.0
		protein for Arf	0.46-86	232.0
485	SH2	Src homology domain 2	0.011	11.4
486	Clq	Clg domain	4.3e-74	259.6
487	dsrm	Double-stranded RNA binding	1.1e-47	171.9
		motif		
489	zf-C2H2	Zinc finger, C2H2 type	4.8e-153	521.9
490	Alpha_adapti	Alpha adaptin carboxyl-terminal	3.4e-222	751.6
	n_C	domai		İ
492	SKI	Shikimate kinase	1.2e-10	48.8
497	ENV_polyprot	ENV polyprotein (coat	2.6e-22	77.6
498	abhydrolase	polyprotein)		<u> </u>
230	2	Phospholipase/Carboxylesterase	0.041	-48.1
500	rrm	DND recognition with		
501	WW	RNA recognition motif.	5.4e-34	126.4
502	ig		4.6e-18	73.4
504	abhydrolase	Immunoglobulin domain	1.1e-10	39.5
504 505	vwa	alpha/beta hydrolase fold	0.045	-3.6
	I wa	von Willebrand factor type A domain	7.1e-62	219.0
508	Na K ATPase	Na+/K+ ATPase C-terminus		
	C ATTUBE	Naty At AlPase C-terminus	2.3e-145	496.3
509	Exonuclease	Exonuclease	1 35 55	201 -
510	Glycos_trans	Glycosyl transferases group 1	1.3e-56	201.5
	f 1	orloosly crameragases dronb 1	2.9e-06	27.0
	Glycos trans	Glycosyl transfers	2.05.05	L
511		Glycosyl transferases group 1	2.9e-06	27.0
511		1		
511	f_1	Glycosyl transferaces crown	1 90 00	30 5
		Glycosyl transferases group 1	1.9e-09	38.5
	f_1 Glycos_trans	Glycosyl transferases group 1 Cyclophilin type peptidyl-	1.9e-09 1.8e-63	38.5

SEQ ID	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	L DECORTORY OF		
NO:	PFAM NAME	DESCRIPTION	p-value	PFAM
515	EGF	EGF-like domain	1.9e-18	74.7
516	Surp	Surp module	4.3e-38	140.0
523	iq	Immunoglobulin domain	3.3e-06	25.0
526	UBX	UBX domain	1.le-34	128.6
528	adh zinc	Zinc-binding dehydrogenases	2.7e-34	127.4
530	SAM	SAM domain (Sterile alpha	0.046	10.0
		motif)	0.040	10.0
531	adh short	short chain dehydrogenase	0.0025	-34.1
532	mito carr	Mitochondrial carrier proteins	2.5e-8I	281.7
533	mito carr	Mitochondrial carrier proteins	2e-61	213.5
534	thiolase	Thiolase	3.5e-183	622.0
535	FMO-like	Flavin-binding monooxygenase-	0	1153.7
		like		
536	SCAN	SCAN domain	4e-55	196.6
537	tRNA-synt_1	tRNA synthetases class I (I, L,	3.1e-136	466.0
		M and V)		
53B	tRNA-synt_1	tRNA synthetases class I (I, L,	3.le-136	466.0
		M and V)	1	1
539	tRNA-synt_1	tRNA synthetases class I (I, L,	1.9e-117	403.6
540	1.5	M and V)		
540	tRNA-synt_1	tRNA synthetases class I (I, L,	3.1e-136	466.0
541	vATP-synt E	M and V)		
543	zf-C2H2	ATP synthase (E/31 kDa) subunit Zinc finger, C2H2 type	5.9e-85	295.7
544	DUF101	Protein of unknown function	5.5e-69	242.6
244	DOFTOI	DUF101	8.5e-38	139.0
545	TGFb propept	TGF-beta propeptide	1.le-67	238.2
	ide	101-beta propeptide	1.16-0,	230.2
547	WD40	WD domain, G-beta repeat	2.6e-32	120.8
548	RHD	Rel homology domain (RHD).	1.6e-238	686.2
549	MMR HSR1	GTPase of unknown function	5.4e-67	236.0
551	HECT	HECT-domain (ubiquitin-	4.3e-127	435.6
		transferase).		
554	MHC_II_alpha	Class II histocompatibility	3.5e-74	259.8
		antigen, alp		
555	zf-UBR1	Putative zinc finger in N-	3.3e-16	67.3
556	Kelch	recognin	<u> </u>	
561	AMP-binding	Kelch motif	5.5e-29	109.7
562	PABP	AMP-binding enzyme	2.8e-06	-163.7
502	FADP	Poly-adenylate binding protein, unique domai	4.9e-38	139.8
564	Gag_p30	Gag P30 core shell protein	1.2e-67	222
566	PWWP	PWWP domain	8.1e-16	238.2 66.0
567	SCAN	SCAN domain	7.3e-68	238.9
569	pkinase	Eukaryotic protein kinase	1.5e-84	294.3
		domain	1.35-04	222.3
570	pkinase	Bukaryotic protein kinase	1.5e-84	294.3
		domain		1
571	CN_hydrolase	Carbon-nitrogen hydrolase	0.00081	-79.7
572	myosin_head	Myosin head (motor domain)	0	1495.2
573	myosin_head	Myosin head (motor domain)	0	1490.4
				91.5
575	Surp	Surp module	1.7e-23	1 27.2
576	Surp	Surp module	1.7e-23 1.7e-23	91.5
576 577	Surp DNA_pol_B	Surp module DNA polymerase family B		
576	Surp	Surp module DNA polymerase family B PDZ domain (Also known as DHR	1.7e-23	91.5
576 577 578	Surp DNA_pol_B PDZ	Surp module DNA polymerase family B PDZ domain (Also known as DHR or GLGF).	1.7e-23 0 8.3e-09	91.5 1138.6 42.7
576 577 578 579	Surp DNA_pol_B PDZ LRR	Surp module  DNA polymerase family B  PDZ domain (Also known as DHR or GLGF).  Leucine Rich Repeat	1.7e-23 0 8.3e-09	91.5 1138.6 42.7
576 577 578	Surp DNA_pol_B PDZ	Surp module  DNA polymerase family B  PDZ domain (Also known as DHR or GLGF).  Leucine Rich Repeat  Neurotransmitter-gated ion-	1.7e-23 0 8.3e-09	91.5 1138.6 42.7
576 577 578 579 580	Surp DNA_pol_B PDZ LRR neur_chan	Surp module  DNA polymerase family B  PDZ domain (Also known as DHR or GLGF).  Leucine Rich Repeat  Neurotransmitter-gated ion-channel	1.7e-23 0 8.3e-09 4.9e-21 5.9e-177	91.5 1138.6 42.7 83.3 601.3
576 577 578 579 580	Surp DNA_pol_B PDZ  LRR neur_chan sushi	Surp module  DNA polymerase family B  PDZ domain (Also known as DHR or GLGF).  Leucine Rich Repeat  Neurotransmitter-gated ion-channel  Sushi domain (SCR repeat)	1.7e-23 0 8.3e-09 4.9e-21 5.9e-177	91.5 1138.6 42.7 83.3 601.3
576 577 578 579 580 583	Surp DNA_pol_B PDZ  LRR neur_chan sushi DEAD	Surp module  DNA polymerase family B  PDZ domain (Also known as DHR or GLGF).  Leucine Rich Repeat  Neurotransmitter-gated ion-channel  Sushi domain (SCR repeat)  DEAD/DEAH box helicase	1.7e-23 0 8.3e-09 4.9e-21 5.9e-177 0 7.3e-36	91.5 1138.6 42.7 83.3 601.3 1673.0 116.3
576 577 578 579 580 583 584 586	Surp DNA_pol_B PDZ  LRR neur_chan sushi DEAD KH-domain	Surp module  DNA polymerase family B  PDZ domain (Also known as DHR or GLGF).  Leucine Rich Repeat  Neurotransmitter-gated ion-channel  Sushi domain (SCR repeat)  DEAD/DEAH box helicase  KH domain	1.7e-23 0 8.3e-09 4.9e-21 5.9e-177 0 7.3e-36 2.9e-13	91.5 1138.6 42.7 83.3 601.3 1673.0 116.3 57.5
576 577 578 579 580 583 584 586 587	Surp DNA_pol_B PDZ  LRR neur_chan sushi DEAD KH-domain G-patch	Surp module  DNA polymerase family B  PDZ domain (Also known as DHR or GLGF).  Leucine Rich Repeat  Neurotransmitter-gated ion-channel  Sushi domain (SCR repeat)  DEAD/DEAH box helicase  KH domain  G-patch domain	1.7e-23 0 8.3e-09 4.9e-21 5.9e-177 0 7.3e-36 2.9e-13 2.3e-14	91.5 1138.6 42.7 83.3 601.3 1673.0 116.3 57.5 61.2
576 577 578 579 580 583 584 586 587 589	Surp DNA_pol_B PDZ  LRR neur_chan sushi DEAD KH-domain G-patch	Surp module  DNA polymerase family B  PDZ domain (Also known as DHR or GLGF).  Leucine Rich Repeat  Neurotransmitter-gated ion-channel  Sushi domain (SCR repeat)  DEAD/DEAH box helicase  KH domain  G-patch domain  LIM domain containing proteins	1.7e-23 0 8.3e-09 4.9e-21 5.9e-177 0 7.3e-36 2.9e-13 2.3e-14 2.3e-36	91.5 1138.6 42.7 83.3 601.3 1673.0 116.3 57.5 61.2
576 577 578 579 580 583 584 586 587	Surp DNA_pol_B PDZ  LRR neur_chan sushi DEAD KH-domain G-patch	Surp module  DNA polymerase family B  PDZ domain (Also known as DHR or GLGF).  Leucine Rich Repeat  Neurotransmitter-gated ion-channel  Sushi domain (SCR repeat)  DEAD/DEAH box helicase  KH domain  G-patch domain	1.7e-23 0 8.3e-09 4.9e-21 5.9e-177 0 7.3e-36 2.9e-13 2.3e-14	91.5 1138.6 42.7 83.3 601.3 1673.0 116.3 57.5 61.2

SCORE	SEQ ID	DENN MAND	DESCRIPTION		-r
Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear hormone   Nuclear ho		PFAM NAME	DESCRIPTION	p-value	PFAM
SP3	592	hormone_rec		3.5e-22	87.1
S94	503	1 10770	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	<del> </del>	
Delinase		L			
S97   ND160   ND domain, G-beta repeat   0.00054   26.7		1			
FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   FG-GAP   F			domain		
Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Sect					
Solution   Substract   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State   State					262.9
domain   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen   Collagen		1 ~ ~ —		1.1e-53	191.8
(20 copies)   (20 copies)   (31 copies)   (32 copies)   (33 copies)   (34 copies)   (35 copies)   (35 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)   (36 copies)	603	pkinase	domain	2.3e-86	300.4
DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE   DATE	605	Collagen		8e-42	152.4
SOB   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   PWMP   P	606	mito carr		6.3e-67	232.3
Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution   Solution	608				
CAP_GIY	609	PWWP		1	
RFX_DNA_bind   RFX_DNA-binding domain   S.2e-5¢   192.9	613	L	1	1	
Side	615	RFX_DNA_bind			
Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Sinc	616	<u> </u>	Kinesin motor domain	1 16-01	294 9
Section					
Finger   MATH   MATH   MATH   Amain   7.8e-05   22.2		3			
Protein-tyrosine phosphatase   1.4e-32   121.6			finger)		
Eukaryotic protein kinase   4.4e-40   146.6					,
domain   BNR		e		<u> </u>	121.6
Molybdopteri	622	pkinase		4.4e-40	146.6
N	623 .		BNR repeat	2.1e-11	51.3
CNMP_binding	624			1.4e-12	
CNMP_binding   Cyclic nucleotide-binding   3.7e-58   206.6	625	TPR	TPR Domain	1.1e-17	72.2
2f-C2H2   Zinc finger, C2H2 type   Zinc-88   307.1	627	cNMP_binding			
631         zf-C2H2         Zinc finger, C2H2 type         2.1e-88         307.1           632         rrm         RNA recognition motif.         4e-05         30.5           635         pkinase         Eukaryotic protein kinase domain         1.6e-104         360.7           636         Fork head         Fork head domain         5.9e-27         103.0           637         pkinase         Eukaryotic protein kinase domain         3.8e-70         246.5           643         pkinase         Eukaryotic protein kinase domain         4.8e-08         40.1           643         efhand         EF hand         1.9e-27         104.6           647         SNF2_N         SNF2 and others N-terminal domain         1.2e-101         351.1           648         PseudoU_synt hdomain         PseudoU_synt hdomain         1.9e-55         197.6           650         zf-C2H2         Zinc finger, C2H2 type         0.0087         22.7           651         ank         Ank repeat         1.3e-17         71.9           652         I_LWEQ         I/LWEQ domain         9.5e-101         341.0           653         neur_chan         Neurotransmitter-gated ion-channel         4.1e-171         581.8           654         t	630	adh short	short chain dehydrogenase	5e-17	70.0
RNA recognition motif.   4e-05   30.5	631	zf-C2H2			
Eukaryotic protein kinase   1.6e-104   360.7	632	rrm			
Fork_head   Fork_head domain   5.9e-27   103.0	635	pkinase		1.6e-104	
Pkinase	636	Fork head		5 9e-27	103.0
642         TPR         TPR Domain         4.8e-08         40.1           643         efhand         1.9e-27         104.6           647         SNF2_N         SNF2 and others N-terminal domain         1.2e-101         351.1           648         PseudoU_synt h2         RNA pseudouridylate synthase h2         1.9e-55         197.6           650         Zf-C2H2         Zinc finger, C2H2 type         0.0087         22.7           651         ank         Ank repeat         1.3e-17         71.9           652         I_LWEQ         I/LWEQ domain         9.5e-101         341.0           653         neur_chan         Neurotransmitter-gated ion-channel         4.1e-171         581.8           654         tsp_1         Thrombospondin type 1 domain         4.1e-47         169.9           659         FHZ         Formin Homology 2 Domain         1e-107         371.2           661         pou         Pou domain - N-terminal to homeobox domain         5.3e-45         162.9           662         C2         C2 domain         6.7e-19         76.2           663         C2         C2 domain         6.7e-19         76.2           664         C2         C2 domain         6.7e-19         76.2<	637		Eukaryotic protein kinase		
643         efhand         EF hand         1.9e-27         104.6           647         SNF2_N         SNF2 and others N-terminal domain         1.2e-101         351.1           648         PseudoU_synt h2         RNA pseudouridylate synthase h2         1.9e-55         197.6           650         zf-C2H2         Zinc finger, C2H2 type         0.0087         22.7           651         ank         Ank repeat         1.3e-17         71.9           652         I_LWEQ         I/LWEQ domain         9.5e-101         341.0           653         neur chan         Neurotransmitter-gated ion-channel         4.1e-171         581.8           654         tsp_1         Thrombospondin type 1 domain         4.1e-47         169.9           659         FH2         Formin Homology 2 Domain         1e-107         371.2           661         pou         Fou domain - N-terminal to homeobox domain         5.3e-45         162.9           662         C2         C2 domain         6.7e-19         76.2           663         C2         C2 domain         6.7e-19         76.2           664         C2         C2 domain         6.7e-19         76.2           667         GST         Glutathione S-transferases	642	ממיזי		1	<del> </del>
647         SNF2_N         SNF2 and others N-terminal domain         1.2e-101         351.1           648         PseudoU_synt h2         RNA pseudouridylate synthase h2         1.9e-55         197.6           650         zf-C2H2         Zinc finger, C2H2 type         0.0087         22.7           651         ank         Ank repeat         1.3e-17         71.9           652         I_LWEQ         I/LWEQ domain         9.5e-101         341.0           653         neur_chan         Neurotransmitter-gated ion-channel         4.1e-171         581.8           654         tsp_1         Thrombospondin type 1 domain         4.1e-47         169.9           659         FH2         Formin Homology 2 Domain         1e-107         371.2           661         pou         Fou domain - N-terminal to homeobox domain         5.3e-45         162.9           662         C2         C2 domain         6.7e-19         76.2           663         C2         C2 domain         6.7e-19         76.2           664         C2         C2 domain         6.7e-19         76.2           667         GST         Glutathione S-transferases         9.3e-34         114.4           668         LRR         Leucine Rich Repe					
				1	1
h_2		•	domain		1
651         ank         Ank repeat         1.3e-17         71.9           652         I_LWEQ         I/LWEQ domain         9.5e-101         341.0           653         neur_chan         Neurotransmitter-gated ion-channel         4.1e-171         581.8           654         tsp_1         Thrombospondin type 1 domain         4.1e-47         169.9           659         FH2         Formin Homology 2 Domain         1e-107         371.2           661         pou         Pou domain - N-terminal to homeobox domain         5.3e-45         162.9           662         C2         C2 domain         6.7e-19         76.2           663         C2         C2 domain         6.7e-19         76.2           664         C2         C2 domain         6.7e-19         76.2           667         GST         Glutathione S-transferases.         9.3e-34         114.4           668         LRR         Leucine Rich Repeat         9.3e-31         115.6           670         Spectrin         Spectrin repeat         4e-57         203.2           671         I_LWEQ         I/LWEQ domain         9.5e-101         341.0           672         ABC tran         ABC transporter         5.3e-60         212		h 2			1
Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Tabl					
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Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Channel   Chan				i i	
659 FH2 Formin Homology 2 Domain 1e-107 371.2 661 pou Pou domain - N-terminal to 5.3e-45 162.9 homeobox domain 6.7e-19 76.2 663 C2 C2 domain 6.7e-19 76.2 664 C2 C2 domain 6.7e-19 76.2 667 GST Glutathione S-transferases. 9.3e-34 114.4 668 LRR Leucine Rich Repeat 9.3e-31 115.6 670 spectrin Spectrin repeat 4e-57 203.2 671 I_LWEQ I/LWEQ domain 9.5e-101 341.0 672 ABC tran ABC transporter 5.3e-60 212.8		<b></b>	channel	4.1e-171	581.8
661 pou Fou domain - N-terminal to 5.3e-45 162.9 homeobox domain 6.7e-19 76.2 663 C2 C2 domain 6.7e-19 76.2 664 C2 C2 domain 6.7e-19 76.2 667 GST Glutathione S-transferases. 9.3e-34 114.4 668 LRR Leucine Rich Repeat 9.3e-31 115.6 670 Spectrin Spectrin repeat 4e-57 203.2 671 I_LWEQ domain 9.5e-101 341.0 672 ABC transporter 5.3e-60 212.8				4.1e-47	169.9
homeobox domain			Formin Homology 2 Domain	1e-107	371.2
663 C2 C2 domain 6.7e-19 76.2 664 C2 C2 domain 6.7e-19 76.2 667 GST Glutathione S-transferases. 9.3e-34 114.4 668 LRR Leucine Rich Repeat 9.3e-31 115.6 670 Spectrin Spectrin repeat 4e-57 203.2 671 I_LWEQ I/LWEQ domain 9.5e-101 341.0 672 ABC tran ABC transporter 5.3e-60 212.8	661	pou		5.3e-45	162.9
663     C2     C2 domain     6.7e-19     76.2       664     C2     C2 domain     6.7e-19     76.2       667     GST     Glutathione S-transferases.     9.3e-34     114.4       668     LRR     Leucine Rich Repeat     9.3e-31     115.6       670     Spectrin     Spectrin repeat     4e-57     203.2       671     I_LWEQ     I/LWEQ domain     9.5e-101     341.0       672     ABC tran     ABC transporter     5.3e-60     212.8	662	C2	C2 domain	6.7e-19	76.2
664         C2         C2 domain         6.7e-19         76.2           667         GST         Glutathione S-transferases.         9.3e-34         114.4           668         LRR         Leucine Rich Repeat         9.3e-31         115.6           670         Spectrin         Spectrin repeat         4e-57         203.2           671         I_LWEQ         I/LWEQ domain         9.5e-101         341.0           672         ABC_tran         ABC transporter         5.3e-60         212.8	663	C2	C2 domain		
667         GST         Glutathione S-transferases.         9.3e-34         114.4           668         LRR         Leucine Rich Repeat         9.3e-31         115.6           670         spectrin         Spectrin repeat         4e-57         203.2           671         I_LMEQ         I/LWEQ domain         9.5e-101         341.0           672         ABC_tran         ABC transporter         5.3e-60         212.8	664				
668         LRR         Leucine Rich Repeat         9.3e-31         115.6           670         spectrin         Spectrin repeat         4e-57         203.2           671         I_LWEQ         I/LWEQ domain         9.5e-101         341.0           672         ABC_tran         ABC transporter         5.3e-60         212.8	667				
670 spectrin Spectrin repeat 4e-57 203.2 671 I_LWEQ I/LWEQ domain 9.5e-101 341.0 672 ABC_tran ABC transporter 5.3e-60 212.8			Leucine Rich Repeat		
671 I_LWEQ I/LWEQ domain 9.5e-101 341.0 672 ABC tran ABC transporter 5.3e-60 212.8	1			<u> </u>	
672 ABC tran ABC transporter 5.3e-60 212.8					
[ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [					
	674	WD40	WD domain, G-beta repeat	4.8e-24	93.3

SEO ID				_
NO:	PFAM NAME	DESCRIPTION	p-value	PFAM
675	WD40	WD domain, G-beta repeat	<del> </del>	
676	LRR	Leucine Rich Repeat	4.8e-24	93.3
679	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H	0.0015	25.2
","	21-cccn	type	2.6e-29	107.7
680	zf-C2H2	Zinc finger, C2H2 type	5.2e-05	30.1
681	CH	Calponin homology (CH) domain	2.4e-17	71.1
682	DSPc	Dual specificity phosphatase,	4.3e-43	
		catalytic doma	4.3e-43	156.6
683	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.051	10.8
687	Synapsin	Synapsin		1890.8
689	PR55	Protein phosphatase 2A	0	1038.8
		regulatory subunit PR	"	1030.0
691	homeobox	Homeobox domain	8.5e-30	112.4
696	Peptidase M2	metallopeptidase family M24	2.6e-59	210.5
	4	medatapeperado ramily M24	2.62-59	210.5
697	RhoGEF	RhoGEF domain	9.5e-35	128.9
698	PHD	PHD-finger	0.008	9.3
701	zf-C2H2	Zinc finger, C2H2 type	5.5e-123	422.0
702	Sulfatase	Sulfatase	3e-231	781.6
703	zf-C2H2	Zinc finger, C2H2 type	5.7e-20	79.8
707	Acyl_transf	Acyl transferase domain	1.le-22	88.8
708	WD40	WD domain, G-beta repeat	4.8e-19	76.7
71.0	Ran BP1	RanBP1 domain.	8.4e-06	-7.3
713	DEAD	DEAD/DEAH box helicase	9.9e-42	
714	PH	PH domain		134.9
715	DSPc	Dual specificity phosphatase,	1.6e-09	39.0
		catalytic doma	1.5e-37	138.2
717	Sialyltransf	Sialyltransferase family	7.5e-31	115.9
718	ig	Immunoglobulin domain	le-29	100.8
719	integrin_B	Integrins, beta chain	0	1125.4
720	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.1e-08	32.4
722	Peptidase_C2	Calpain family cysteine	3e-145	495.9
723	ig	protease Immunoglobulin domain	<del> </del>	
724	F-box		2.2e-05	22.4
725	Nop	F-box domain.	0.007	23.0
726	Nop	Putative snoRNA binding domain	8.1e-58	205.5
727	WD40	Putative snoRNA binding domain	8.1e-58	205.5
730	_ 1	WD domain, G-beta repeat	7.5e-26	99.3
730	derm	Double-stranded RNA binding motif	0.027	12.1
731	dynamin	Dynamin family	4.2e-16	66.9
733	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H	2.8e-10	41.7
	_ [	type	2.00 20	1
735	CDP-	CDP-alcohol	4.2e-26	100.1
	OH_P_transf	phosphatidyltransferase		]
738	DEAD	DEAD/DEAH box helicase	B.6e-57	182.5
739	TSC22	TSC-22/dip/bun family	6.5e-32	119.5
742	ras	Ras family	2.2e-100	346.9
743	PMI_typeI	Phosphomannosc isomerase type I	1.2e-243	822.9
747	trypsin	Trypsin	6.4e-88	279.4
748	kazal	Kazal-type serine protease		
<del></del>		inhibitor domain	2.2e-52	187.4
749	efhand		6.3e-06	33.1
751	efhand PHD	inhibitor domain  EF hand  PHD-finger		33.1
751 752	efhand	inhibitor domain  EF hand  PHD-finger	6.3e-06 4.9e-16	33.1 66.7
751	efhand PHD	inhibitor domain  EF hand  PHD-finger  Zinc finger, C2H2 type haloacid dehalogenase-like	6.3e-06	33.1
751 752	efhand PHD zf-C2H2 Hydrolase Ribosomal_L3	inhibitor domain  EF hand  PHD-finger  Zinc finger, C2H2 type	6.3e-06 4.9e-16 3.2e-21	33.1 66.7 83.9
751 752 753 754	efhand PHD zf-C2H2 Hydrolase Ribosomal_L3	inhibitor domain  EF hand  PHD-finger  Zinc finger, C2H2 type haloacid dehalogenase-like hydrolase  Ribosomal L39 protein	6.3e-06 4.9e-16 3.2e-21 6.1e-11	33.1 66.7 83.9 49.8
751 752 753 754 755	efhand PHD zf-C2H2 Hydrolase Ribosomal_L3 9 PH	inhibitor domain  EF hand  PHD-finger  Zinc finger, C2H2 type haloacid dehalogenase-like hydrolase  Ribosomal L39 protein  PH domain	6.3e-06 4.9e-16 3.2e-21 6.1e-11	33.1 66.7 83.9 49.8
751 752 753 754 755 758	efhand PHD zf-C2H2 Hydrolase Ribosomal_L3 9 PH SCAN	inhibitor domain  EF hand  PHD-finger  Zinc finger, C2H2 type haloacid dehalogenase-like hydrolase  Ribosomal L39 protein	6.3e-06 4.9e-16 3.2e-21 6.1e-11	33.1 66.7 83.9 49.8
751 752 753 754 755 758 759	efhand PHD zf-C2H2 Hydrolase Ribosomal_L3 9 PH SCAN PA	inhibitor domain  EF hand  PHD-finger  Zinc finger, C2H2 type haloacid dehalogenase-like hydrolase Ribosomal L39 protein  PH domain  SCAN domain PA domain	6.3e-06 4.9e-16 3.2e-21 6.1e-11 0.00018 3.6e-14 1.4e-53	33.1 66.7 83.9 49.8 26.7 55.7
751 752 753 754 755 758	efhand PHD zf-C2H2 Hydrolase Ribosomal_L3 9 PH SCAN	inhibitor domain  EF hand  PHD-finger  Zinc finger, C2H2 type haloacid dehalogenase-like hydrolase Ribosomal L39 protein  PH domain  SCAN domain	6.3e-06 4.9e-16 3.2e-21 6.1e-11 0.00018	33.1 66.7 83.9 49.8 26.7

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PPAM
NO:				SCORE
762	histone	Core histone H2A/H2B/H3/H4	9.9e-53	188.6
763	zf-MYND	MYND finger	4.1e-14	60.3
764	bon	Pou domain - N-terminal to	1e-52	188.6
		homeobox domain		
767	VWC	von Willebrand factor type C	2.9e-34	127.3
		domain	İ	
769	efhand	EF hand	4.8e-11	50.1
770	zf-C4	Zinc finger, C4 type (two ·	2.4e-53	181.6
		domains)		ŀ
772	ras	Ras family	7e-90	312.0
773	Sulfatase	Sulfatase	le-142	487.5
775	zf-C2H2	Zinc finger, C2H2 type	1.1e-12	55.5
776	zf-C2H2	Zinc finger, C2H2 type	1.1e-12	55.5
777	zf-C2H2	Zinc finger, C2H2 type	1.1e-12	55.5
778	rrm	RNA recognition motif.	2.1e-32	121.1
779	G6PD ·	Glucose-6-phosphate	1.5e-76	236.6
		dehydrogenase	1	
780	spectrin	Spectrin repeat	3.7e-29	110.3
781	mito_carr	Mitochondrial carrier proteins	4.6e-57	198.5
782	SCAN	SCAN domain	1.3e-24	95.2
783	PDZ	PDZ domain (Also known as DHR	4.1e-07	37.1
		or GLGF).		1
785	DEAD	DEAD/DEAH box helicase	6e-06	21.7
786	ras	Ras family	5.3e-39	143.0
787	RNase_HII	Ribonuclease HII	2.5e-67	237.1
790	PI3 PI4 kina	Phosphatidylinositol 3- and 4-	5.4e-108	372.2
	se	kinases	10.12.200	3,2.2
795	cadherin	Cadherin domain	2.5e-40	147.4
796	ARID	ARID DNA binding domain	1.6e-20	81.6
797	trypsin	Trypsin	9.9e-20	64.8
799	CH	Calponin homology (CH) domain	3.7e-15	63.8
801	Gal-	Vertebrate galactoside-binding	4.1e-25	88.7
	bind lectin	lectin		00.7
803	WD40	WD domain, G-beta repeat	0.00082	26.1
806	TBC	TBC domain	1.8e-26	101.4
807	TBC	TBC domain	1.8e-26	101.4
808	CN_hydrolase	Carbon-nitrogen hydrolase	8.8e-80	278.5
811	CBFD NFYB HM	Histone-like transcription	6e-14	59.8
	F	factor		1 32.0
812	adh_short	short chain dehydrogenase	8.1e-20	79.3
814	IMP4	Domain of unknown function	3.3e-71	250.0
815	zf-C2H2	Zinc finger, C2H2 type	8.2e-66	232.1
816	Pept_tRNA hy	Peptidyl-tRNA hydrolase	1.6e-37	138.0
	dro			
817	ARID	ARID DNA binding domain	2.5e-18	74.3
826	IFS_eIF4_eIF	eIF4-gamma/eIF5/eIF2-epsilon	1.6e-32	121.5
	2			122.5
830	ArfGap	Putative GTP-ase activating	1.5e-53	191.3
	1 -	protein for Arf		1
831	LRR	Leucine Rich Repeat	2.1e-26	101.1
832	laminin EGF	Laminin EGF-like (Domains III	2e-57	204.2
			1223,	201.2
	_	and V)	1	1
839	rrm		1.36-22	88 5
839 840		RNA recognition motif.	1.3e-22	88.5
	rrm Y_phosphatas		1.3e-22 2.6c-119	88.5
	Y_phosphatas	RNA recognition motif. Protein-tyrosinc phosphatase	2.60-119	409:8
840	Y_phosphatas e	RNA recognition motif. Protein-tyrosinc phosphatase Bukaryotic protein kinase		
840	Y_phosphatas e pkinase	RNA recognition motif.  Protein-tyrosinc phosphatase  Bukaryotic protein kinase domain	2.6c-119 3.4e-100	409!8 346.3
840	Y_phosphatas e	RNA recognition motif. Protein-tyrosinc phosphatase Bukaryotic protein kinase	2.60-119	409:8
841 844	Y_phosphatas e pkinase Ribosomal_L2 2e	RNA recognition motif. Protein-tyrosinc phosphatase  Eukaryotic protein kinase domain Ribosomal L22e protein family	2.6c-119 3.4e-100 1e-64	409!8 346.3 228.4
840 841 844 846	Y_phosphatas e pkinase Ribosomal_L2 2e IBR	RNA recognition motif.  Protein-tyrosinc phosphatase  Bukaryotic protein kinase domain  Ribosomal L22e protein family  IBR domain	2.6c-119 3.4e-100 1e-64 9e-15	409:8 346.3 228.4 62.5
840	Y_phosphatas e pkinase Ribosomal_L2 2e	RNA recognition motif.  Protein-tyrosinc phosphatase  Bukaryotic protein kinase domain Ribosomal L22e protein family  IBR domain Zinc finger, C3HC4 type (RING	2.6c-119 3.4e-100 1e-64	409!8 346.3 228.4
841 841 844 846 849	Y_phosphatas e pkinase Ribosomal_L2 2e IBR zf-C3HC4	RNA recognition motif.  Protein-tyrosinc phosphatase  Bukaryotic protein kinase domain  Ribosomal L22e protein family  IBR domain  Zinc finger, C3HC4 type (RING finger)	2.6c-119 3.4e-100 1e-64 9e-15 7.4e-07	409:8 346.3 228.4 62.5 26.5
840 841 844 846	Y_phosphatas e pkinase Ribosomal_L2 2e IBR	RNA recognition motif.  Protein-tyrosinc phosphatase  Bukaryotic protein kinase domain  Ribosomal L22e protein family  IBR domain  Zinc finger, C3HC4 type (RING finger)  Zinc finger, C3HC4 type (RING	2.6c-119 3.4e-100 1e-64 9e-15	409:8 346.3 228.4 62.5
841 844 846 846 849	Y_phosphatas e pkinase  Ribosomal_L2 2e  IBR zf-C3HC4  zf-C3HC4	RNA recognition motif.  Protein-tyrosinc phosphatase  Bukaryotic protein kinase domain  Ribosomal L22e protein family  IBR domain  Zinc finger, C3HC4 type (RING finger)  Zinc finger, C3HC4 type (RING finger)	2.6c-119 3.4e-100 1e-64 9e-15 7.4e-07 0.00016	409:8 346.3 228.4 62.5 26.5
841 841 844 846 849	Y_phosphatas e pkinase Ribosomal_L2 2e IBR zf-C3HC4	RNA recognition motif.  Protein-tyrosinc phosphatase  Bukaryotic protein kinase domain  Ribosomal L22e protein family  IBR domain  Zinc finger, C3HC4 type (RING finger)  Zinc finger, C3HC4 type (RING	2.6c-119 3.4e-100 1e-64 9e-15 7.4e-07	409:8 346.3 228.4 62.5 26.5

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:				SCORE
		rich domain		
853	SRCR	Scavenger receptor cysteine- rich domain	0	1025.4
857	lactamase_B	Metallo-beta-lactamase superfamily	0.012	-6.0
858	COX6A	Cytochrome c oxidase subunit	3.4e-58	206.7
B59	rrm	RNA recognition motif.	<del></del>	
861	PRK	Phosphoribulokinase	5.4e-45	162.9
863	mito carr	Mitochondrial carrier proteins	5.1e-62	219.4
864	HSP90	Hsp90 protein	2.9e-53	185.5
866	ig		4.7e-158	538.5
867	zf-C2H2	Immunoglobulin domain Zinc finger, C2H2 type	4e-12	44.1
872	histone	Core histone H2A/H2B/H3/H4	7e-135	461.5
874	CPSase_L_cha		4.9e-41	149.8
	in	(CPSase)	2.1e-218	739.0
879	Ribosomal_S1 2e	Ribosomal protein Sl2e	2.1e-98	340.3
882	serpin	Serpins (serine protease inhibitors)	2.5e-42	145.7
883	Patatin	Patatin	1.2e-51	182.0
884	RA	Ras association (RalGDS/AF-6) domain	0.044	8.0
887	DUF92	Integral membrane protein DUF92	2.7e-12	54.3
889	sugar tr	Sugar (and other) transporter	8.2e-63	222.1
893	DUF28	Domain of unknown function	1.3e-43	158.3
896	IP trans	DUF28 Phosphatidylinositol transfer	6.5e-98	
898	DEAD	protein		338.7
899	KE2	DEAD/DEAH box helicase	1.5e-48	156.5
900	KE2	KE2 family protein KE2 family protein	7e-61	215.7
901	zf-C2H2	Zinc finger, C2H2 type	4.3e-51	183.2
902	ras	Ras family	2.7e-57	203.8
904	TPR	TPR Domain	2.3e-75 3.2e-22	263.8 87.2
906	GBP	Guanylate-binding protein	8.9e-253	853.1
907	GBP	Guanylate-binding protein	1.1e-239	809.6
908	WD40	WD domain, G-beta repeat	2.6e-26	100.8
909	PH	PH domain	1.3e-09	39.4
910	zf-C2H2	Zinc finger, C2H2 type	2.5e-39	144.1
913	Epimerase	NAD dependent epimerase/dehydratase family	5e-07	-88.5
921	TBC	TBC domain	1.5e-09	30.7
922	WD40	WD domain, G-beta repeat	1.6e-25	98.2
923	WD40	WD domain, G-beta repeat	8.2e-07	36.1
924	Hydrolase	haloacid dehalogenase-like hydrolase	2.9e-05	29.1
925	UQ_con	Ubiquitin-conjugating enzyme	0.00033	-27.6
926	CH	Calponin homology (CH) domain	3.3e~53	190.2
928	WD40	WD domain, G-beta repeat	5.9e-48	172.7
929	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	3.1e-10	37.4
930	Ribul_P_3_ep	Ribulose-phosphate 3 epimerase family	7.2e-105	361.8
931	Ribul_P_3_ep	Ribulose-phosphate 3 epimerase	1.2e-96	334.4
936	C2	family C2 domain	8	
937	NAP_family	Nucleosome assembly protein	2.2e-62 1.1e-22	220.7 84.6
940	abhydrolase	(NAP)		
944	Tropomyosin	alpha/beta hydrolase fold	0.011	3.1
48	pkinase	Tropomyosins Eukaryotic protein kinase	3.2e-07	25.1
_		domain	3.4e-75	263.2
A Q				
50	WD40 Acyltransfer	WD domain, G-beta repeat Acyltransferase	1.8e-27 1.6e-07	104.7 38.4

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:				SCORE
951	SAM	SAM domain (Sterile alpha motif)	0.014	14.5
954	GFO_IDH_MocA	Oxidoreductase family	1.3e-11	52.0
955	BTB	BTB/POZ domain	7e-22	86.1
956	BTB	BTB/POZ domain	7e-22	86.1
957	CDP-	CDP-alcohol	0.053	-22.2
	OH_P_transf	phosphatidyltransferase		
959	ras	Ras family	2.4e-97	336.8
960	ras	Ras family	8.4e-43	155.6
961	Acetyltransf	Acetyltransferase (GNAT) family	1.2e-08	42.2
962	adh_short	short chain dehydrogenase	2.4e-31	117.6
963	mutT	Bacterial mutT protein	5.6e-06	26.2
969 .	IF-2B	Initiation factor 2 subunit family	8.4e-193	653.9
970	RNase_PH	3' exoribonuclease family	9e-24	92.4
975	WW	WW domain	5.7e-25	96.4
977	PDZ	PDZ domain (Also known as DHR or GLGF).	3.6e-21	83.7
978	Ribosomal_L1 7	Ribosomal protein L17	2.4e-20	81.0
979	LIM	LIM domain containing proteins	5.8e-42	152.8
980	Calsequestri n	Calsequestrin	1.7e-297	1001.7
982	HSP20	Hsp20/alpha crystallin family	1.2e-10	43.2
983	oxidored_q6	NADH ubiquinone oxidoreductase, 20 Kd sub	4.8e-63	222.9
988	TBC	TBC domain	2.2e-50	180.8
989	TBC	TBC domain	2.2e-50	180.8
993	tRNA_int_end	tRNA intron endonuclease	0.0017	-34.2
994	homeobox	Homeobox domain	4e-18	73.6
997	pyr_redox	Pyridine nucleotide-disulphide	0.012	11.6
1000		oxidoreducta	A 8- 153	421.2
1000	mito_carr	Mitochondrial carrier proteins Ras association (RalGDS/AF-6)	9.7e-123 1.2e-15	65.4
		domain		
1004	DUF81	Domain of unknown function DUF81	0.099	10.2
1005	actin	Actin	1.3e-174	574.3
1006	actin	Actin	3.1e-130	428.6
1007	cpn60_TCP1	TCP-1/cpn60 chaperonin family TPR Domain	3.7e-195 8.1e-44	661.8
1009	zf-C2H2			159.0 216.6
1011	zf-C2H2	Zinc finger, C2H2 type	3.6e-61 3.6e-61	216.6
1012	zf-C3HC4	Zinc finger, C2H2 type Zinc finger, C3HC4 type (RING	4.7e-15	53.1
		finger)		
1016	tRNA-synt_2c	tRNA synthetases class II (A)	2.3e-15	55.2 274.3
1018	PGAM	Rhogap domain	1.6e-78 3.8e-18	69.7
1022	HMG box	Phosphoglycerate mutase family	3.8e-18 8.4e-20	79.2
		HMG (high mobility group) box TBC domain	7.3e-45	
1027	TBC UQ_con	Ubiquitin-conjugating enzyme		162.5
1032	PDZ	PDZ domain (Also known as DHR	1.4e-49 0.028	178.1
1034	Hydrolase	or GLGF). haloacid dehalogenasc-like hydrolase	2e-21	84.6
1037	KRAB	KRAB box	4.8e-06	32.4
1038	Cation_efflu x	Cation efflux family	7.1e-42	152.5
1040	ART	NAD:arginine ADF- ribosyltransferase	4.7e-47	169.1
1042	WD40	WD domain, G-beta repeat	1.9e-18	74.7
1042	zf-C2H2	Zinc finger, C2H2 type	3.7e-24	93.7
1045	lectin c	Lectin C-type domain	1.9e-28	108.0
1045	Glucosamine	Glucosamine-6-phosphate	0.00013	-25.1
	, ~~~~~~~m±116		4.46673	1 ~~

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
1047	ligase-CoA	CoA-ligases	4.5e-80	279.4
1047		Immunoglobulin domain	1.7e-09	35.6
1050	ig Ribosomal L2	Ribosomal protein L24e	2e-33	124.5
1020	4e	RIDOSOMAI DIOCEIN 124e		
1054	Amidase	Amidase	4.3e-152	518.7
1055	rrm	RNA recognition motif.	3.8e-26	100.3
1058	annexin	Annexin	6.9e-44	159.2
1059	PMP22_Claudi	PMP-22/EMP/MP20/Claudin family	0.023	-23.6
1060	homeobox	Homeobox domain	3.2e-31	117.2
1062	Acyltransfer	Acyltransferase	0.00065	10.5
1064	AMP-binding	AMP-binding enzyme	6.6e-100	345.3
1065	LRR	Leucine Rich Repeat	3.3e-14	60.6
1066	GTP1_OBG	GTP1/OBG family	4.8e-41	141.8
		Immunoglobulin domain	8.4e-48	159.1
1071	ig		6.8e-07	36.3
1072	PHD	PHD-finger		121.5
1074	DENN	DENN (AEX-3) domain	8.3e-33	
1075	SCP	SCP-like extracellular protein	4.7e-41	149.8
1077 .	OLF	Olfactomedin-like domain	2.2e-66	234.0
1078	mito_carr	Mitochondrial carrier proteins	1e-42	149.3
1079	WD40	WD domain, G-beta repeat	6.2e-45	162.7
1087	START	START domain	1.5e-48	174.7
1093	DSPc	Dual specificity phosphatase, catalytic doma	3.3e-63	223.4
1094	GSHPx	Glutathione peroxidases	9.6e-41	148.8
1095	DUF25	Domain of unknown function DUF25	2e-75	264.0
1096	DUF25	Domain of unknown function DUF25	6e-75	262.4
1105	Nitroreducta se	Nitroreductase family	1.3e-13	58.6
1106	PTE	Phosphotriesterase family	1.3e-179	610.1
1107	DAGKC	Diacylglycerol kinase catalytic domain	0.00049	19.6
1109	ras	Ras family	1.3e-15	40.7
1115	ArfGap	Putative GTP-ase activating protein for Arf	9.7e-47	168.7
1116	HMG14 17	HMG14 and HMG17	4.4e-21	83.5
1117	HMG14 17	HMG14 and HMG17	9.9e-12	52.4
1119	FAA_hydrolas	Fumarylacetoacetate (FAA) hydrolase fam	2e-83	290.6
1120	pkinase	Eukaryotic protein kinase domain	1.4e-94	327.6
1123	abhydrolase	alpha/beta hydrolase fold	9.2e-23	89.0
1129	pro_isomeras	Cyclophilin type peptidyl- prolyl cis-tr	2.2e-56	197.1
1131	DnaJ	DnaJ domain	1.6e-30	114.9
1132	WD40	WD domain, G-beta repeat	1.3e-19	78.6
1133	WD40	WD domain, G-beta repeat	1.8e-15	64.9
1134	PH	PH domain	0.0015	17.8
1136	Adap_comp_su	Adaptor complexes medium subunit family	1.2e-256	866.0
1137	Adap_comp_su	Adaptor complexes medium subunit family	2.5e-209	708.8
1139	ras	Ras family	1.5e-86	301.0
1141	pkinase	Eukaryotic protein kinase domain	9.4e-74	258.4
1152	Acyltransfer ase	Acyltransferase	1.2e-05	29.9
1157	IRS	PTB domain (IRS-1.type)	5.4e-55	196.1
1153		Immunoglobulin domain	1.3e-31	106.9
1155 1157	Asparaginase	Asparaginase	6.4e-72	252.3
1159 1160	GMC_oxred	GMC oxidoreductases	4.7e-142	485.3
		AN1-like Zinc finger	0.00021	

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
1163	linker_histo	linker histone H1 and H5 family	3.8e-14	60.4
1164	DED	Death effector domain	3.9e-05	30.5
1165	IRS	PTB domain (IRS-1 type)	2.6e-43	157.3
1166	IRS	PTB domain (IRS-1 type)	2.6e-43	157.3
		SAM domain (Sterile alpha	0.04	10.5
1168	SAM	motif)		
1170	abhydrolase	alpha/beta hydrolase fold	0.098	-7.5
1174	SAP	SAP domain	3.9e-10	47.1
1177	PP2C	Protein phosphatase 2C	5.3e-31	112.5
1178	WD40	WD domain, G-beta repeat	4.7e-35	129.9
1180	Ets	Ets-domain	1.8e-09	33.3
1181	Collagen	Collagen triple helix repeat (20 copies)	0.00016	24.7
1182	TCL1 MTCP1	TCL1/MTCP1 family	9.5e-56	198.6
1184	RasGEF	RasGEF domain	1.7e-88	307.4
1185	mito carr	Mitochondrial carrier proteins	1.5e-62	217.3
1187	UPAR LY6	u-PAR/Ly-6 domain	0.0042	15.6
1188	Orn DAP Arg	Pyridoxal-dependent	6.2e-128	430.6
	deC	decarboxylase		1
1193	Stathmin	Stathmin family	1.8e-90	314.0
1194	Stathmin	Stathmin family	1.8e-90	314.0
1195	Secl	Sec1 family	3.2e-183	622.1
1196	pyr_redox	Pyridine nucleotide-disulphide oxidoreducta	3.1e-32	111.B
1197	Glyco_transf	Glycosyl transferase family 8	1.2e-09	45.5
1202	K_tetra	K+ channel tetramerisation domain	0.022	-16.8
1203	adh short	short chain dehydrogenase	8.3e-45	162.3
1206	Ubie methylt	ubiE/COQ5 methyltransferase family	1.3e-121	417.4
1208	7tm 3	7 transmembrane receptor	7.2e-09	29.0
1208	ank	Ank repeat	3.9e-15	63.7
1210	vATP-	ATP synthase (C/AC39) subunit	2.5e-128	439.7
	synt_AC39			<del> </del>
1212	zf-C2H2	Zinc finger, C2H2 type	5.5e-17	69.9
1213	efhand	EF hand	3.2e-07	37.4
1219	rrm	RNA recognition motif.	2.1e-40	147.7
1220	DUF6	Integral membrane protein DUF6	0.015	21.5
1222	SCAN	SCAN domain	1.5e-71	251.1
1223	G-gamma	GGL domain	3.6e-36	129.5
1227	catalase	Catalase	0	1158.9
1232	PX	PX domain	2.2e-15	64.5
1233	PX	PX domain	2.2e-15	64.5
1236	FCH	Fes/CIP4 homology domain	3.3e-09	44.0
1241	Peptidase_M2	Peptidase family M20/M25/M40	2e-63	224.1
1243	WW	WW domain	0.044	17.9
1247	UPF0006	Metalloenzyme of unknown	6.3e-61	215.8
1248	Glycos_trans	function UPF0006 Glycosyl transferases	4.5e-10	46.9
	f_2		<del>                                     </del>	50.4
1249	efhand	EF hand	4e-11	
1254	UQ_con_	Ubiquitin-conjugating enzyme	2.1e-73	257.3
1255	ras	Ras family	2.2e-62	220.7
1256	formyl_trans	Formyl transferase	4.9e-30	108.3
1259	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	5.3e-13	46.4
1261	Dikfolate_re	Dihydrofolate reductase	2.1e-69	241.7
1262	G_glu_transp ept	Gamma-glutamyltranspeptidase	1.8e-110	380.4
1263	PAS	PAS domain	1.3e-08	36.9
1265	LRR	Leucine Rich Repeat	4.2e-22	86.9

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
1266	SCP	SCP-like extracellular protein	6e-29	108.0
1267	K_tetra	K+ channel tetramerisation	2.8e-27	104.0
		domain	1.3e-85	297.9
1269	ras	Ras family		37.0
1275	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	4.2e-10	
1276	abhydrolase	alpha/beta hydrolase fold	5.4e-23	89.8
1277	abhydrolase	alpha/beta hydrolase fold	5.6e-21	83.1
1279	trypsin	Trypsin	4.4e-41	132.0
1280	PBP	Phosphatidylethanolamine- binding protein	1.3e-13	58.7
1285	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	5.6e-14	49.6
1287	ank	Ank repeat	1.7e-52	187.8
1294	fn3	Fibronectin type III domain	0.026	20.9
1295	GBP	Guanylate-binding protein	0.00026	-70.0
1296	PMP22_Claudi	PMP-22/EMP/MP20/Claudin family	6.9e-41	149.3
1297	n Rhodanese	Rhodanese-like domain	3.2e-14	60.7
1297	LIM	LIM domain containing proteins	5.8e-21	79.1
1301	rnaseA	Pancreatic ribonucleases	4.9e-43	145.2
1301		Mitochondrial carrier proteins	2.1e-53	186.0
	mito_carr	WD domain, G-beta repeat	1.6e-17	71.6
1308	WD40		7.1e-20	75.5
1310	UPAR_LY6	u-PAR/Ly-6 domain Thioredoxin	3.6e-05	21.6
1313	thiored		1.5e-67	237.9
1314	Aa_trans	Transmembrane amino acid transporter protein		
1316	trypsin	Trypsin	4.4e-41	132.0
1320	Ribosomal_L1 3	Ribosomal protein L13	3.9e-62	219.8
1327	Armadillo_se	Armadillo/beta-catenin-like repeats	0.0054	23.4
1328	KRAB	KRAB box	0.052	-5.6
1329	rrm	RNA recognition motif.	2.1e-40	147.7
1330	Bcl-2	Apoptosis regulator proteins, Bcl-2 family	0.014	-1.6
1331	PX	PX domain	2.1e-10	48.0
1333	KRAB	KRAB box	1.8e-36	134.6
1334	UPP_syntheta	Putative undecaprenyl diphosphate synt	2.3e-89	310.3
1335	UPP_syntheta	Putative undecaprenyl diphosphate synt	1.8e-59	211.0
1336	DSPC	Dual specificity phosphatase, catalytic doma	1.2e-31	118.6
1337	DSPc	Dual specificity phosphatase, catalytic doma	2.3e-12	54.5
1338	TPR	TPR Domain	0.00021	28.1
	metalthio	Metallothionein	0.013	20.3
1340	I MECATCHIO	Bacterial mutT protein	5.8e-09	36.5
12/1	POLIT PER			
1341	mutT	PEDM domain (Band 4 1 family)		122.5
1343	Band_41	FERM domain (Band 4.1 family)	1.3e-38	
1343 1344	Band_41 Kelch	PERM domain (Band 4.1 family) Kelch motif	1.3e-38 1.4e-44	161.5
1343 1344 1345	Band_41 Kelch Antifreeze	FERM domain (Band 4.1 family) Kelch motif Antifreeze protein	1.3e-38 1.4e-44 1.2e-10	161.5 48.8
1343 1344 1345 1347	Band 41 Kelch Antifreeze 3Beta_HSD	FERM domain (Band 4.1 family) Kelch motif Antifreeze protein 3-beta hydroxysteroid dehydrogenase/isomera	1.3e-38 1.4e-44 1.2e-10 0.086	161.5 48.8 -177.2
1343 1344 1345 1347	Band 41 Kelch Antifreeze 3Beta_HSD	PERM domain (Band 4.1 family) Kelch motif Antifreeze protein 3-beta hydroxysteroid dehydrogenase/isomera BTB/POZ domain	1.3e-38 1.4e-44 1.2e-10 0.086	161.5 48.8 -177.2
1343 1344 1345 1347	Band 41 Kelch Antifreeze 3Beta_HSD BTB DUF6	PERM domain (Band 4.1 family) Kelch motif Antifreeze protein 3-beta hydroxysteroid dehydrogenase/isomera BTB/POZ domain Integral membrane protein DUF6	1.3e-38 1.4e-44 1.2e-10 0.086 5.3e-28 0.033	161.5 48.8 -177.2 106.5 15.8
1343 1344 1345 1347	Band 41 Kelch Antifreeze 3Beta_HSD	FERM domain (Band 4.1 family) Kelch motif Antifreeze protein 3-beta hydroxysteroid dehydrogenase/isomera BTB/POZ domain Integral membrane protein DUF6 Myosin head (motor domain)	1.3e-38 1.4e-44 1.2e-10 0.086 5.3e-28 0.033	161.5 48.8 -177.2 106.5 15.8 1088.7
1343 1344 1345 1347 1346 1349	Band 41 Kelch Antifreeze 3Beta_HSD BTB DUF6	PERM domain (Band 4.1 family) Kelch motif Antifreeze protein 3-beta hydroxysteroid dehydrogenase/isomera BTB/POZ domain Integral membrane protein DUF6	1.3e-38 1.4e-44 1.2e-10 0.086 5.3e-28 0.033	161.5 48.8 -177.2 106.5 15.8 1088.7 686.6
1343 1344 1345 1347 1348 1349 1350	Band 41 Kelch Antifreeze 3Beta_HSD BTB DUF6 myosin_head	FERM domain (Band 4.1 family) Kelch motif Antifreeze protein 3-beta hydroxysteroid dehydrogenase/isomera BTB/FOZ domain Integral membrane protein DUF6 Myosin head (motor domain) Natural resistance-associated macrophage pro S-100/ICaBP type calcium	1.3e-38 1.4e-44 1.2e-10 0.086 5.3e-28 0.033	161.5 48.8 -177.2 106.5 15.8 1088.7
1343 1344 1345 1347 1348 1349 1350 1352	Band 41 Kelch Antifreeze 3Beta_HSD BTB DUF6 myosin_head Nramp S_100	PERM domain (Band 4.1 family) Kelch motif Antifreeze protein 3-beta hydroxysteroid dehydrogenase/isomera BTB/POZ domain Integral membrane protein DUF6 Myosin head (motor domain) Natural resistance-associated macrophage pro S-100/ICaBP type calcium binding domain	1.3e-38 1.4e-44 1.2e-10 0.086 5.3e-28 0.033 0 1.2e-202	161.5 48.8 -177.2 106.5 15.8 1088.7 686.6
1343 1344 1345 1347 1348 1349 1350 1352 1353	Band_41 Kelch Antifreeze 3Beta_HSD BTB DUF6 myosin_head Nramp S_100 DEAD	PERM domain (Band 4.1 family) Kelch motif Antifreeze protein 3-beta hydroxysteroid dehydrogenase/isomera BTB/POZ domain Integral membrane protein DUF6 Myosin head (motor domain) Natural resistance-associated macrophage pro S-100/ICaBP type calcium binding domain DEAD/DEAH box helicase	1.3e-38 1.4e-44 1.2e-10 0.086 5.3e-28 0.033 0 1.2e-202 5.3e-23	161.5 48.8 -177.2 106.5 15.8 1088.7 686.6
1343 1344 1345 1347 1348 1349 1350 1352 1353	Band_41 Kelch Antifreeze 3Beta_HSD BTB DUF6 myosin_head Nramp S_100 DEAD C2	PERM domain (Band 4.1 family) Kelch motif Antifreeze protein 3-beta hydroxysteroid dehydrogenase/isomera BTB/POZ domain Integral membrane protein DUF6 Myosin head (motor domain) Natural resistance-associated macrophage pro S-100/ICaBP type calcium binding domain DEAD/DEAH box helicase C2 domain	1.3e-38 1.4e-44 1.2e-10 0.086 5.3e-28 0.033 0 1.2e-202 5.3e-23 3.6e-65	161.5 48.8 -177.2 106.5 15.8 1088.7 686.6 89.9
1343 1344 1345 1347 1348 1349 1350 1352 1353	Band_41 Kelch Antifreeze 3Beta_HSD BTB DUF6 myosin_head Nramp S_100 DEAD	PERM domain (Band 4.1 family) Kelch motif Antifreeze protein 3-beta hydroxysteroid dehydrogenase/isomera BTB/POZ domain Integral membrane protein DUF6 Myosin head (motor domain) Natural resistance-associated macrophage pro S-100/ICaBP type calcium binding domain DEAD/DEAH box helicase	1.3e-38 1.4e-44 1.2e-10 0.086 5.3e-28 0.033 0 1.2e-202 5.3e-23 3.6e-65 2.4e-15	161.5 48.8 -177.2 106.5 15.8 1088.7 686.6 89.9

C050 75	1 5554 5545	L DEGOD F DETON	T	1 500004
SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
1362	sis	SIS domain	3.8e-30	113.6
1363	SIS	SIS domain	1.3e-28	108.5
1364	iq	Immunoglobulin domain	0.00026	19.0
1368	K tetra	K+ channel tetramerisation	1.1e-16	68.9
	_	domain		
1371	Collagen	Collagen triple helix repeat (20 copies)	2.2e-113	390.1
1372	DnaJ	DnaJ domain	6.6e-36	132.7
1376	KRAB	KRAB box	2.1e-38	141.0
1378	ELM2	RLM2 domain	2e-23	91.3
1380	thiored	Thioredoxin	1.2e-23	82.8
1381	ank	Ank repeat	2.3e-83	290.4
1382	втв	BTB/POZ domain	3e-11	50.8
1383	WD40	WD domain, G-beta repeat	1.6e-19	78.3
1384	WD40	WD domain, G-beta repeat	6.3e-24	92.9
1387	zf-C3HC4	Zinc finger, C3HC4 type (RING	1.1e-09	35.6
		finger)		
1389	zf-C2H2	Zinc finger, C2H2 type	5.5e-50	179.5
1390	zf-C2H2	Zinc finger, C2H2 type	2.5e-85	296.9
1393	kinesin	Kinesin motor domain	7.8e-188	637.4
1394	zf-C2H2	Zinc finger, C2H2 type	1.2e-49	178.4
1398	KRAB	KRAB box	5.1e-22	86.6
1402	bZIP	bZIP transcription factor	0.035	13.1
1405	sugar tr	Sugar (and other) transporter	0.003	-101.5
1406	RhoGAP	RhoGAP domain	8.9e-47	168.8
1407	rrm	RNA recognition motif.	1e-35	132.1
1408	LRR	Leucine Rich Repeat	2.1e-13	58.0
1409	Nebulin_repe	Nebulin repeat	6e-54	192.6
3 4 3 0	at			
1410	ank	Ank repeat	1.6e-17	71.6
1412	Ribosomal_L5	ribosomal L5P family C-terminus	8.2e-58	205.5
1415	trypsin	Trypsin	4.7e-85	.270.4
1416	aminotran_1	Aminotransferases class-I	4.4e-05	-91.2
1417	S1	S1 RNA binding domain	1.6e-07	33.1
1419	WD40	WD domain, G-beta repeat	2.2e-09	44.6
1422	cadherin	Cadherin domain	8.3e-42	152.3
1424	SH3	SH3 domain	2.5e-80	280.3
1425	PHD	PHD-finger	3.2e-17	70.6
1426	PHD	PHD-finger	3.2e-17	70.6
1427	ArfGap	Putative GTP-ase activating protein for Arf	1e-37	138.8
1428	helicase_C	Helicases conserved C-terminal	1e-26	102.2
1429		1	L	1
1429			2 00 07	777
1430	WD40	WD domain, G-beta repeat	3.9e-07	37.2
	inositol P	Inositol monophosphatase family	2.5e-10	40.2
	inositol_P mito_carr	Inositol monophosphatase family Mitochondrial carrier proteins	2.5e-10 4.3e-83	40.2
1433	inositol_P mito_carr Clq	Inositol monophosphatase family Mitochondrial carrier proteins Ciq domain	2.5e-10 4.3e-83 2.9e-16	40.2 287.7 66.2
1433	inositol_P mito_carr Clq WD40	Inositol monophosphatase family Mitochondrial carrier proteins Ciq domain WD domain, G-beta repeat	2.5e-10 4.3e-83 2.9e-16 1.6e-13	40.2 287.7 66.2 58.3
1433	inositol_P mito_carr Clq	Inositol monophosphatase family Mitochondrial carrier proteins Ciq domain	2.5e-10 4.3e-83 2.9e-16	40.2 287.7 66.2
1433	inositol_p mito_carr Clq WD40 Inos-1-	Inositol monophosphatase family Mitochondrial carrier proteins Ciq domain WD domain, G-beta repeat Myo-inositol-1-phosphate	2.5e-10 4.3e-83 2.9e-16 1.6e-13	40.2 287.7 66.2 58.3
1433 1434 1435	inositol_P mito_carr Clq WD40 Inos-1- P_synth	Inositol monophosphatase family Mitochondrial carrier proteins Ciq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif.	2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228	40.2 287.7 66.2 58.3 770.4
1433 1434 1435	inositol_P mito_carr Clq WD40 Inos-1- P_synth rrm ig	Inositol monophosphatase family Mitochondrial carrier proteins Ciq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain	2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12	40.2 287.7 66.2 58.3 770.4
1433 1434 1435 1436 1438 1440	inositol_P mito_carr Clq WD40 Inos-1- P_synth rrm ig G_Adapt_CT	Inositol monophosphatase family Mitochondrial carrier proteins Ciq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus	2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12 3.4e-67	40.2 287.7 66.2 58.3 770.4 128.3 45.6 236.7
1433 1434 1435 1436 1438 1440 1441	inositol_P mito_carr Clq WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT	Inositol monophosphatase family Mitochondrial carrier proteins Clq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus	2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12 3.4e-67	40.2 287.7 66.2 58.3 770.4 128.3 45.6 236.7
1433 1434 1435 1436 1438 1440 1441 1443	inositol_P mito_carr Clq WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch	Inositol monophosphatase family Mitochondrial carrier proteins Ciq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif	2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12 3.4e-67 0.00013	40.2 287.7 66.2 58.3 770.4 128.3 45.6 236.7 236.7
1434 1435 1436 1438 1440 1441 1443	inositol_P mito_carr Clq WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch ARID	Inositol monophosphatase family Mitochondrial carrier proteins Ciq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif ARID DNA binding domain	2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12 3.4e-67 0.00013 1.8e-21	40.2 287.7 66.2 58.3 770.4 128.3 45.6 236.7 236.7 28.7 84.7
1434 1434 1435 1436 1438 1440 1441 1443 1446 1447	inositol_P mito_carr Clq WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch ARID zf-C2H2	Inositol monophosphatase family Mitochondrial carrier proteins Ciq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif ARID DNA binding domain Zinc finger, CZH2 type	2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12 3.4e-67 3.4e-67 0.00013 1.8e-21 9.4e-28	40.2 287.7 66.2 58.3 770.4 128.3 45.6 236.7 236.7 28.7 84.7 105.6
1433 1434 1435 1436 1438 1440 1441 1443 1446 1447	inositol_P mito_carr Clq WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch ARID zf-C2H2 AMP-binding	Inositol monophosphatase family Mitochondrial carrier proteins Ciq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif ARID DNA binding domain Zinc finger, CZHZ type AMP-binding enzyme	2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12 3.4e-67 3.4e-67 0.00013 1.8e-21 9.4e-28 2.6e-07	40.2 287.7 66.2 58.3 770.4 128.3 45.6 236.7 236.7 28.7 84.7 105.6 -145.1
1433 1434 1435 1436 1438 1440 1441 1443 1446 1447 1448	inositol_P mito_carr Clq WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch ARID zf-C2H2 AMP-binding rrm	Inositol monophosphatase family Mitochondrial carrier proteins Ciq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif ARID DNA binding domain Zinc finger, CZHZ type AMP-binding enzyme RNA recognition motif.	2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12 3.4e-67 0.00013 1.8e-21 9.4e-28 2.6e-07 6.5e-21	40.2 287.7 66.2 58.3 770.4 128.3 45.6 236.7 236.7 28.7 84.7 105.6 -145.1 82.9
1433 1434 1435 1436 1438 1440 1441 1443 1446 1447 1448 1451 1454	inositol_P mito_carr Clq WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch ARID zf-C2H2 AMP-binding rrm ig	Inositol monophosphatase family Mitochondrial carrier proteins Ciq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif ARID DNA binding domain Zinc finger, CZH2 type AMP-binding enzyme RNA recognition motif. Immunoglobulin domain	2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12 3.4e-67 0.00013 1.8e-21 9.4e-28 2.6e-07 6.5e-21 5.6e-44	40.2 287.7 66.2 58.3 770.4 128.3 45.6 236.7 236.7 28.7 84.7 105.6 -145.1 82.9 146.7
1433 1434 1435 1436 1438 1440 1441 1443 1446 1447 1448 1448 1451 1454	inositol_P mito_carr Clq WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch ARID zf-C2H2 AMP-binding rrm ig Sialyltransf	Inositol monophosphatase family Mitochondrial carrier proteins Ciq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif ARID DNA binding domain Zinc finger, CZH2 type AMP-binding enzyme RNA recognition motif. Immunoglobulin domain Sialyltransferase family	2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12 3.4e-67 0.00013 1.8e-21 9.4e-28 2.6e-07 6.5e-21 5.6e-44 5.4e-21	40.2 287.7 66.2 58.3 770.4 128.3 45.6 236.7 236.7 28.7 84.7 105.6 -145.1 82.9 146.7 83.2
1433 1434 1435 1436 1438 1440 1441 1443 1446 1447 1448 1451 1454 1455	inositol_P mito_carr Clq WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch ARID zf-C2H2 AMP-binding rrm ig Sialyltransf Aldose_epim	Inositol monophosphatase family Mitochondrial carrier proteins Ciq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif ARID DNA binding domain Zinc finger, CZH2 type AMP-binding enzyme RNA recognition motif. Immunoglobulin domain Sialyltransferase family Aldose 1-epimerase	2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12 3.4e-67 0.00013 1.8e-21 9.4e-28 2.6e-07 6.5e-21 5.6e-44 5.4e-21 1.9e-35	40.2 287.7 66.2 58.3 770.4 128.3 45.6 236.7 236.7 28.7 84.7 105.6 -145.1 82.9 146.7 83.2 131.2
1433 1434 1435 1436 1438 1440 1440 1441 1443 1446 1447 1448 1451 1454 1455 1460	inositol_P mito_carr Clq WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch ARID zf-C2H2 AMP-binding rrm ig Sialyltransf Aldose_epim C2	Inositol monophosphatase family Mitochondrial carrier proteins Ciq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif ARID DNA binding domain Zinc finger, CZHZ type AMP-binding enzyme RNA recognition motif. Immunoglobulin domain Sialyltransferase family Aldose 1-epimerase C2 domain	2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12 3.4e-67 0.00013 1.8e-21 9.4e-28 2.6e-07 6.5e-21 5.6e-44 5.4e-21 1.9e-35 4e-18	40.2 287.7 66.2 58.3 770.4 128.3 45.6 236.7 236.7 28.7 84.7 105.6 -145.1 82.9 146.7 83.2 131.2 73.6
1433 1434 1435 1436 1438 1440 1441 1443 1446 1447 1448 1451 1454 1455	inositol_P mito_carr Clq WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch ARID zf-C2H2 AMP-binding rrm ig Sialyltransf Aldose_epim	Inositol monophosphatase family Mitochondrial carrier proteins Ciq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif ARID DNA binding domain Zinc finger, CZH2 type AMP-binding enzyme RNA recognition motif. Immunoglobulin domain Sialyltransferase family Aldose 1-epimerase	2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12 3.4e-67 0.00013 1.8e-21 9.4e-28 2.6e-07 6.5e-21 5.6e-44 5.4e-21 1.9e-35	40.2 287.7 66.2 58.3 770.4 128.3 45.6 236.7 236.7 28.7 84.7 105.6 -145.1 82.9 146.7 83.2 131.2

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
	h 2			-
1474	DENN	DENN (AEX-3) domain	1.3e-44	161.6
1475	Cation efflu	Cation efflux family	4.6e-49	176.4
	x	2		
1477	TBC	TBC domain	8e-47	169.0
1478	rrm	RNA recognition motif.	2e-21	84.6
1480	ig	Immunoglobulin domain	5.5e-06	24.3
1484	Telo bind al	Telomere-binding protein alpha	0.028	-225.9
	pha	subuni		
1485	zf-C2H2	Zinc finger, C2H2 type	1.8e-68	240.9
1486	pkinase	Eukaryotic protein kinase	9.5e-13	49.9
1488	helicase_C	domain Helicases conserved C-terminal domain	1.4e-15	65.2
1489	DUF89	Protein of unknown function DUF89	0.079	-132.4
1490	ECH	Enoyl-CoA hydratase/isomerase family	5.2e-41	149.7
1491	guanylate_cy	Adenylate and Guanylate cyclase catalyt	5.9e-46	166.1
1492	LRR	Leucine Rich Repeat	3.4e-19	77.2
1495	zf-C3HC4	Zinc finger, C3HC4 type (RING	7.1e-10	36.3
1497	pkinase	finger)  Bukaryotic protein kinase domain	le-22	85.8
1500	SH3	SH3 domain	9.3e-05	27.2
1500	homeobox	Homeobox domain	0.084	13.8
1502	homeobox	.)	0.084	13.8
		Homeobox domain		90.8
1505	EGF	EGF-like domain	2.7e-23	
1506	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	2.7e-21	84.2
1508	Peptidase_M2 0	Peptidase family M20/M25/M40	2.8e-28	101.8
1511	PX	PX domain	1.9e-11	51.5
1512	Sulfatase	Sulfatase	2.8e-35	130.7
1516	Syntaxin	Syntaxin	0.011	-62.3
1518	aminotran_3	Aminotransferases class-III pyridoxal-pho	9.7e-106	305.6
1520	ig	Immunoglobulin domain	0.075	11.0
1521	RA	Ras association (RalGDS/AF-6)	0.013	13.3
1523	RhoGAP	RhoGAP domain	2.5e-05	18.7
1528	WD40	WD domain, G-beta repeat	5.4e-24	93.1
1535	IMS	impB/mucB/samB family	7.8e-95	328.5
1538	FYVE	FYVE zinc finger	3.2e-27	101.5
1539	DAGKC	Diacylglycerol kinase catalytic domain	6e-07	36.5
1540	Ocular_alb	Ocular albinism type 1 protein	0	1184.7
1653 1654	SAP Amino_oxidas	SAP domain Flavin containing amine oxidase	6e-06 3.2e-43	33.2 157.0
1655	e Amino_oxidas	Flavin containing amine oxidase	3.2e-43	157.0
	е		L	
1656	RhoGEF	RhoGEF domain	1.4e-24	95.1
1657	MMR_HSR1	GTPase of unknown function	0.0011	-45.5
1659	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	2.5e-11	51.1
1660	actin	Actin	6.6e-21	69.9
1661	BAH	BAH domain	1.7e-82	287.5
1662	vwa	von Willebrand factor type A domain	0	1909.4
1663	WD40	WD domain, G-beta repeat	1.4e-67	237.9
1667	zf-C2H2	Zinc finger, C2H2 type	1.3e-93	324.4
1669	Nol1_Nop2_Su	NOL1/NOP2/sun family	1.3e-23	84.3
1591	n	<u> </u>		1
1671	SH2	Src homology domain 2	5.4e-15	46.9

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	FFAM SCORE
1672	chromo	'chromo' (CHRromatin Organization MOdifier)	2.1e-18	67.7
1674	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H	0.0025	17.6
1676	Glyco_hydro_	type Glycosyl hydrolase family 47	1.8e-187	636.2
1677	Glyco_hydro_	Glycosyl hydrolase family 47	4.5e-74	259.5
1680	47 WD40	WD domain, G-beta repeat	1.1e-27	105.5
1681	W240	WD domain, G-beta repeat	1.1e-27	105.5
1683	MMR HSR1	GTPase of unknown function	1.8e-78	274.1
1691	rrm	RNA recognition motif.	1.8e-37	137.9
1692	rrm	RNA recognition motif.	1.8e-37	137.9
1693	AAA	ATPases associated with various cellular act	1.3e-81	284.5
1697	Ferric_reduc	Ferric reductase like	8.4e-82	285.2
1698	Ferric_reduc	Ferric reductase like	3.5e-53	190.1
1699	zf-C2H2	Zinc finger, C2H2 type	4.4e-34	126.6
1700	arf	ADP-ribosylation factor family	9e-19	75.8
1702	GTP_EFTU	Elongation factor Tu family	0.014	11.4
1702	SCAN	SCAN domain	1.8e-54	194.4
1707	pkinase	Eukaryotic protein kinase domain	1.2e-88	307.9
1709	WD40	WD domain, G-beta repeat	0.0035	24.0
1710	LRR	Leucine Rich Repeat	1.2e-30	115.3
1711	WW	WW domain	7.6e-12	52.8
1712	ank	Ank repeat	4.2e-34	126.7
1713	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H	2.6e-09	38.3
1714	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H	2.6e-09	38.3
1715	ras	Ras family	4.4e-41	149.9
1718	HMG box	HMG (high mobility group) box	8.3e-21	82.6
1719	TBC	TBC domain	1.1e-45	165.2
1721	HLH	Helix-loop-helix DNA-binding domain	9.2e-10	45.9
1723	derm	Double-stranded RNA binding motif	2.9e-05	30.9
1724	RrnaAD	Ribosomal RNA adenine dimethylases	0.045	9.2
1725	CIDE-N	CIDE-N domain	5.9e-40	146.2
1726	HAT	HAT (Half-A-TPR) repeats	2.9e-44	160.5
1728	efhand	EF hand	5.1e-20	79.9
1733	Hist_deacety	Histone deacetylase family	1.7e-104	360.6
1735	LRR	Leucine Rich Repeat	4.6e-34	126.6
1739	PI-PLC-X	Phosphatidylinositol-specific phospholipase	0.0023	16.1
1743	ras	Ras family	3.7e-10	-21.3
1744	ras	Ras family	3.7e-10	-21.3
1745	RasGEF	RasGEF domain	3.2e-49	176.9
1746	adh_short	short chain dehydrogenase	7.1e-08	34.6
1751	zf-C2H2	Zinc finger, C2H2 type	9e-39	142.2
1754	fn3	Fibronectin type III domain	5.5e-101	348.9
1756	zf-C2H2	Zinc finger, C2H2 type	6.3e-93	322.1
1758	xxm	RNA recognition motif.	0.017	21.2
1760	Nop	Putative snoRNA binding domain	6.le-95	328.8
1761	Мор	Putative snoRNA binding domain	6.1e-95	328.8
1765	MMR_HSR1	GTPase of unknown function	6.4e-41	149.4
1769	CN_hydrolase	Carbon-nitrogen hydrolase	3e-06	-43.9
1775	ank	Ank repeat	4.1e-07	37.1
1779	Oxysterol_BP	Oxysterol-binding protein	4.7e-56	199.6
1783	RhoGEF	RhoGEF domain	1.6e-23	91.6
1784	RhoGEF	RhoGEF domain	1.6e-23	1 21.0

SEQ ID	PFAM NAME	DESCRIPTION .	p-value	PFAM SCORE
1785	rrm	RNA recognition motif.	6.4e-14	59.7

TRADOCS:1416227.1(%CRN01!.DOC)

TABLE 5

SEQ ID NO:	POSITION OF	MaxS (MAXIMUM	MeanS (MEAN
	SIGNAL IN AMINO	SCORE)	SCORE)
1	ACID SEQUENCE	0.991	0.955
2	1-31	0.995	0.944
3	1-33	0.949	0.736
4	1-19	0.970	0.951
5	1-26	0.971	0.863
6	1-26	0.971	0.863
7	1-26	0.971	0.863
8	1-26	0.971	0.863
9	1-46	0.982	0.901
10	1-21	0.991	0.955
12	1-23	0.989	0.803
13	1-18	0.932	0.625
14	1-18	0.938	0.876
15	1-25	0.941	0.811
16	1-17	0.972	0.939
17	1-27	0.964	0.777
18	1-16	0.914	0.657
19	1-19	0.953	0.840
20	1-20	0.935	0.701
21	1-22	0.974	0.850
22	1-33	0.961	0.895
23	1-19	0.991	0.959
24	1-31	0.995	0.944
25 26	1-22	0.976	0.935
27	1-24	0.953	0.739
28	1-21	0.906	0.688
29	1-31	0.986	0.841
30	1-28	0.980	0.893
31	1-19	0.993	0.976
32	1-22	0.998	0.909
35	1-33	0.949	0.736
36	1-33	0.949	0.736
46	1-19	0.970	0.951
67	1-25	0.968	0.848
71 72	1-18	0.949	0.919
75	1-29	0.958	0.854
88	1-20	0.986	0.945
94	1-33	0.994	0.943
97	1-46	0.964	0.595
103	1-49	0.983	0.570
108	1-26	0.978	0.885
111	1-23	0.989	0.899
126	1-25	0.955	0.803
129	1-19	0.963	0.918
138	1-29	0.971	0.844
143	1-18	0.914	0.628
156	1-25	0.941	0.811
158	1-22	0.979	0.927
160	1-17	0.972	0.939
161	1-48	0.903	0.571
162	1-25	0.937	0.729
168	1-16	0.939	0.826
171	1-27	0.964	0.777
178	1-21	0.945	0.825
180	1-27	0.981	0.941
187	1-28	0.982	0.936
190	1-19	0.953	0.840
196	1-22	0.975	0.916
197	1-22	0.963	0.936

SEQ ID NO:	POSITION OF	MaxS (MAXIMUM	MeanS (MEAN
	SIGNAL IN AMINO	SCORE)	SCORE)
	ACID SEQUENCE		
199	1-20	0.935	0.701
200	1-23	0.977	0.773
206	1-30	0.984	0.890
207	1-19	0.990	0.850
208	1-22		0.670
210	1-40	0.940	0.849
211	1-28	0.971	0.956
216	1-24	0.986	0.895
218	1-33	0.970	0.871
219	1-19	0.904	0.553
221	1-21	0.917	0.555
	1-19	0.991	0.959
230	1-26	0.953	0.800
231	1-25	0.988	0.826
232	1-23	0.969	0.828
	1-17	0.982	0.955
240 241	1-17	0.982	0.955
245	1-30	0.970	0.722
248	1-22	0.976	0.935
249	1-23	0.968	0.940
252	1-18	0.971	0,923
261	1-24	0.883	0.587
265	1-18	0.939	0.868
272	1-24	0.953	0.739
283	. 1-21	0.906	0.688
284	1-29	0.997	0.854
290	1-31	0.986	0.841
302	1-28	0.980	0.893
304	1-16	0.907	0.635
312	1-19	0.993	0.976
313	1-17	0.930	0.753
323	1-22	0.998	0.909
324	1-17	0.982	0.954
328	1-19	0.971	0.865
329	1-22	0.963	0.924
330	1-33	0.978	0.841
331	1-24	0.920	0.712
332	1-24	0.975	0.881
333	1-19	0.984	0.941
334	1-20	0.899	0.567 .
335	1-27	0.942	0.813
336	1-20	0.952	0.850
337	1-38	0.942	0.772
338	1-27	0.973	
339	1-36	0.979	0.804
340	1-27	0.888	0.865
343	1-19	0.971	0.928
344	1-22	0.994	0.687
345	1-17	0.986	0.822
346	1-19	0.963	0.924
347	1-24	0.982	0.966
		0.918	0.815
351 352	1-21	0.988	0.912
354	1-31	0.974	0.839
355	1-31	0.932	0.632
356	<del>-  </del>	0.994	0.969
357	1-33	0.935	0.726
360	1-33	0.938	0.827
361	1-25	0.954	0.674
362	1-25	0.929	0.788
363	1-21	0.323	0.715
364	1-33	0.978	0.841
		,	

SEQ ID NO:	POSITION OF	MaxS (MAXIMUM	MeanS (MEAN
	SIGNAL IN AMINO	SCORE)	SCORE)
	ACID SEQUENCE		<u> </u>
366	1-21	0.916	0.820
367	1-19	0.936	0.822
368	1-29	0.972	0.874
370 371	1-24	0.920	0.712
372	1-24	0.919	0.768
373	1-19	0.986	0.945
375	1-32	0.994	0.932
376	1-34	0.987	0.810
377	1-17	0.995	0.950
378	1-49	0.971	0.749
380	1-20	0.968	0.874
381	1-20	0.928	0.782
382	1-19	0.986	0.934
383	1-28	0.965	0.829
384	1-39	0.970	0.551
386	1-24	0.975	0.881
388	1-30	0.989	0.868
389	1-19	0.984	0.941
390	1-26	0.971	0.782
392	1-20	0.981	0.900
393	1-16	0.968	0.890
394	1-23	0.937	0.701
397	1-22	0.985	0.854
399	1-46	0.977	0.698
401	1-20	0.899	0.567
402	1-22	0.967	0.931
403	1-27	0.992	0.934
404	1-19	0.991	0.973
405	1-23	0.994	0.921
407	1-35	0.987	0.658
408	1-39	0.976	0.551
409	1-33	0.897	0.570
410	1-25	0.990	0.827
411	1-20	0.944	0.768
413	1-20	0.988	0.965
414	1-46	0.993	0.638
415	1-23	0.981	0.940
417	1-29	0.941	0.672
418	1-20	0.952	0.850
419	1-19	0.986	0.967
420	1-29	0.965	0.861
421	1-22	0.889	0.785
422	1-48	0.982	0.862
424	1-19	0.979	0.933
428	1-38	0.942	0.653
430	1-18	0.947	0.595
432	1-33	0.957	0.789
433	1-26	0.979	0.904
434	1-27	0.962	0.777
435	1-24	0.998	0.977
436	1-27	0.973	0.772
443	1-15	0.966	0.940
448	1-36	0.979	0.804
453	1-41	0.958	0.609
455	1-33	0.943	0.606
457	1-27	0.888	0.597
462	1-16	0.925	0.681
486	1-27	0.972	0.845
495	1-24	0.917	0.636
498	1-26	0.993	0.890
505	1-20	0.976	0.926
507 510	1-17	0.966	0.687
710	1-23	0.930	0.593

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
511	1-23	0.930	0.593
512	1-23	0.930	0.593
515	1-18	0.978	0.956
523	1-19	0.936	0.822
529	1-22	0.963	0.924
<u> </u>		l	0.966
545	1-24	0.982	
550	1-30	0.933	0.713
552	1-21	0.973	0.912
554	1-23	0.969	0.784
571	1-21	0.918	0.815
574	1-31	0.988	0.912
580	1-39	0.925	0.556
			0.839
594	1-31	0.974	
608	1-29	0.932	0.632
609	1-29	0.932	0.632
610	1-21	0.990	0.948
621	1-15	0.994	0.969
623	1-33	0.935	0.726
653	1-27	0.938	0.827
	1	1	0.788
668	1-22	0.929	
677 .	1-16	0.948	0.807
685	1-21	0.881	0.715
699	1-22	0.975	0.816
702	1-31	0.968	0.898
707	1-16	0.860	0.562
713	1-25	0.966	0.743
718	1-19	0.936	0.822
L			0.824
719	1-20	0.961	
729	1-29	0.972	0.874
735	1-46	0.903	0.598
746	1-14	0.916	0.730
747	1-22	0.965	0.876
748	1-29	0.968	0.785
759	1-24	0.961	0.773
767	1-27	0.919	0.768
768	1-33	0.900	0.585
		l	0.702
773	1-42	0.959	
779	1-19	0.986	0.945
797	1-19	0.944	0.759
798	1-19	0.900	0.568
820	1-17	0.995	0.950
827	1-49	0.971	0.749
848	1-20	0.968	0.874
L	1-20	0.928	0.782
864		1	
866	1-19	0.986	0.934
873	1-23	0.948	0.886
881	1-28	0.965	0.829
887	1-39	0.970	0.551
927	1-30	0.989	0.868
934	1-48	0.988	0.777
939	1-39	0.994	0.889
944	1-26	0.971	0.782
950	1-29	0.957	0.845
963	1-20	0.981	0.900
964	1-20	0.886	0.558
973	1-16	0.968	0.890
980	1-34	0.961	0.749
	<u> </u>		0.822
981	1-20	0.953	
984	1-12	0.938	0.780
1015	1-22	0.985	0.854
1040	1-46	0.977	0.698
1052	1-18	0.969	0.842
1059	1-20	0.927	0.867
1065	1-33	0.983	0.918
1069	1-22	0.993	0.935
		1 4.333	1

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
1075	1-27	0.992	0.934
1080	1-19	0.931	0.829
1092	1-19	0.991	0.973
1094	1-46	0.992	0.653
1095	1-30	0.974	0.929
1105	1-23	0.994	0.921
1123	1-35	0.987	0.658
1138	1-32	0.954	0.613
1140	1-38	0.989	0.789
1142	1-33	0.897	0.570
1152	1-25	0.990	0.962
1170	1-38	0.977	0.827
1176	1-20	0.944	0.768
1187	1-20	0.988	0.965
1189	1-35	0.967	0.839
1192	1-46	0.993	0.638
	<del></del>	L	
1193	1-16	0.925	0.710
1197	1-29	0.985	0.853
1208	1-23	0.981	0.940
1225	1-29	0.941	0.672
1245	1-19	0.986	0.967
1258	1-29	0.965	0.861
1265	1-22	0.889	0.785
1266	1-20	0.944	0.809
1276	1-48	0.982	0.862
1292	1-19	0.979	0.933
1296	1-21	0.984	0.944
1297	1-19	0.984	0.953
1332	1-38	0.942	0.653
1358	1-18	0.947	0.595
1371	1-33	0.957	0.789
1380	1-26	0.979	0.904
1397	1-27	0.962	0.777
1399	1-23	0.997	0.960
1404	1-24	0.998	0.977
1410	1-15	0.946	0.845
1414	1-24	0.913	0.588
1415	1-19	0.982	0.929
1416	1-12	0.931	0.891
1418	1-30	0.933	0.563
1420	1-20	0.881	0.561
1421	1-19	0.990	0.968
1423	1-17	0.968	0.863
1424	1-21	0.885	0.591
1425	1-24	0.913	0.588
1426	1-24	0.913	0.588
1428	1-25	0.957	0.899
1430	1-34	0.977	0.819
1432			
	1-36	0.957	0.613
1433	1-32	0.921	0.753
1434	1-39	0.983	0.621
1435	1-25	0.910	0.631
1436	1-42	0.988	0.868
1437	1-22	0.998	0.980
1442	1-20	0.918	0.753
1448	1-12	0.931	0.891
1462	1-18	0.968	0.888
1490	1-20	0.881	0.561
1518	1-17	0.968	0.863
1525	1-21	0.885	0.591
1547	1-28	0.974	0.891
1561	1-25	0.967	0.899
1580	1-17	0.923	0.824
1593	1-28	0.979	0.923

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	Maxs (MAXIMUM SCORE)	MeanS (MEAN SCORE)
1596	1-16	0.929	0.709
1601	1-36	0.957	0.613
1606	1-22	0.979	0.831
1607	1-20	0.974	0.770
1608	1-32	0.921	0.753
1614	1-33	0.969	0.829
1616	1-20	0.959	0.869
1625	1-39	0.983	0.621
1632	1-25	0.910	0.631
1636	1-33	0.897	0.591
1639	1-42	0.988	0.868
1645	1-20	0.927	0.568
1647	1-17	0.923	0.742
1648	1-22	0.998	0.980

TRADOCS:1416234.1(%CR%01!.DOC)

TABLE 6

TABLE 6					
SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
of full-	NO: of	of contig	NO:	docket number_	NO:in
length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide		segrence	priority	1
	sequence			application	
1	1787	3573	5359	784CIP2_1	1103
2	1788	3574	5360	784CIP2_2	2673
3	1789	357,5	5361	784CIP2_3	4117
4	1790	3576	5362	784CIP2_4	5556
5	1791	3577	5363	784CIP2_5	5562
6	1792	3578	5364	784CIP2_6	5562
7	1793	3579	5365	784CIP2_7	5562
8	1794	3580	5366	784CIP2_8	5562
9	1795	3581	5367	784CIP2_9	5563
10	1796	3582	5368	784CIP2_10	5564
11	1797	3583	5369	784CIP2_11	5565
1.2	1798	3584	5370	784CIP2_12	5689
13	1799	3585	5371	784CIP2_13	5729
14	1800	3586	5372	784CIP2_14	5745
15	1801	3587	5373	784CIP2_15	5777
16	1802	3588	5374	784CIP2_16	5777
17	1803	3589	5375	784CIP2_17	5789
18	1804	3590	5376	784CIP2_18	5792
19	1805	3591	5377	784CIP2_19	5804
20	1806	3592	5378	784CIP2 20	5805
21	1807	3593	5379	784CIP2 21	5805
22	1808	3594	5380	784CIP2 22	5844
23	1809	3595	5381	784CIP2 23	5844
24	1810	3596	5382	784CIP2 24	5850
25	1811	3597	5383	784CIP2 25	5867
26	1812	3598	5384	784CIP2 26	5973
27	1813	3599	5385	784CIP2 27	5995
28	1814	3600	5386	784CIP2 28	5995
29	1815	3601	5387	784CIP2 29	6005
30	1816	3602	5388	784CIP2 30	6007
31	1817	3603	5389	784CIP2 31	6007
32	1818	3604	5390	784CIP2 32	6009
33	1819	3605	5391	784CIP2_33	6012
34	1820	3606	5392	784CIP2_34	6015
35	1821	3607	5393	784CIP2_35	6016
36	1822	3608	5394	784CIP2_36	6016
37	1823	3609	5395	784CIP2_37	6018
38	1824	3610	5396	784CIP2_38	6018
39	1825	3611	5397	784CIP2_39	6018
40	1826	3612	5398	784CIP2_40	6023
41	1827	3613	5399	784CIP2_41	6070
42	1828	3614	5400	784CIP2_42	6081
43	1829	3615	5401	784CIP2_43	6089
44	1830	3616	5402	784CIP2_44	6118
45	1831	3617	5403	784CIP2_45	6118
46	1832	3618	5404	784CIP2_46	6130
47	1833	3619	5405	784CIP2_47	6177
48	1834	3620	5406	784CIP2_48	6189
49	1835	3621	5407	784CIP2_49	6191
50	1836	3622	5408	784CIP2_50	6204
51	1837	3623	5409	784CIP2 51 -	6204
52	1838	3624	5410	784CIP2 52	6284
53	1839	3625	5411	784CIP2 53	6367
54	1840	3626	5412	784CIP2 54	6436
55	1841	3627	5413	784CIP2 55	6442
56	1842	3628	5414	784CIP2 56	6445
57	1843	3629	5415	784CIP2 57	6457
58	1844	3630	5416	784CIP2 58	6458
59	1845	3631	5417	784CIP2 59	6458
	1	3034			

SEO ID NO:	SEQ ID	SEO ID NO:	SEQ ID	Priority	SEQ ID
of full-	NO: of	of contig	NO:	docket number	NO:in
length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide	1 -	sequence	priority	
L	sequence	L		application	
60	1846	3632	5418	784CIP2_60	6462
61	1847	3633	5419	784CIP2_61	6472
62	1848	3634	5420	784CIP2_62	6499
63	1849	3635	5421	784CIP2_63	6499
64	1850	3636	5422	784CIP2_64	6505
65	1851	3637	5423	784CIP2_65	6534
66	1852	3638	5424	784CIP2_66	6534
67	1853	3639	5425	784CIP2_67	6540
68	1854	3640	5426	784CIP2_68	6550
69	1855	3641	5427	784CIP2_69	6550
70	1856	3642	5428	784CIP2_70	6592
71	1857	3643	5429	784CIP2_71	6645
72	1858	3644	5430	784CIP2_72	6671
73	1859	3645	5431	784CIP2_73	6763
74	1860	3646	5432	784CIP2_74	6763
75	1861	3647	5433	784CIP2_75	6786
76	1862	3648	5434	784CIP2_76	6824
77	1863	3649	5435	784CIP2_77	6830
78	1864	3650	5436	784CIP2_78	6831
79	1865	3651	5437	784ClP2_79	6832
80	1866	3652	5438	784C1P2_80	6834
. 81	1867	3653	5439	784CIP2_81	6834
82	1868	3654	5440	784CIP2_82	6835
83	1859	3655	5441	784CIP2_83	6837
84	1870	3656	5442	784CIP2_84	6843
85	1871	3657	5443	784C1P2_85	6859
86	1872	3658	5444	784C1P2_86	6915
87	1873	3659	5445	784CIP2_87	6932
88	1874	3660	5446	784CIP2_88	6957
89	1875	3661	5417	784C1P2_89	6961
90	1876	3662	5448	784CIP2_90	6973
91	1877	3663	5449	784CIP2_91	6973
92	1878	3664	5450	784CIP2_93	7007
93	. 1879	3665	5451	784CIP2_94	7018
94	1880	3666	5452	784CIP2_95	7019
95	1881	3667	5453	784CIP2_96	7020
96	1882	3668	5454	784CIP2_97	7,020
97	1883	3669	5455	784CIP2_98	7021
98 99	1884	3670	5456	784CIP2_99 784CIP2_100	7023 7027
100	1885 1886	3671	5457		7027
100		3672	5458	784CIP2_101	7028
101 .	1887	3673	5459 5460	784CIP2_102	7029
102	1888 1889	3674	5460 5461	784CIP2_103 784CIP2_104	7031
103	1899	3675 3676	5462	784CIP2_104 784CIP2_105	7032
104	1890	3675	5462	784CIP2_105 784CIP2_106	7033
					7035
106	1892	3678	5464	784CIP2_107 784CIP2_108	7036
107 108	1893	3679	5465		7043
	1894	3680	5466	784CIP2_109	7043
109	1895	3681	5467	784CIP2_110	
110	1896	3682	5468	784CIP2_111	7046
111	1897	3683	5469	784CIP2_112	7054 7061
112	1898	3684	5470	784CIP2_113 784CIP2_114	7077
113	1899	3685	5471		7077
114	1900	3686	5472	784CIP2_115	
115	1901	3687	5473	784CIP2_116	7094
116	1902	3688	5474	784CIP2_117	7106
117	1903	3689	5475	784CIP2_118	7107
118	1904	3690	5476	784CIP2_119	7111
119	1905	3691	5477	784CIP2_120	7123
120	1906	3692	5478	784CIP2_121	7142
121	1907	3693	5479	784CIP2_122	7142

of full- length nucleotide sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence seq	SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
nucleotide sequence sequence sequence sequence peptide sequence peptide sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequenc	of full-			NO:		1 ~
sequence sequence         sequence sequence         sequence sequence         sequence sequence         sequence application           122         1968         3694         5680         784CIP2 123         7154           123         1909         3695         5681         784CIP2 125         7169           124         1910         3696         5482         784CIP2 125         7169           125         1911         3697         5483         784CIP2 127         7197           126         1912         3698         5484         784CIP2 127         7197           127         1913         3699         5485         796CIP2 128         7219           126         1914         3700         5486         784CIP2 139         7226           130         1916         3702         5488         784CIP2 131         7234           131         1917         3703         5489         784CIP2 133         7234           131         1918         3706         5492         784CIP2 131         7235           133         1918         3705         5491         784CIP2 131         7235           134         1920         3706         5492         784CIP2 137<	length	full-	nucleotide	of contig	corresponding	U.S.S.N.
Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   122   1908   3694   5480   794CIP2   123   7154   123   1909   3695   5481   794CIP2   125   7169   125   1911   3697   5482   784CIP2   125   7169   125   1911   3697   5483   784CIP2   126   7165   126   1912   3698   5484   784CIP2   126   7165   127   1913   3699   5485   764CIP2   128   7219   128   1914   3700   5486   744CIP2   128   7219   129   1915   3701   5487   784CIP2   130   7229   1316   3702   5488   784CIP2   130   7229   1316   3702   5488   784CIP2   130   7229   1311   1917   3703   5489   784CIP2   132   7235   133   1919   3705   5491   784CIP2   133   7235   133   1919   3705   5491   784CIP2   134   7239   134   1920   3706   5492   784CIP2   134   7239   135   1329   3707   5493   784CIP2   136   7247   7247   137   1323   3709   5495   784CIP2   137   7247   7247   137   1323   3709   5495   784CIP2   137   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7247   7	nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
122	sequence	peptide	ì	sequence	priority	i
123		sequence	ţ		application	
124			3694		·	
125	123	1909	3695	5481		
126		1910	3696	L		
127	125	1911	3697		1	
126						
129						L
130	128			L		1
131		1915	3701		<del> </del>	l
132	1	l				
133						L
134						
135	l			I	<b>—</b>	
136	1					
137	L			I		
138						
139	L					
140		_	1			
141		L				
142						
143						L
144						
14S						
146				1		L
147         1933         3719         5505         784CIP2_148         7312           148         1934         3720         5506         784CIP2_149         7313           149         1935         3721         5507         784CIP2_150         7315           150         1936         3722         5508         784CIP2_151         7318           151         1937         3723         5509         784CIP2_152         7321           152         1938         3724         5510         784CIP2_153         7330           153         1939         3725         5511         784CIP2_154         7331           154         1940         3726         5512         784CIP2_156         7350           155         1941         3727         5513         784CIP2_156         7350           156         1942         3728         5514         784CIP2_156         7350           156         1942         3728         5515         784CIP2_157         7352           157         1943         3729         5515         784CIP2_159         7403           159         1945         3731         5517         784CIP2_159         7403	l					
148         1934         3720         5506         784CIP2_149         7313           149         1935         3721         5507         784CIP2_150         7315           150         1936         3722         5508         784CIP2_151         7318           151         1937         3723         5509         784CIP2_152         7321           152         1938         3724         5510         784CIP2_153         7330           153         1939         3725         5511         784CIP2_154         7331           154         1940         3726         5512         784CIP2_156         7350           155         1941         3727         5513         784CIP2_156         7350           156         1942         3728         5514         784CIP2_157         7352           157         1943         3729         5515         784CIP2_157         7352           157         1944         3730         5516         784CIP2_159         7403           158         1944         3730         5516         784CIP2_159         7403           159         1945         3731         5517         784CIP2_160         7431				1		
149				L	·	I
150	L	<del></del>			<b>-</b>	
151	l	<u> </u>		<u>.                                    </u>		
152			L			l ·
153         1939         3725         5511         784CIP2_154         7331           154         1940         3726         5512         784CIP2_155         7333           155         1941         3727         5513         784CIP2_156         7350           156         1942         3728         5514         784CIP2_157         7352           157         1943         3729         5515         784CIP2_158         7384           158         1944         3730         5516         784CIP2_159         7403           159         1945         3731         5517         784CIP2_160         7431           160         1946         3732         5518         784CIP2_160         7431           161         1947         3733         5519         784CIP2_160         7431           161         1947         3733         5519         784CIP2_162         7453           162         1948         3734         5520         784CIP2_162         7453           163         1949         3735         5521         784CIP2_164         7471           164         1950         3736         5522         784CIP2_164         7471	1					L
154         1940         3726         5512         784CIP2_155         7333           155         1941         3727         5513         784CIP2_156         7350           156         1942         3728         5514         784CIP2_157         7352           157         1943         3729         5515         784CIP2_158         7384           158         1944         3730         5516         784CIP2_159         7403           159         1945         3731         5517         78aCIP2_160         7431           160         1946         3732         5518         784CIP2_161         7441           161         1947         3733         5519         784CIP2_161         7441           161         1947         3733         5519         784CIP2_162         7453           162         1948         3734         5520         784CIP2_163         7467           163         1949         3735         5521         784CIP2_165         7493           165         1951         3737         5523         784CIP2_165         7493           165         1952         3738         5524         784CIP2_167         7511	and the second second	I		l		
155         1941         3727         5513         784CIP2_156         7350           156         1942         3728         5514         784CIP2_157         7352           157         1943         3729         5515         784CIP2_158         7384           158         1944         3730         5516         784CIP2_169         7403           159         1945         3731         5517         784CIP2_160         7431           160         1946         3732         5518         784CIP2_161         7441           161         1947         3733         5519         784CIP2_163         7467           162         1948         3734         5520         784CIP2_163         7467           163         1949         3735         5521         784CIP2_164         7471           164         1950         3736         5522         784CIP2_165         7493           165         1951         3737         5523         784CIP2_165         7493           165         1952         3738         5524         784CIP2_167         7511           167         1953         3739         5525         784CIP2_168         7514						
156         1942         3728         5514         784CIP2_157         7352           157         1943         3729         5515         784CIP2_158         7384           158         1944         3730         5516         784CIP2_159         7403           159         1945         3731         5517         784CIP2_160         7431           160         1946         3732         5518         784CIP2_161         7441           161         1947         3733         5519         784CIP2_162         7453           162         1948         3734         5520         784CIP2_163         7467           163         1949         3735         5521         784CIP2_164         7471           164         1950         3736         5522         784CIP2_165         7493           165         1951         3737         5523         784CIP2_166         7502           166         1952         3738         5524         784CIP2_166         7502           166         1953         3739         5525         784CIP2_168         7514           167         1953         3739         5525         784CIP2_168         7514	<u> </u>					
157         1943         3729         5515         784CIF2_158         7384           158         1944         3730         5516         784CIP2_159         7403           159         1945         3731         5517         784CIP2_160         7431           160         1946         3732         5518         784CIP2_161         7441           161         1947         3733         5519         784CIP2_162         7453           162         1948         3734         5520         784CIP2_163         7467           163         1949         3735         5521         784CIP2_164         7471           164         1950         3736         5522         784CIP2_165         7493           165         1951         3737         5523         784CIP2_166         7502           166         1952         3738         5524         784CIP2_166         7502           166         1953         3737         5523         784CIP2_168         7514           167         1953         3740         5526         784CIP2_168         7514           168         1954         3740         5526         784CIP2_170         7541				1		
158         1944         3730         5516         784CIP2_159         7403           159         1945         3731         5517         784CIP2_160         7431           160         1946         3732         5518         784CIP2_161         7441           161         1947         3733         5519         784CIP2_162         7453           162         1948         3734         5520         784CIP2_163         7467           163         1949         3735         5521         784CIP2_164         7471           164         1950         3736         5522         784CIP2_165         7493           165         1951         3737         5523         784CIP2_165         7493           165         1951         3737         5523         784CIP2_166         7502           166         1952         3738         5524         784CIP2_167         7511           167         1953         3739         5525         784CIP2_168         7514           168         1954         3740         5526         784CIP2_170         7541           170         1956         3742         5528         784CIP2_171         7570						
159         1945         3731         5517         784CIP2_160         7431           160         1946         3732         5518         784CIP2_161         7441           161         1947         3733         5519         784CIP2_162         7453           162         1948         3734         5520         784CIP2_163         7467           163         1949         3735         5521         784CIP2_164         7471           164         1.950         3736         5522         784CIP2_165         7493           165         1.951         3737         5523         784CIP2_166         7502           166         1.952         3738         5524         784CIP2_166         7502           166         1.953         3739         5525         784CIP2_166         7514           167         1.953         3739         5525         784CIP2_168         7514           168         1.954         3740         5526         784CIP2_168         7514           169         1.955         3741         5527         784CIP2_170         7541           170         1.956         3742         5528         784CIP2_171         7570     <						
160         1946         3732         5518         784CIP2_161         7441           161         1947         3733         5519         784CIP2_162         7453           162         1948         3734         5520         784CIP2_163         7467           163         1949         3735         5521         784CIP2_164         7471           164         1.950         3736         5522         784CIP2_165         7493           165         1951         3737         5523         784CIP2_165         7493           165         1951         3737         5523         784CIP2_166         7502           166         1952         3738         5524         784CIP2_166         7502           166         1953         3739         5525         784CIP2_168         7514           167         1953         3740         5526         784CIP2_169         7520           169         1955         3741         5527         784CIP2_169         7520           169         1955         3741         5527         784CIP2_171         7570           171         1957         3743         5529         784CIP2_172         7578				L		
161         1947         3733         5519         784CIP2_162         7453           162         1948         3734         5520         784CIP2_163         7467           163         1949         3735         5521         784CIP2_164         7471           164         1950         3736         5522         784CIP2_165         7493           165         1951         3737         5523         784CIP2_166         7502           166         1952         3738         5524         784CIP2_167         7511           167         1953         3739         5525         784CIP2_168         7514           168         1954         3740         5526         784CIP2_169         7520           169         1955         3741         5527         784CIP2_170         7541           170         1956         3742         5528         784CIP2_170         7541           170         1958         3743         5529         784CIP2_172         7578           172         1958         3744         5530         784CIP2_173         7583           173         1959         3745         5531         784CIP2_173         7583					_ <del>-</del>	1
162         1948         3734         5520         784CIP2_163         7467           163         1949         3735         5521         784CIP2_164         7471           164         1950         3736         5522         784CIP2_165         7493           165         1951         3737         5523         784CIP2_166         7502           166         1952         3738         5524         784CIP2_167         7511           167         1953         3739         5525         784CIP2_167         7511           168         1954         3740         5526         784CIP2_169         7520           169         1955         3741         5527         784CIP2_170         7541           170         1956         3742         5528         784CIP2_170         7541           170         1956         3743         5529         784CIP2_172         7578           172         1958         3744         5530         784CIP2_173         7583           173         1959         3745         5531         784CIP2_173         7593           174         1960         3746         5532         784CIP2_176         7601					· · · · · · · · · · · · · · · · · · ·	
163         1949         3735         5521         784CIP2_164         7471           164         1950         3736         5522         784CIP2_165         7493           165         1951         3737         5523         784CIP2_166         7502           166         1952         3738         5524         784CIP2_167         7511           167         1953         3739         5525         784CIP2_168         7514           168         1954         3740         5526         784CIP2_169         7520           169         1955         3741         5527         784CIP2_170         7541           170         1956         3742         5528         784CIP2_171         7570           171         1957         3743         5529         784CIP2_172         7578           172         1958         3744         5530         784CIP2_173         7583           173         1959         3745         5531         784CIP2_173         7592           174         1960         3746         5532         784CIP2_174         7592           174         1960         3746         5532         784CIP2_175         7601						L
164         1.950         3736         5522         784CIP2_165         7493           165         1.951         3737         5523         784CIP2_166         7502           166         1.952         3738         5524         784CIP2_167         7511           167         1.953         3739         5525         784CIP2_168         7514           168         1.954         3740         5526         784CIP2_169         7520           169         1.955         3741         5527         784CIP2_170         7541           170         1.956         3742         5528         784CIP2_171         7570           171         1.957         3743         5529         784CIP2_172         7578           172         1.958         3744         5530         784CIP2_172         7578           172         1.958         3744         5530         784CIP2_173         7583           173         1.959         3745         5531         784CIP2_174         7592           174         1.960         3746         5532         784CIP2_174         7592           175         1.961         3747         5533         784CIP2_176         7602	163					I
166         1952         3738         5524         784CIP2_167         7511           167         1953         3739         5525         784CIP2_168         7514           168         1954         3740         5526         784CIP2_169         7520           169         1955         3741         5527         784CIP2_170         7541           170         1956         3742         5528         784CIP2_171         7570           171         1957         3743         5529         784CIP2_172         7578           172         1958         3744         5530         784CIP2_172         7578           173         1959         3745         5531         784CIP2_174         7592           174         1960         3746         5532         784CIP2_175         7601           175         1961         3747         5533         784CIP2_176         7602           176         1962         3748         5534         784CIP2_176         7608           177         1963         3749         5535         784CIP2_179         7617           179         1965         3751         5536         784CIP2_181         7624	164			5522		7493
167         1953         3739         5525         784CIP2_168         7514           168         1954         3740         5526         784CIP2_169         7520           169         1955         3741         5527         784CIP2_170         7541           170         1956         3742         5528         784CIP2_171         7570           171         1957         3743         5529         784CIP2_172         7578           172         1958         3744         5530         784CIP2_173         7583           173         1959         3745         5531         784CIP2_174         7592           174         1960         3746         5532         784CIP2_175         7601           175         1961         3747         5533         784CIP2_176         7602           176         1962         3748         5534         784CIP2_177         7608           177         1963         3749         5535         784CIP2_179         7617           179         1965         3751         5537         784CIP2_181         7624           180         1966         3752         5538         784CIP2_182         7626	165	1951	3737	5523	784CIP2_166	7502
168         1954         3740         5526         784CIP2_169         7520           169         1955         3741         5527         784CIP2_170         7541           170         1956         3742         5528         784CIP2_171         7570           171         1957         3743         5529         784CIP2_172         7578           172         1958         3744         5530         784CIP2_173         7583           173         1959         3745         5531         784CIP2_174         7592           174         1960         3746         5532         784CIP2_175         7601           175         1961         3747         5533         784CIP2_176         7602           176         1962         3748         5534         784CIP2_177         7608           177         1963         3749         5535         784CIP2_179         7615           178         1964         3750         5536         784CIP2_179         7617           179         1965         3751         5537         784CIP2_181         7624           180         1966         3752         5538         784CIP2_182         7626	166	1952	3738	5524	784CIP2_167	
169         1955         3741         5527         784CIP2_170         7541           170         1956         3742         5528         784CIP2_171         7570           171         1957         3743         5529         784CIP2_172         7578           172         1958         3744         5530         784CIP2_173         7583           173         1959         3745         5531         784CIP2_174         7592           174         1960         3746         5532         784CIP2_175         7601           175         1961         3747         5533         784CIP2_176         7602           176         1962         3748         5534         784CIP2_177         7608           177         1963         3749         5535         784CIP2_177         7608           178         1964         3750         5536         784CIP2_179         7617           179         1965         3751         5537         784CIP2_181         7624           180         1966         3752         5538         784CIP2_182         7626           181         1967         3753         5539         784CIP2_184         7640	167	1953	3739	5525	784CIP2_168	7514
170         1956         3742         5528         784CIP2_171         7570           171         1957         3743         5529         784CIP2_172         7578           172         1958         3744         5530         784CIP2_173         7583           173         1959         3745         5531         784CIP2_174         7592           174         1960         3746         5532         784CIP2_175         7601           175         1961         3747         5533         784CIP2_176         7602           176         1962         3748         5534         784CIP2_177         7608           177         1963         3749         5535         784CIP2_178         7615           178         1964         3750         5536         784CIP2_179         7617           179         1965         3751         5537         784CIP2_181         7624           180         1966         3752         5538         784CIP2_182         7626           181         1967         3753         5539         784CIP2_184         7640           182         1968         3754         5540         784CIP2_184         7641 <td>168</td> <td>1954</td> <td>3740</td> <td>5526</td> <td>784CIP2_169</td> <td>7520</td>	168	1954	3740	5526	784CIP2_169	7520
171     1957     3743     5529     784CIP2_172     7578       172     1958     3744     5530     784CIP2_173     7583       173     1959     3745     5531     784CIP2_174     7592       174     1960     3746     5532     784CIP2_175     7601       175     1961     3747     5533     784CIP2_176     7602       176     1962     3748     5534     784CIP2_177     7608       177     1963     3749     5535     784CIP2_178     7615       178     1964     3750     5536     784CIP2_179     7617       179     1965     3751     5537     784CIP2_181     7624       180     1966     3752     5538     784CIP2_182     7626       181     1967     3753     5539     784CIP2_183     7640       182     1968     3754     5540     784CIP2_184     7641	169	1955	3741	5527	784CIP2_170	7541
172     1958     3744     5530     784CIP2_173     7583       173     1959     3745     5531     784CIP2_174     7592       174     1960     3746     5532     784CIP2_175     7601       175     1961     3747     5533     784CIP2_176     7602       176     1962     3748     5534     784CIP2_177     7608       177     1963     3749     5535     784CIP2_178     7615       178     1964     3750     5536     784CIP2_179     7617       179     1965     3751     5537     784CIP2_181     7624       180     1966     3752     5538     784CIP2_182     7626       181     1967     3753     5539     784CIP2_183     7640       182     1968     3754     5540     784CIP2_184     7641			3742	5528	784CIP2_171	
173     1959     3745     5531     784CIP2_174     7592       174     1960     3746     5532     784CIP2_175     7601       175     1961     3747     5533     784CIP2_176     7602       176     1962     3748     5534     784CIP2_177     7608       177     1963     3749     5535     784CIP2_178     7615       178     1964     3750     5536     784CIP2_179     7617       179     1965     3751     5537     784CIP2_181     7624       180     1966     3752     5538     784CIP2_182     7626       181     1967     3753     5539     784CIP2_183     7640       182     1968     3754     5540     784CIP2_184     7641			3743	5529		
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175     1961     3747     5533     784CIP2_176     7602       176     1962     3748     5534     784CIP2_177     7608       177     1963     3749     5535     784CIP2_178     7615       178     1964     3750     5536     784CIP2_179     7617       179     1965     3751     5537     784CIP2_181     7624       180     1966     3752     5538     784CIP2_182     7626       181     1967     3753     5539     784CIP2_183     7640       182     1968     3754     5540     784CIP2_184     7641			3745	5531		
176     1962     3748     5534     784CIP2_177     7608       177     1963     3749     5535     784CIP2_178     7615       178     1964     3750     5536     784CIP2_179     7617       179     1965     3751     5537     784CIP2_181     7624       180     1966     3752     5538     784CIP2_182     7626       181     1967     3753     5539     784CIP2_183     7640       182     1968     3754     5540     784CIP2_184     7641			3746	5532	784CIP2_175	
177     1963     3749     5535     784CIP2_178     7615       178     1964     3750     5536     784CIP2_179     7617       179     1965     3751     5537     784CIP2_181     7624       180     1966     3752     5538     784CIP2_182     7626       181     1967     3753     5539     784CIP2_183     7640       182     1968     3754     5540     784CIP2_184     7641			3747	5533	784CIP2_176	
178     1964     3750     5536     784CIP2_179     7617       179     1965     3751     5537     784CIP2_181     7624       180     1966     3752     5538     784CIP2_182     7626       181     1967     3753     5539     784CIP2_183     7640       182     1968     3754     5540     784CIP2_184     7641			3748		784CIP2_177	
179     1965     3751     5537     784CIP2 181     7624       180     1966     3752     5538     784CIP2 182     7626       181     1967     3753     5539     784CIP2 183     7640       182     1968     3754     5540     784CIP2 184     7641	177	1963	3749	5535	784CIP2_178	
180     1966     3752     5538     784CIP2 182     7626       181     1967     3753     5539     784CIP2 183     7640       182     1968     3754     5540     784CIP2 184     7641	178	1964	3750	5536	784CIP2_179	
181     1967     3753     5539     784CIP2 183     7640       182     1968     3754     5540     784CIP2 184     7641	179	1965	3751	5537	784CIP2_181	
182 1968 3754 5540 784CIP2_184 7641	180	1966	3752	5538	784CIP2_182	
	181	1967	3753	5539	784CIP2_183	
183 1969 3755 5541 784CIP2_185 7641			3754	5540	784CIP2_184	
	183	1969	3755	5541	784CIP2_185	7641

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of full-	SEQ ID NO: of	SEQ ID NO:	SEQ ID	docket number	NO: in
length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide	-	sequence	priority	
	sequence	}		application	· ·
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185	1971	3757	5543	784CIP2_187	7642
186	1972	3758	5544	784CIP2_188	7649
187	1973	3759	5545	784CIP2_189	7656
188	1974	3760	5546	784CIP2_190	7657
189	1975	3761	5547	784CIP2_191	7657
190	1976	3762	5548	784CIP2_192	7662
191	1977	3763	5549	784CIP2_193	766B
192	1978	3764	5550	784CIP2_194	7673
193	1979	3765	5551	784CIP2_195	7690
194	1980	3766	5552	784CIP2_196	7700
195	1981	3767	5553	784CIP2_197	7709
196	1982	3768	5554	784CIP2_198	7736
197	1983	3769	5555	784CIP2_199	7737
198	1984	3770	5556	784CIP2_200	7744
199	1985	3771	5557	784CIP2_201	7771
200	1986	3772	5558	784CIP2_202 784CIP2_203	7786 7791
201	1987	3773	5559		7797
202	1988	3774	5560	784CIP2_204	7806
203	1989	3775	5561	784CIP2_205 784CIP2_206	7812
204	1990	3776	5562 5563	784CIP2_206	7812
205	1991	3777 3778	5564	784CIP2_207	7812
206 207	1992	3779	5565	784CIP2_208	7822
207	1993	3780	5566	784CIP2 210	7827
209	1995	3781	5567	784CIP2 211	7830
210	1995	3782	5568	784CIP2 212	7835
211	1997	3783	5569	784CIP2 214	7840
212	1998	3784	5570	784CIP2 215	7858
213	1999	3785	5571	784CIP2 216	7858
214	2000	3786	5572	784CIP2 217	7861
215	2001	3787	5573	784CIP2 218	7866
216	2002	3788	5574	784CIP2_219	7868
217	2003	3789	5575	784CIP2_220	7896
218	2004	3790	5576	784CIP2_221	7898
219	2005	3791	5577	784CIP2_222	7900
220	2006	3792	5578	784CIP2_223	7906
221	2007	3793	5579	784CIP2_224	7908
222	2008	3794	5580	784CIP2_225	7909
223	2009	3795	5581	784CIP2_226	7917
224	2010	3796	5582	784CIP2_227	7932
225	2011	3797	5583	784CIP2_228	7940
226	2012	3798	5584	784CIP2_229	7940
227	2013	3799	5585	784CIP2_230	7984
228	2014	3800	5586	784CIP2_231	7984
229	2015	3801	5587	784CIP2_232	8001
230	2016	3802	5588	784CIP2_233	8021
231	2017	3803	5589	784CIP2_234	8029
232	2018	3804	5590	784CIP2_235	8033
233	2019	3805	5591	784CIP2_236	8040
234	2020	3806	5592	784CIP2_237	8052
235	2021	3807	5593	784CIP2_238	8096
236	2022	3808	5594	784CIP2_239	8096
237	2023	3809	5595	784CIP2_240	8113
238	2024	3810	5596	784CIP2_241	8126
239	2025	3811	5597	784CIP2_242	8132
240	2026	3812	5598	784CIP2_243	8137
241	2027	3813	5599	784CIP2_244	8137
242	2028	3814	5600	784CIP2_245	8159 8159
243	2029	3815	5601	784CIP2_246	8159
244	2030	3816	5602	784CIP2_247	8176
245	2031	3817	5603	784CIP2_248	1 07.10

SEO ID NO:	SEQ ID	SEO ID NO:	SEQ ID	Priority	SEQ ID
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length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
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246	sequence 2032	3818	5604	application 784CIP2 249	8196
247	2032	3819	5605	784CIP2 250	8200
248	2034	3820	5606	784CIP2 251	8212
249	2035	3821	5607	784CIP2 252	8220
250	2036	3822	5608	784CIP2_253	8238
251	2037	3823	5609	784C1P2_254	8254
252	2038	3824	5610	784CIP2_255	8255
253	2039	3825	5611	784CIP2_256	8288
254	2040	3826	5612	784CIP2_257	8296
255	2041	3827	5613	784CIP2_258	8329
256	2042	3828	5614	784CTP2_259 784CIP2_260	8362 8429
257	2043	3829 3830	5615 5616	784CIP2_260 784CIP2_261	8436
258 259	2044	3831	5617	784CIP2_261	8448
259	2045	3832	5618	784CIP2 263	8472
261	2047	3833	5619	784CIP2 264	8502
262	2048	3834	5620	784CIP2 265	8504
263	2049	3835	5621	784CIP2_266	8507
264	2050	3836	5622	784CIP2_268	8509
265	2051	3837	5623	784CIP2_269	8515
266	2052	3838	5624	784CIP2_270	8519
267	2053	3839	5625	784CIP2_271	8530
268	2054	3840	5626	784CIP2_272	8532
269	2055	3841	5627	784CIP2_273 784CIP2_274	8532 8539
270 271	2056	3842 3843	5628 5629	784CIP2_274 784CIP2_275	8541
272	2057	3844	5630	784CIP2 276	8543
273	2059	3845	5631	784CIP2 277	8593
274	2060	3846	5632	784CIP2 278	8595
275	2061	3847	5633	784CIP2 279	8615
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277	2063	3849	5635	784CIP2_281	8621
278	2064	3850	5636	784CIP2_282	8623
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280	2066	3852	5638	784CIP2_284	8628
281	2067	3853	5639	784CIP2_285	8628 8629
282	2068	3854	5640	784CIP2_286 784CIP2_287	8630
283 284	2069	3855 3856	5641 5642	784CIP2_287	8631
285	2071	3857	5643	784CIP2 289	8633
286	2072	3858	5644	784CIP2 290	8634
287	2073	3859	5645	784CIP2_291	8635
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290	2076	3862	5548	784CIP2_294	8660
291	2077	3863	5649	784CIP2_295	8667
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293	2079	3865	5651	784CIP2_297	8685
294	2080	3866	5652	784CIP2_298 784CIP2_299	8896
295	2081	3867	5653	784CIP2_299 784CIP2_300	8978
296 297	2082	3868 3869	5654 5655	784CIP2_300 784CIP2_301	9046
298	2084	3870	5656	784CIP2_301	9048
299	2085	3871	5657	784CIP2 303	9116
300	2086	3872	5658	784CIP2_304	9195
301	2087	3873	5659	784CIP2_305	9201
302	2088	3874	5660	784CIP2 306	9307
303	2089	3875	5661	784CIP2_307	9321
304	2090	3876	5662	784CIP2_308	9397
305	2091	3877	5663	784CIP2_309	9405
306	2092	3878	5664	784CIP2_310	9406 9422
307	2093	3879	5665	784CIP2 311	

SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority docket number	SEQ ID NO:in
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Length nucleoti <b>d</b> e	length'	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide	sequence	sequence	priority	
ecd acree	sequence	i	•	application	
308	2094	3880	5666	784CIP2_312	9494
309	2095	3881	5667	784CIP2_313	9512
310	2096	3882	5668	784CIP2_314	9632
311	2097	3883	5669	784CIP2_315	9661
312	2098	3884	5670	784CIP2_316	9664
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314	2100	3886	5672	784CIP2_318	9700
315	2101	3887	5673	784CIP2_319	9716
316	2102	3888	5674	784CIP2_320	9721
317	2103	3889	5675	784CIP2_321	9870
318	2104	3890	5676	784CIP2_322	9887
319	2105	3891	5677	784CIP2_323	9923
320	2106	3892	5678	784CIP2_324	9938
321	2107	3893	5679	784CIP2_325	9964
322	2108	3894	5680	784CIP2_326	10007
323	2109	3895	5681	784CIP2_327	10009
324	2110	3896	5682	784CIP2_328	10046
325	2111	3897	5683	784CIP2_329	10156
326	2112	3898	5684	784CIP2_330	10276
327	2113	3899	5685	784CIP2_331	10283
328	2114	3900	5686	784CIP2B_1	152 167
329	2115	3901	5687	784CIP2B_2	205
330	2116	3902	5688	784CIP2B_3	210
331	2117	3903	5689	784CIP2B_4	225
332	2118	3904	5690	784CIP2B_5 784CIP2B 6	225
333	2119	3905	5691 5692	784CIP2B 7	264
334	2120	3906	5693	784CIP2B 8	268
335	2121	3907 3908	5694	784CIP2B 9	293
336	2122	3908	5695	784CIP2B 10	293
337	2124	3910	5696	784CIP2B 11	293
338	2125	3910	5697	784CIP2B 12	302
339 340	2125	3912	5698	784CIP2B 13	311
341	2127	3913	5699	784CIP2B 14	352
342	2128	3914	5700	784CIP2B 15	358
343	2129	3915	5701	784CIP2B 16	368
344	2130	3916	5702	784CIP2B 17	393
345	2131	3917	. 5703	784CIP2B_18	477
346	2132	3918	5704	784CIP2B_19	508
347	2133	3919	5705	784CIP2B_20	508
348	2134	3920	5706	784CIP2B_21	515
349	2135	3921	5707	784CIP2B_22	578
350	2136	3922	5708	784CIP2B_23	588
351	2137	3923	5709	784CIP2B_24	591
352	2138	3924	5710	784CIP2B_25	593
353	2139	3925	5711	784CIP2B_26	594
354	2140	3926	5712	784CIP2B_27	619
355	2141	3927	5713	784CIP2B_28	620
356	2142	3928	5714	784CIP2B_29	654
357	2143	3929	5715	784CIP2B_30	692
358	2144	3930	5716	784CIP2B_31	753
359	2145	3931	5717	784CIP2B_32	758
360	2146	3932	5718	784CIP2B_33	787
361	2147	3933	5719	784CIP2B_34	833
362	2148	3934	5720	784CIP2B_35	838
363	2149	3935	5721	784CIP2B_36	870
364	2150	3936	5722	784CIP2B_37	891
365	2151	3937	5723	784CIP2B_38	891
366	2152	3938	5724	784CIP2B_39	921
367	2153	3939	5725	784CIP2B_40	924
368	2154	3940	5726	784CIP2B_41	932
369	2155	3941	5727	784CIP2B_42	942

SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
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length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide	j	sequence	priority	1
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370	2156	3942	5728	784CIP2B_43	958
371	2157	3943	5729	784CIP2B_44	968
372	2158	3944	5730	784CIP2B_45	992
373	2159	3945	5731	784CIP2B_46	1025
374	2160	3946	5732	784CIP2B_47	1074
375	2161	3947	5733	784CIP2B_48	1104
376	2162	3948	5734	784CIP2B_49	1114
377	2163	3949	5735	784CIP2B_50	
378	2164	3950	5736	784CIP2B_51 784CIP2B_52	1262
379	2165	3951	5737	784CIP2B_52 784CIP2B_53	1319
380	2166	3952	5738		1319
381	2167	3953	5739 5740	784CIP2B_54 784CIP2B_55	1436
382	2168	3954	5741	784CIP2B_55	1464
383	2169	3955	5742	784CIP2B_57	1584
384	2170	3956 3957	5742	784CIP2B_57	1617
385	2171	3957	5744	784CIP2B_58	1724
386	2172	3958	5745	784CIP2B 60	1728
387	2173	3959	5746	784CIP2B 61	1772
389	2175	3961	5747	784CIP2B 62	1809
390	2175	3962	5748	784CIP2B 63	1868
391	2177	3963	5749	784CIP2B 64	1898
392	2178	3964	5750	784CIP2B 65	1926
393	2179	3965	5751	784CIP2B 66	1965
394	2180	3966	5752	784CIP2B 67	1967
395	2181	3967	5753	784CIP2B 68	1995
396	2182	3968	5754	784CIP2B 69	2005.
397	2183	3969	5755	784CIP2B 70	2027
398	2184	3970	5756	784CIP2B 71	2055
399	2185	3971	. 5757	784CIP2B 72	2103
400	2186	3972	5758	784CIP2B 73	2106
401	2187	3973	5759	784CIP2B 74	2166
402	2188	3974	5760	784CIP2B 75	2175
403	2189	3975	5761	784CIP2B 76	2176
404	2190	3976	5762	784CIP2B 78	2236
405	2191	3977	5763	784CIP2B_79	2250
406	2192	3978	5764	784CIP2B_80	2300 .
407	2193	3979	· 5765	784CIP2B_81	2323
408	2194	3980	5766	784CIP2B_82	2340
409	2195	3981	5767	784CIP2B_83	2371
410	2196	3982	5768	784CIP2B_84	2399
411	2197	3983	5769	784CIP2B_85	2411
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413	2199	3985	5771	784CIP2B_87	2430
414	2200	3986	5772	784CIP2B_88	2439
415	2201	3987	5773	784CIP2B_89	2447
416	2202	3988	5774	784CIP2B_90	2461
417	2203	3989	5775	784CIP2B_91	2487
418	2204	3990	5776	784CIP2B_92	2492
419	2205	3991	5777	784CIP2B_93	2512
420	2206	3992	5778	784CIP2B_94	2564
421	2207	3993	5779	784CIP2B_95	2678
422	2208	3994	5780	784CIPZB_96	2816
423	2209	3995	5781	784CIP2B_97	2818
424	2210	3996	5782	784CIP2B_98	2819
425	2211	3997	5783	784CIP2B_99	2943
426	2212	3998	5784	784CIP2B_100	3137
427	2213	3999	5785	784CIP2B_101	31,37
428	2214	4000	5786	784CIP2B_102	3160
429	2215	4001	5787	784CIP2B_103	3323
430	2216	4002	5788	784CIP2B_104	3360
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SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
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length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide	} -	sequence	priority	1
<u> </u>	sequence		_	application	i
432	2218	4004	5790	784CIP2B 106	3417
433	2219	4005	5791	784CIP2B 107	3418
434	2220	4006	5792	784CIP2B 108	3442
435	2221	4007	5793	784CIP2B 109	3442
436	2222	4008	5794	784CIP2B 110	3444
437	2223	4009	5795	784CIP2B 111	3855
438	2224	4010	5796	784CIP2B_111	3863
				784CIP2B_112	
439	2225	4011	5797		4090
440	2226	4012	5798	784CIP2B_114	4105
441	2227	4013	5799	784CIP2B_115	4142
442	2228	4014	5800	784CIP2B_116	4142
443	2229	4015	5801	784CIP2B_117	4149
444	2230	4016	5802	784CIP2B_118	4196
445	2231	4017	5803	784CIP2B_119	4202
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447	2233	4019	5805	784CIP2B_121	4304
448	2234	4020	5806	784CIP2B 122	4306
449	2235	4021	5807	784CIP2B 123	4311
450	2236	4022	5808	784CIP2B 124	4321
451	2237	4023	5809	784CIP2B 125	4323
452	2238	4024	5810	784CIP2B 126	4332
453	2239	4025	5811	784CIP2B 127	4488
454	2240	4026	5812	784CIP2B 128	4588
455				784CIP2B 129	
456	2241	4027	5813		5569 5573
	2242	4028	5814	784CIP2B_130	
457	2243	4029	5815	784CIP2B_131	5577
458	2244	4030	5816	784CIP2B_132	5579
459	2245	4031	5817	784CIP2B_133	5582
460	2246	4032	5818	784CIP2B_134	5583
461	2247	4033	5819	784CIP2B_135	5584
462	2248	4034	5820	784CIP2B_136	5585
463	2249	4035	5821	784CIP2B_137	5591
464	2250	4036	5822	784CIP2B_138	5593
465	2251	4037	5823	784CIP2B_139	5594
466	2252	4038	5824	784CIP2B_140	5594
467	2253	4039	5825	784CIP2B_141	5598
468	2254	4040	5826	784CIP2B_142	5602
469	2255	4041	5827	784CIP2B 143	5605
470	2256	4042	5828	784CIP2B 144	5608
471	2257	4043	5829	784CIP2B 145	5617
472	2258	4044	5830	784CIP2B 146	5620
473	2259	4045	5831	784CIP2B 147	5622
474	2260	4046	5832	784CIP2B 148	5623
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482	2268	4054	5840	784CIP2B_156	5641
483	2269	4055	5841	784CIP2B_157	5643
484	2270	4056	5842	784CIP2B_158	5647
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487	2273	4059	5845	784CIP2B_161	5659
488	2274	4060	5846	784CIP2B_162	5667
489	2275	4061	5847	784CIP2B 163	5672
490	2276	4062	5848	784CIP2B 164	5674
491	2277	4063	5849	784CIP2B 165	5678
492	2278	4064	5850	784CIP2B 166	5680
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SEO ID NO:	Lego In	1 000 TD NO	1 650 - 55	C Book and the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contro	7
of full-	SEQ ID NO: of	SEQ ID NO:	SEQ ID	Priority	SEQ ID
length	full-	of contig	NO: of contig	docket number_	NO:in
nucleotide	length	sequence	peptide	corresponding SEQ ID NO: in	U.S.S.N.
sequence	peptide	sequence	- ~		09/488,725
beguence	sequence		sequence	priority	
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495	2281	4067	5853	784CIP2B_169	5694
496	2282	4068	5854	784CIP2B_170	5698
497	2283	4069	5855	784CIP2B_171	5699
498	2284	4070	5856	784CIP2B_172	5712
499	2285	4071	5857	784CIP2B_173	5719
500	2286	4072	5858	784CIP2B 174	5720
501	2287	4073	5859	784CIP2B 175	5727
502	2288	4074	5860	784CIP2B 176	5730
503	2289	4075	5861	784CIP2B 177	5734
504	2290	4076	5862	784CIP2B 178	5738
505	2291	4077	5863	784CIP2B 179	5739
506	2292	4078	5864	784CIP2B 180	5740
507	2293	4079	5865	784CIP2B 181	5744
508	2294	4080	5866	784CIP2B 182	5748
509	2295	4081	5867		
510	2296			784CIP2B 183	5749
	2296	4082	5868	784CIP2B_184	5750
511		4083	5869	784CIP2B_185	5750
512	2298	4084	5870	784CIP2B_186	5750
513	2299	4085	5871	784CIP2B_187	5761
514	2300	4086	5872	784CIP2B_188	5762
515	2301	4087	5873	784CIP2B_189	5767
516	2302	4088	5874	784CIP2B_190	5773
517	2303	4089	5875	784CIP2B_191	5783
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519	2305	4091	5877	784CIP2B 193	5788
520	2306	4092	5878	784CIP2B 194	5798
521	2307	4093	5879	784CIP2B 196	5807
522	2308	4094	5880	784CIP2B 197	5818
523	2309	4095	5881	784CIP2B 198	5819
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526	2312	4098	5884	784CIP2B 201	5842
527	2313	4099	5885	784CIP2B_201	l
528	2314	4100			5853
529	2315		5886	784CIP2B_203	5861
530		4101	5887	784CIP2B_204	5864
	2316	4102	5888	784CIP2B_205	5865
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532	2318	4104	5890	784CIP2B_207	5873
533	2319	4105	5891	784CIP2B_208	5873
534	2320	4106	5892	784CIP2B_209	5875
535	2321	4107	5893	784CIP2B_210	5878
536	2322	4108	5894	784CIP2B_211	5879
537	2323	4109	5895	784CIP2B_212	5880
538	2324	4110	5896	784CIP2B_213	5880
539	2325	4111	5897	784CIP2B_214	5880
540	2326	4112	5898	784CIP2B 215	5880
541	2327	4113	5899	784CIP2B 216	5885
542	2328	4114	5900	784CIP2B 217	5895
543	2329	4115	5901	784CIP2B 218	5898
544	2330	4116	5902	784CIP2B 219	5902
545	2331	4117	5903	784CIP2B 220	
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547	2332	4118	5904	784CIP2B_221	5918
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548	2334	4120	5906	784CIP2B_223	5927
549	2335	4121	5907	784CIP2B_224	5932
550	2336	4122	5908	784CIP2B_225	5939
551	2337	4123	5909	784CIP2B_226	5945
552	2338	4124	5910	784CIP2B 227	5946
553	2339	4125	5911	784CIP2B 228	5947
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559	2345	4131	5917	784CIP2B_235	5979
560	2346	4132	5918	784CIP2B_236	5980
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563	2349	4135	5921	784CIP2B_239	5991
564	2350	4136	5922	784CIP2B_240	5997
565	2351	4137	5923	784CIF2B_241	5998
566	2352	4138	5924	784CIP2B_242	6003
567	2353	4139	5925	784CIP2B_243	6004
568	2354	4140	5926	784CIP2B_244	6013
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570	2356	4142	5928	784CIP2B_246	6028
571	2357	4143	5929	784CIP2B_247	6029
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574	2360	4146	5932	784CIP2B_250	6032
575	2361	4147	5933	784CIP2B_251	6037
576	2362	4148	5934	784CIP2B_252	6037
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578	2364	4150	5936	784CIP2B_254	6044
579	2365	4151	5937	784CIP2B_255	6046
580	2366	4152	5938	784CIP2B_256	6048
581	2367	4153	5939	784CIP2B_257	6049
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595	2381	4167	5953	784CIP2B 272	6088
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671	2457	4243	6029	784CIP2B 353	6337
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	sequence			application	l
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683	2469	4255	6041	784CIP2B 365	6376
684	2470	4256	6042	784CIP2B 366	6379
685	2471	4257	6043	784CIP2B 367	6380
686	2472	4258	6044	784CIP2B 368	
687	2473		1		6381
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688	2474	4260	6046	784CIP2B_370	6395
689	2475	4261	6047	784CIP2B_371	6397
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691	2477	4263	6049	784CIP2B 373	6401
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697	2483	4269	6055	784CIP2B_379	. 6422
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700	2486	4272	6058	784CIP2B 382	6427
701	2487	4273	6059	784CIP2B 383	6428
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704		4276	6062	784CIP2B_386	6432
	2491	4277	6063	784CIP2B_387	6432
706	2492	4278	6064	784CIP2B_388	6438
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711	2497	4283	6069	784CIP2B 394	6461
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723	2509	4295	6081	784CIP2B 407	6544
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727	2513	4299	6085	784CIP2B_411	6552
728	2514	4300	6086	784CIP2B_412	6554
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732	2518	4304	6090	784CIP2B 416	6564
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734	2520				
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	2521	4307	6093	784CIP2B_419	6575
736	2522	4308	6094	784CIP2B_420	6577
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740	2526	4312	6098	784CIP2B 424	6625
741	2527	4313	6099	784CIP2B 425	6625
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777         2563         4349         6135         784CIP2B_461         6730           778         2564         4350         6136         784CIP2B_462         6732           779         2565         4351         6137         784CIP2B_463         6733           780         2566         4352         6138         784CIP2B_464         6737           781         2567         4353         6139         784CIP2B_465         6745           782         2568         4354         6140         784CIP2B_466         6751           783         2569         4355         6141         784CIP2B_467         6754           784         2570         4356         6142         784CIP2B_469         6761           786         2571         4357         6143         784CIP2B_469         6761           786         2572         4358         6144         784CIP2B_471         6765           787         2573         4359         6145         784CIP2B_471         6768           788         2574         4360         6146         784CIP2B_471         6768           788         2574         4360         6146         784CIP2B_471         6768					_	
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779         2565         4351         6137         784CIP2B_463         6733           780         2566         4352         6138         784CIP2B_464         6737           781         2567         4353         6139         784CIP2B_465         6745           782         2568         4354         6140         784CIP2B_466         6751           783         2569         4355         6141         784CIP2B_467         6754           784         2570         4356         6142         784CIP2B_469         6761           784         2570         4356         6142         784CIP2B_469         6761           785         2571         4357         6143         784CIP2B_469         6761           786         2572         4358         6144         784CIP2B_470         6765           787         2573         4359         6145         784CIP2B_471         6768           788         2574         4360         6146         784CIP2B_471         6768           789         2575         4361         6147         784CIP2B_473         6776           790         2576         4362         6148         784CIP2B_474         6796						
780         2565         4352         6138         784CIP2B 464         6737           781         2567         4353         6139         784CIP2B 465         6745           782         2568         4354         6140         784CIP2B 466         6751           783         2569         4355         6141         784CIP2B 467         6754           784         2570         4356         6142         784CIP2B 468         6758           785         2571         4357         6143         784CIP2B 469         6761           786         2572         4358         6144         784CIP2B 470         6765           787         2573         4359         6145         784CIP2B 471         6768           788         2574         4360         6146         784CIP2B 472         6773           789         2575         4361         6147         784CIP2B 473         6776           790         2576         4362         6148         784CIP2B 474         6796           791         2577         4363         6149         784CIP2B 475         6798           792         .2578         4364         6150         784CIP2B 476         6823						
781         2567         4353         6139         784CIP2B 465         6745           782         2568         4354         6140         784CIP2B 466         6751           783         2569         4355         6141         784CIP2B 467         6754           784         2570         4356         6142         784CIP2B 469         6758           785         2571         4357         6143         784CIP2B 469         6761           786         2572         4358         6144         784CIP2B 470         6765           787         2573         4359         6145         784CIP2B 471         6768           788         2574         4360         5146         784CIP2B 472         6773           789         2575         4361         6147         784CIP2B 473         6776           790         2576         4362         6148         784CIP2B 474         6796           791         2577         4363         6149         784CIP2B 475         6798           792         2578         4364         6150         784CIP2B 476         6823           793         2579         4365         6151         784CIP2B 477         6825						
782         2568         4354         6140         784CIP2B_466         6751           783         2569         4355         6141         784CIP2B_467         6754           784         2570         4356         6142         784CIP2B_468         6758           785         2571         4357         6143         784CIP2B_469         6761           786         2572         4358         6144         784CIP2B_470         6765           787         2573         4359         6145         784CIP2B_471         6768           788         2574         4360         6146         784CIP2B_472         6773           789         2575         4361         6147         784CIP2B_473         6776           790         2576         4362         6148         784CIP2B_473         6776           791         2577         4363         6149         784CIP2B_475         6798           792         .2578         4364         6150         784CIP2B_476         6823           793         2579         4365         6151         784CIP2B_476         6823           794         2580         4366         6152         784CIP2B_478         6826	781					
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784         2570         4356         6142         784CIP2B_468         6758           785         2571         4357         6143         784CIP2B_469         6761           786         2572         4358         6144         784CIP2B_470         6765           787         2573         4359         6145         784CIP2B_471         6768           788         2574         4360         6146         784CIP2B_472         6773           789         2575         4361         6147         784CIP2B_473         6776           790         2576         4362         6148         784CIP2B_474         6796           791         2577         4363         6149         784CIP2B_475         6798           792         .2578         4364         6150         784CIP2B_476         6823           793         2579         4365         6151         784CIP2B_477         6825           794         2580         4366         6152         784CIP2B_478         6826           795         2581         4367         6153         784CIP2B_480         6844           797         2583         4368         6154         784CIP2B_480         6844	783	2569	4355	6141		
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Sequence	seguence	peptide	_	sequence		1 00, 100, 123
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993 2779 4565 6381 784CIP2B_680 7613 994 2780 4565 6381 784CIP2B_680 7613 994 2780 4566 6381 784CIP2B_680 7623 995 2781 4567 6353 784CIP2B_680 7623 996 2782 4568 6354 784CIP2B_680 7639 997 2783 4569 6355 784CIP2B_680 7633 998 2784 4570 6356 784CIP2B_680 7633 998 2784 4570 6356 784CIP2B_680 7635 1000 2786 4571 6357 784CIP2B_680 7638 1001 2786 4572 6358 784CIP2B_680 7638 1001 2786 4572 6358 784CIP2B_680 7639 1001 2786 4573 6359 784CIP2B_680 7639 1001 2786 4575 6361 784CIP2B_680 7647 1002 2788 4574 6360 784CIP2B_690 7648 1004 2790 4576 6362 784CIP2B_690 7648 1005 2791 4577 6363 784CIP2B_690 7648 1006 2792 4578 6364 784CIP2B_690 7648 1007 2793 4579 6365 784CIP2B_690 7648 1008 2794 4580 5366 784CIP2B_691 7657 1009 2795 4581 6364 784CIP2B_695 7664 1000 2796 4576 6366 784CIP2B_690 7648 1000 2797 4580 6364 784CIP2B_690 7648 1000 2798 4579 6365 784CIP2B_691 7658 1000 2799 4576 6366 784CIP2B_691 7664 1000 2799 4576 6366 784CIP2B_691 7664 1000 2799 4576 6364 784CIP2B_690 7668 1000 2799 4579 6365 784CIP2B_691 7664 1000 2799 4579 6365 784CIP2B_691 7664 1000 2799 4579 6365 784CIP2B_691 7664 1001 2799 4580 5366 784CIP2B_695 7661 1002 2798 4580 5366 784CIP2B_695 7661 1003 2798 4580 5366 784CIP2B_695 7661 1004 2790 4580 5366 784CIP2B_695 7661 1005 2791 4597 7658 1006 2794 4580 5366 784CIP2B_697 7668 1007 2793 4590 5366 784CIP2B_697 7668 1008 2794 4580 5366 784CIP2B_700 7673 1009 2795 4581 6367 784CIP2B_700 7668 1001 2796 4582 6368 784CIP2B_700 7668 1001 2796 4582 6368 784CIP2B_700 7668 1001 2798 4584 5370 784CIP2B_700 7668 1001 2798 4584 5370 784CIP2B_700 7668 1001 2798 4584 5370 784CIP2B_700 7775 1001 2800 4586 5372 784CIP2B_700 7775 1001 2800 4586 5372 784CIP2B_700 7774 1002 2806 4599 5398 784CIP2B_700 7776 1003 2800 4589 6389 784CIP2B_700 7776 1004 2800 4580 6380 784CIP2B_700 7776 1009 2805 4591 6397 784CIP2B_700 7776 1009 2805 4591 6397 784CIP2B_700 7776 1009 2805 4591 6397 784CIP2B_700 7776 1009 2805 4591 6397 784CIP2B_700 7776 1009 2805 4606 6392 784CIP2B_700 7778 1009 2805 4606 6392 784CIP2B_700 7776 1009 2805 4606 6392		2777	4563	6349	784CIP2B 678	
994 2780 4566 6352 784CIP25 681 7623 955 2781 4567 6353 784CIP25 681 7623 956 2782 4568 6354 784CIP26 683 7639 957 2783 4569 6355 784CIP26 683 7639 958 2784 4570 6356 784CIP26 684 7633 959 2785 4571 6357 784CIP26 686 7638 1000 2786 4572 6358 784CIP26 686 7638 1000 2786 4572 6358 784CIP26 686 7638 1001 2787 4573 6359 784CIP26 686 7639 1001 2787 4573 6359 784CIP26 686 7639 1002 2788 4574 6360 784CIP26 689 7647 1003 2799 4575 6361 784CIP26 689 7647 1003 2799 4576 6362 784CIP26 689 7647 1005 2791 4577 5363 784CIP26 699 7668 1006 2792 4578 6364 784CIP26 699 7668 1007 2793 4579 6364 784CIP26 699 7668 1008 2794 4580 5366 784CIP26 699 7668 1009 2795 4581 6367 784CIP26 699 7667 1010 2796 4576 6366 784CIP26 699 7668 1009 2795 4581 6367 784CIP26 699 7667 1010 2796 4580 5368 784CIP26 699 7668 1010 2796 4580 5368 784CIP26 699 7668 1010 2796 4580 5368 784CIP26 699 7668 1010 2796 4580 5368 784CIP26 699 7668 1010 2796 4581 6367 784CIP26 699 7668 1010 2796 4580 5368 784CIP26 699 7668 1010 2796 4581 6367 784CIP26 699 7668 1010 2798 4581 6367 784CIP2B 699 7668 1011 2797 4583 5369 784CIP26 699 7668 1012 2798 4584 5370 784CIP2B 699 7668 1013 2799 4585 5371 784CIP2B 700 7693 1014 2800 4586 5372 784CIP2B 700 7693 1015 2801 4587 5373 784CIP2B 700 7736 1016 2802 4588 5371 784CIP2B 700 7736 1017 2803 4599 6375 784CIP2B 707 7736 1018 2804 4589 6375 784CIP2B 707 7736 1019 2806 4589 6375 784CIP2B 707 7739 1020 2806 4589 6376 784CIP2B 707 7739 1021 2807 4583 6389 784CIP2B 700 7733 1022 2808 4589 6380 784CIP2B 706 7733 1023 2808 4589 6380 784CIP2B 707 7739 1024 2810 4596 6382 784CIP2B 708 7735 1025 2801 4597 6383 784CIP2B 707 7739 1026 2806 6392 784CIP2B 708 7733 1027 2813 4599 6385 784CIP2B 708 7733 1029 2808 4599 6395 784CIP2B 708 7736 1031 2817 4603 6389 784CIP2B 707 7739 1029 2815 4601 6387 784CIP2B 709 7778 1029 2815 4601 6387 784CIP2B 709 7778 1029 2815 4601 6387 784CIP2B 709 7778 1029 2815 4601 6396 784CIP2B 713 7748 1039 2815 4601 6396 784CIP2B 713 7778 1044 2830 4609 6392 784CIP2B 713 7778 10404 2832 4613 6399 784CIP2B 713 7778 1044			4564	6350	784CIP2B_679	7609
995 2781 4567 6353 784C1P28 682 7629 996 2782 4558 6354 784C1P28 683 7630 997 2783 4559 6355 784C1P28 683 7630 998 2784 4570 6356 784C1P28 685 7633 998 2784 4570 6356 784C1P28 686 7638 1000 2786 4571 6357 784C1P28 686 7638 1001 2787 4573 6358 784C1P28 687 7639 1001 2787 4573 6359 784C1P28 687 7639 1001 2787 4573 6359 784C1P28 688 7639 1001 2787 4573 6359 784C1P28 689 7639 1002 2788 4574 6360 784C1P28 689 7636 1003 2789 4575 6361 784C1P28 689 7637 1004 2790 4575 6361 784C1P28 699 7648 1005 2791 4577 6363 784C1P28 699 7658 1006 2792 4578 6362 784C1P28 699 7658 1007 2793 4579 6365 784C1P28 699 7658 1008 2794 4580 5366 784C1P28 699 7658 1009 2795 4581 6367 784C1P28 699 7675 1009 2795 4582 6368 784C1P28 699 7668 1010 2798 4588 6369 784C1P28 699 7668 1010 2798 4588 6369 784C1P28 699 7668 1011 2797 4583 6369 784C1P28 699 7668 1012 2798 4584 6370 784C1P28 699 7668 1014 2800 4588 6370 784C1P28 699 7668 1014 2800 4588 6370 784C1P28 709 7668 1015 2801 4587 6373 784C1P28 709 7668 1016 2802 4588 6371 784C1P28 709 7681 1017 2803 4589 6376 784C1P28 709 7735 1018 2800 4589 6370 784C1P28 709 7735 1019 2805 4591 6377 784C1P28 709 7735 1019 2805 4591 6377 784C1P28 709 7735 1022 2808 4599 6376 784C1P28 709 7731 1039 2795 4589 6370 784C1P28 709 7731 1040 2800 4589 6370 784C1P28 709 7731 1051 2801 4597 6333 784C1P28 709 7731 1052 2809 4599 6376 784C1P28 709 7733 1021 2807 4593 6399 784C1P28 709 7733 1022 2808 4599 6380 784C1P28 709 7733 1021 2807 4593 6399 784C1P28 709 7733 1022 2808 4599 6380 784C1P28 709 7733 1023 2809 4595 6380 784C1P28 709 7733 1024 2810 4596 6382 784C1P28 709 7733 1025 2808 4599 6380 784C1P28 709 7733 1026 2813 4599 6399 6390 784C1P28 709 7733 1027 2803 4599 6390 784C1P28 709 7733 1028 2814 4600 6386 784C1P28 719 7766 1030 2816 4602 6389 784C1P28 719 7766 1031 2817 4603 6389 784C1P28 719 7767 1039 2815 4604 6390 784C1P28 719 7769 1030 2816 4604 6390 784C1P28 719 7778 1031 2817 4603 6389 784C1P28 719 7778 1039 2818 4604 6399 784C1P28 719 7778 1039 2818 4604 6399 784C1P28 719 7778 1044 2820 4606 6391 784C1P28 719		2779	4565	6351	784CIP2B 680	7613
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1004 2790 4576 5362 784CIP2B 590 7658 1005 2791 4577 5363 784CIP2B 692 7664 1006 2792 4577 6363 784CIP2B 692 7664 1006 2792 4578 6364 784CIP2B 693 7664 1007 2793 4579 6365 784CIP2B 695 7664 1008 2794 4580 6366 784CIP2B 695 7675 1009 2795 4581 6367 784CIP2B 697 7676 1010 2796 4582 6368 784CIP2B 697 7676 1011 2797 4583 6369 784CIP2B 697 7676 1011 2797 4583 6369 784CIP2B 698 7681 1011 2797 4583 6369 784CIP2B 698 7681 1012 2798 4584 6370 784CIP2B 698 7681 1013 2799 4585 6371 784CIP2B 700 7693 1014 2800 4586 6372 784CIP2B 702 7715 1016 2802 4588 6374 784CIP2B 703 7716 1016 2802 4588 6374 784CIP2B 703 7716 1017 2803 4589 6375 784CIP2B 707 7721 1018 2804 4589 6375 784CIP2B 708 7721 1019 2805 4591 6377 784CIP2B 707 7729 1020 2806 4592 6378 784CIP2B 707 7729 1020 2806 4593 6376 784CIP2B 707 7729 1020 2806 4593 6376 784CIP2B 707 7729 1021 2807 4593 6379 784CIP2B 707 7733 1021 2809 4595 6387 784CIP2B 707 7735 1022 2808 4599 6388 784CIP2B 707 7735 1022 2808 4599 6388 784CIP2B 707 7735 1023 2809 4595 6388 784CIP2B 707 7735 1024 2810 4596 6382 784CIP2B 710 7741 1025 2811 4597 6383 784CIP2B 710 7741 1026 2812 4598 6384 784CIP2B 710 7741 1027 2813 4599 6386 784CIP2B 710 7741 1028 2814 4600 6386 784CIP2B 711 7748 1029 2815 4601 6387 784CIP2B 711 7749 1029 2815 4601 6387 784CIP2B 712 7748 1029 2815 4601 6387 784CIP2B 711 7749 1029 2815 4601 6387 784CIP2B 712 7748 1029 2816 4606 6392 784CIP2B 712 7767 1039 2815 4601 6387 784CIP2B 712 7767 1031 2817 4603 6389 784CIP2B 713 7767 1032 2818 4604 6390 784CIP2B 713 7767 1033 2819 4605 6391 784CIP2B 713 7769 1034 2824 4610 6396 784CIP2B 713 7769 1035 2811 4607 6393 784CIP2B 713 7769 1031 2817 4603 6389 784CIP2B 713 7769 1032 2818 4604 6390 784CIP2B 713 7769 1033 2819 4605 6391 784CIP2B 713 7769 1034 2823 4609 6395 784CIP2B 713 7769 1035 2821 4604 6396 784CIP2B 713 7769 1036 2822 4608 6394 784CIP2B 722 7767 1037 2823 4609 6395 784CIP2B 722 7767 1037 2823 4609 6396 784CIP2B 723 7781 1038 2824 4610 6396 784CIP2B 723 7781 1040 2826 4611 6397 784CIP2B 733 77624 1041 2823 4618 6404 784CIP2B 73					784CIP2B_689	7647
1005				<u> </u>	784CIP2B_690	7648
1006 2792 4578 6364 784CIP2B_693 7664 1007 2793 4579 6365 784CIP2B_695 7674 1008 2794 4580 6366 784CIP2B_695 7674 1008 2794 4580 6366 784CIP2B_695 7675 1009 2795 4581 6367 784CIP2B_697 7676 1010 2796 4582 6368 784CIP2B_697 7676 1011 2797 4583 6369 784CIP2B_699 7688 1011 2797 4583 6369 784CIP2B_699 7688 1012 2798 4584 6370 784CIP2B_699 7688 1013 2799 4585 6370 784CIP2B_700 7693 1013 2799 4585 6371 784CIP2B_700 7693 1014 2800 4586 6372 784CIP2B_702 7715 1015 2801 4587 6373 784CIP2B_703 7716 1016 2802 4588 6374 784CIP2B_703 7716 1017 2803 4589 6375 784CIP2B_703 7716 1019 2805 4591 6377 784CIP2B_707 7729 1020 2806 4592 6378 784CIP2B_708 7733 1021 2807 4593 6376 784CIP2B_708 7733 1021 2807 4593 6376 784CIP2B_708 7733 1022 2808 4599 6380 784CIP2B_708 7733 1024 2810 4596 6381 784CIP2B_710 7741 1025 2811 4597 6381 784CIP2B_710 7741 1026 2810 4596 6381 784CIP2B_710 7743 1027 2831 4599 6396 784CIP2B_710 7743 1028 2810 4596 6381 784CIP2B_710 7743 1029 2810 4596 6381 784CIP2B_711 7743 1029 2810 4596 6381 784CIP2B_711 7743 1025 2811 4597 6383 784CIP2B_711 7745 1027 2833 4599 6386 784CIP2B_711 7745 1028 2814 4600 6386 784CIP2B_711 7745 1029 2815 4601 6387 784CIP2B_716 7759 1029 2815 4601 6387 784CIP2B_716 7759 1029 2815 4601 6387 784CIP2B_716 7759 1029 2815 4601 6387 784CIP2B_716 7759 1029 2815 4601 6387 784CIP2B_711 7760 1031 2817 4603 6386 784CIP2B_712 7766 1031 2817 4603 6389 784CIP2B_712 7766 1032 2818 4604 6390 784CIP2B_712 7766 1034 2820 4606 6392 784CIP2B_721 7766 1035 2821 4607 6393 784CIP2B_721 7766 1036 2822 4608 6394 784CIP2B_722 7767 1037 2823 4609 6395 784CIP2B_723 7769 1038 2824 4610 6396 784CIP2B_723 7769 1039 2815 4601 6397 784CIP2B_723 7769 1031 2817 4603 6399 784CIP2B_723 7769 1034 2820 4606 6392 784CIP2B_723 7769 1035 2821 4607 6393 784CIP2B_723 7769 1036 2822 4608 6394 784CIP2B_723 7769 1037 2823 4609 6395 784CIP2B_723 7769 1038 2824 4610 6396 784CIP2B_723 7769 1039 2825 4611 6397 784CIP2B_723 7769 1040 2826 4612 6398 784CIP2B_723 7799 1040 2826 4612 6399 784CIP2B_733 7801 1040 2826 4612 6399 784CIP2B_733						7658
1007 2793 4579 6365 784CIP2B-695 7674 1008 2794 4580 5366 784CIP2B-695 7675 1009 2795 4581 6367 784CIP2B-696 7675 1010 2796 4582 6368 784CIP2B-698 7681 1011 2797 4583 6368 784CIP2B-698 7681 1011 2797 4583 6368 784CIP2B-699 7688 1012 2798 4584 6370 784CIP2B-699 7688 1012 2798 4584 6370 784CIP2B-701 7694 1014 2800 4586 6372 784CIP2B-701 7694 1014 2800 4586 6372 784CIP2B-703 7716 1015 2801 4587 6373 784CIP2B-703 7716 1016 2802 4588 6374 784CIP2B-703 7716 1016 2802 4588 6374 784CIP2B-704 7718 1017 2803 4589 6375 784CIP2B-706 7723 1018 2804 4530 6376 784CIP2B-706 7723 1019 2805 4591 6377 784CIP2B-706 7723 1020 2806 4592 6378 784CIP2B-707 7735 1021 2807 4593 6379 784CIP2B-708 7733 1021 2807 4593 6379 784CIP2B-708 7733 1022 2808 4594 6580 784CIP2B-710 7741 1023 2809 4595 6381 784CIP2B-710 7741 1024 2810 4596 6382 784CIP2B-710 7741 1025 2811 4597 6383 784CIP2B-710 7741 1026 2812 4598 6384 784CIP2B-710 7741 1027 2813 4599 6385 784CIP2B-710 7741 1028 2814 4600 6386 784CIP2B-711 7743 1029 2815 4601 6387 784CIP2B-711 7750 1028 2814 4600 6386 784CIP2B-714 7750 1039 2815 4601 6387 784CIP2B-716 7755 1039 2815 4601 6387 784CIP2B-716 7759 1030 2816 4602 6388 784CIP2B-716 7759 1031 2817 4603 6389 784CIP2B-716 7759 1032 2818 4604 6390 784CIP2B-716 7759 1039 2815 4601 6387 784CIP2B-717 7766 1031 2817 4603 6389 784CIP2B-718 7766 1031 2817 4603 6389 784CIP2B-718 7766 1032 2818 4604 6390 784CIP2B-719 7765 1033 2819 4605 6391 784CIP2B-72 7776 1038 2824 4610 6396 784CIP2B-72 7777 1038 2824 4610 6396 784CIP2B-72 7777 1038 2824 4610 6396 784CIP2B-72 7777 1039 2815 4601 6397 784CIP2B-72 7777 1039 2815 4601 6397 784CIP2B-72 7777 1039 2816 4607 6393 784CIP2B-72 7777 1039 2823 4609 6395 784CIP2B-72 7777 1039 2823 4609 6395 784CIP2B-72 7777 1039 2823 4609 6395 784CIP2B-72 7777 1039 2824 4610 6396 784CIP2B-72 7777 1039 2824 4610 6396 784CIP2B-72 7777 1039 2825 4611 6397 784CIP2B-72 7777 1040 2826 4612 6398 784CIP2B-73 7782 1044 2830 4616 6402 784CIP2B-73 7783 1044 2830 4616 6402 784CIP2B-73 7785 1049 2835 4621 6400 784CIP2B-73 7782						7664
1008   2794   4580   6366   784CIP2B_595   7675     1009   2795   4581   6367   784CIP2B_597   7676     1010   2796   4582   6368   784CIP2B_697   7676     1011   2797   4583   6369   784CIP2B_699   7668     1011   2798   4584   6370   784CIP2B_699   7668     1012   2798   4584   6370   784CIP2B_700   7693     1013   2799   4585   6371   784CIP2B_701   7694     1014   2800   4586   6372   784CIP2B_702   7715     1015   2801   4587   6373   784CIP2B_703   7716     1016   2802   4588   6374   784CIP2B_703   7716     1016   2802   4588   6374   784CIP2B_704   7718     1017   2803   4589   6376   784CIP2B_705   7723     1018   2804   4589   6376   784CIP2B_705   7723     1019   2805   4581   6377   784CIP2B_706   7723     1020   2806   4592   6378   784CIP2B_707   7733     1021   2807   4593   6379   784CIP2B_709   7733     1022   2808   4594   6380   784CIP2B_709   7735     1023   2809   4595   6381   784CIP2B_709   7741     1024   2810   4596   6382   784CIP2B_710   7741     1025   2811   4597   6383   784CIP2B_712   7748     1026   2812   4598   6384   784CIP2B_713   7745     1027   2813   4599   6385   784CIP2B_713   7745     1029   2815   4601   6387   784CIP2B_713   7750     1030   2816   4602   6388   784CIP2B_713   7760     1031   2817   4603   6387   784CIP2B_715   7766     1031   2817   4603   6395   784CIP2B_716   7759     1032   2818   4604   6390   784CIP2B_717   7766     1034   2820   4606   6392   784CIP2B_717   7766     1035   2821   4607   6393   784CIP2B_717   7766     1036   2822   4608   6395   784CIP2B_717   7767     1039   2825   4611   6396   784CIP2B_718   7767     1039   2825   4611   6396   784CIP2B_718   7767     1039   2825   4611   6397   784CIP2B_723   7769     1031   2821   4607   6393   784CIP2B_723   7769     1032   2828   4614   6400   784CIP2B_723   7769     1034   2820   4606   6392   784CIP2B_723   7769     1035   2821   4607   6393   784CIP2B_723   7769     1040   2826   4612   6398   784CIP2B_723   7769     1040   2826   4612   6398   784CIP2B_733   7892     1041   2823   46				1	L	1
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1118	2904	4690	6476	784CIP2B_807	8046
1119	2905	4691	6477	784CIP2B_808	8047
1120	2906	4692	6478	784CIP2B_809	8051
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1172	2956 2957 2958	4742 4743 4744	6528 . 6529 6530	784CIP2B_859	
1172 1173	2956 2957 2958 2959	4742 4743 4744 4745	6528 . 6529 . 6530 . 6531	784CIP2B_859 784CIP2B_860 784CIP2B_861 784CIP2B_862	8209 8211 8214
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1356	3142	4928	6714	784CIP2B_1046	9435
1357	3143	4929	6715	784CIP2B_1047	9437
1358	3144	4930	6716	784CIP2B_1048	9469
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1392	3177	4963	6749	784CIP2B_1081	9916
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1398	3184	4970	6756	784CIP2B_1087 784CIP2B_1088	9959
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1407	3193	4979	6765	784CIP2B_1098	10132
1408	3194	4980	6766	784CIP2B_1099	10169
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1420	3205	4992	6777	784CIP2C_6	953
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of full-	NO: of	of contig	NO:	Priority docket number	SEQ ID
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sequence	peptide	beguessee	sequence	priority	09/400,725
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nucleotide   length   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence	length	full-				
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1490   3275   5062   5648   784CIP2C 75   3381     1491   3277   5063   5849   784CIP2C 80   3383     1492   3278   5064   6850   784CIP2C 81   4295     1493   3279   5065   5651   784CIP2C 82   4360     1494   3280   5066   6852   784CIP2C 82   4360     1495   3281   5067   6853   784CIP2C 84   4362     1496   3282   5068   6854   784CIP2C 85   4371     1497   3223   5069   6855   784CIP2C 86   4373     1498   3284   5070   6856   784CIP2C 86   4373     1499   3285   5071   6857   784CIP2C 86   4376     1499   3285   5071   6857   784CIP2C 89   4378     1500   3286   5072   6658   784CIP2C 80   4382     1501   3287   5073   6659   784CIP2C 81     1503   3289   5074   6860   784CIP2C 81     1504   3290   5076   6866   784CIP2C 92   4421     1505   3281   5077   6863   784CIP2C 93   4421     1506   3292   5078   6864   784CIP2C 93   4421     1507   3293   5079   6865   784CIP2C 94   4426     1508   3291   5077   6863   784CIP2C 95   4430     1509   3294   5080   6866   784CIP2C 95   4430     1509   3295   5077   6863   784CIP2C 97   4436     1509   3291   5077   6865   784CIP2C 98   4435     1509   3294   5080   6866   784CIP2C 98   4435     1509   3295   5081   6867   784CIP2C 98   4435     1501   3297   5083   6866   784CIP2C 98   4436     1511   3297   5083   6866   784CIP2C 98   4436     1511   3297   5083   6869   784CIP2C 100   4441     1512   3298   5084   6870   784CIP2C 101     1441   3300   5086   6868   784CIP2C 102   4456     1518   3301   5087   6868   784CIP2C 103   4466     1519   3303   5089   6871   784CIP2C 103   4465     1518   3304   5096   6886   784CIP2C 104   4466     1519   3303   5089   6872   784CIP2C 105     1481   3300   5086   6882   784CIP2C 105     1481   3300   5086   6882   784CIP2C 105     1481   3300   5086   6882   784CIP2C 105     1524   3310   5087   6883   784CIP2C 105     1524   3310   5087   6883   784CIP2C 105     1524   3310   5096   6882   784CIP2C 114     1525   3311   5087   6883   784CIP2C 115     1526   3312   5098   6886   784CIP2C 115     1527   3313   5099   6		<u> </u>	5060	6846	784CIP2C_77	3935
1491   3277   5063   5645   784CTP2C   80   3388   1492   3278   5064   6850   784CTP2C   81   4295   1493   3279   5065   6851   784CTP2C   82   4360   1494   3280   5066   6852   784CTP2C   83   4362   1495   3281   5367   6853   784CTP2C   84   4362   1496   3282   5068   6654   784CTP2C   87   4376   1497   3223   5069   6855   784CTP2C   87   4376   1497   3223   5069   6855   784CTP2C   87   4376   1498   3284   5070   6856   784CTP2C   87   4376   1498   3284   5070   6856   784CTP2C   87   4376   1499   3285   5071   6857   784CTP2C   87   4376   1499   3285   5071   6857   784CTP2C   87   4376   1500   3286   5072   6858   784CTP2C   87   4376   1500   3286   5072   6858   784CTP2C   90   4378   1500   3287   5073   6859   784CTP2C   90   4421   1504   3290   5076   6862   784CTP2C   92   4421   1504   3290   5076   6862   784CTP2C   95   4430   1506   3292   5078   6864   784CTP2C   95   4430   1506   3292   5078   6864   784CTP2C   95   4430   1506   3292   5078   6864   784CTP2C   97   4440   1500   3296   5082   6866   784CTP2C   98   4435   1500   3295   5081   6867   784CTP2C   99   4440   1511   3297   5083   6866   784CTP2C   99   4440   1511   3297   5083   6866   784CTP2C   99   4440   1511   3297   5083   6866   784CTP2C   99   4440   1511   3297   5083   6867   784CTP2C   100   4441   1511   3297   5083   6867   784CTP2C   100   4441   1511   3297   5083   6869   784CTP2C   100   4441   1511   3303   5085   6871   784CTP2C   102   4455   1513   3301   5087   6873   784CTP2C   102   4455   1513   3301   5087   6873   784CTP2C   102   4456   1515   3301   5087   6873   784CTP2C   102   4456   1515   3301   5087   6873   784CTP2C   102   4456   1515   3301   5087   6873   784CTP2C   102   4456   1515   3301   5087   6873   784CTP2C   102   4466   1515   3301   5087   6873   784CTP2C   102   4456   1515   3301   5087   6883   784CTP2C   103   4466   1515   3301   5087   6883   784CTP2C   103   4466   1515   3301   5087   6883   784CTP2C   104   4466   1515   3301   5095   6882   784CTP2C   10			5061	6847	784CIP2C_78	3959
1492   3278   \$064   6850   784CIP2C 81   4295     1494   3280   5065   6851   784CIP2C 82   4300     1494   3280   5065   6851   784CIP2C 82   4360     1495   3281   5067   6853   784CIP2C 84   4362     1496   3282   5068   6854   784CIP2C 84   4362     1497   3283   5069   6855   784CIP2C 86   4371     1497   3283   5069   6855   784CIP2C 86   4373     1498   3284   5070   6856   784CIP2C 86   4373     1499   3285   5071   6857   784CIP2C 89   4378     1500   3286   5072   6858   784CIP2C 99   4378     1501   3287   5073   6859   784CIP2C 99   4378     1502   3288   5074   6850   784CIP2C 91   4409     1503   3289   5075   6861   784CIP2C 93   4421     1503   3289   5075   6861   784CIP2C 93   4421     1504   3290   5076   6862   784CIP2C 93   4421     1505   3291   5077   6863   784CIP2C 94   4426     1506   3292   5078   6864   784CIP2C 95   4430     1507   3293   5079   6865   784CIP2C 96   4335     1508   3294   5080   6866   784CIP2C 98   4436     1510   3285   5081   6867   784CIP2C 99   4440     1511   3297   5083   6866   784CIP2C 98   4439     1509   3295   5081   6867   784CIP2C 99   4440     1511   3297   5083   6869   784CIP2C 90   4441     1511   3298   5084   6870   784CIP2C 100   4441     1511   3298   5084   6870   784CIP2C 101   4442     1513   3298   5084   6870   784CIP2C 101   4442     1514   3300   5086   6873   784CIP2C 101   4442     1515   3298   5084   6870   784CIP2C 101   4466     1516   3302   5089   6871   784CIP2C 104   4466     1517   3303   5089   6873   784CIP2C 106   4479     1517   3303   5089   6873   784CIP2C 107   4481     1519   3305   5095   6878   784CIP2C 107   4481     1519   3306   5095   6878   784CIP2C 107   4481     1520   3306   5095   6878   784CIP2C 107   4481     1521   3307   5093   6879   784CIP2C 107     1524   3310   5095   6885   784CIP2C 110   4486     1521   3307   5093   6879   784CIP2C 110     1522   3308   5094   6880   784CIP2C 110     1524   3310   5095   6885   784CIP2C 110     1526   3312   5098   6897   784CIP2C 110     1528   3314   5100   6		1	5062	6848	784CIP2C_79	3981
1493 3279 5065 6851 784CIP2C 82 4300 1494 3280 5066 6852 784CIP2C 83 4360 1495 3281 5067 6853 784CIP2C 83 4362 1496 3282 5068 6854 784CIP2C 85 4371 1497 3283 5069 6855 784CIP2C 86 4373 1498 3284 5070 6856 784CIP2C 87 4376 1498 3284 5070 6856 784CIP2C 87 4376 1498 3285 5071 6857 784CIP2C 87 4376 1500 3286 5072 6858 784CIP2C 90 4382 1501 3287 5073 6859 784CIP2C 91 4409 1502 3288 5074 6860 784CIP2C 93 4378 1503 3289 5075 6861 784CIP2C 93 4421 1503 3289 5076 6862 784CIP2C 93 4421 1504 3290 5076 6862 784CIP2C 93 4421 1505 3291 5077 6863 784CIP2C 93 4421 1506 3292 5078 6864 784CIP2C 93 4426 1507 3293 5079 6865 784CIP2C 94 4435 1509 3295 5076 6866 784CIP2C 95 4430 1509 3295 5076 6866 784CIP2C 95 4430 1509 3295 5076 6866 784CIP2C 96 4435 1501 3297 5080 6866 784CIP2C 97 4436 1509 3295 5080 6866 784CIP2C 97 4436 1509 3295 5080 6866 784CIP2C 98 4439 1509 3295 5081 6867 784CIP2C 99 4440 1511 3297 5083 6869 784CIP2C 99 4440 1511 3297 5083 6869 784CIP2C 99 4440 1511 3297 5083 6869 784CIP2C 99 4440 1511 3297 5083 6869 784CIP2C 99 4440 1511 3297 5083 6869 784CIP2C 99 4440 1511 3297 5083 6869 784CIP2C 99 4440 1511 3297 5083 6869 784CIP2C 99 4440 1511 3297 5083 6869 784CIP2C 99 4440 1511 3297 5083 6869 784CIP2C 99 4440 1511 3297 5083 6869 784CIP2C 99 4440 1511 3297 5083 6869 784CIP2C 99 4440 1512 3298 5084 6870 784CIP2C 100 4441 1513 3299 5085 6871 784CIP2C 101 4442 1514 3300 5086 6872 784CIP2C 101 4442 1519 3305 5089 6873 784CIP2C 101 4481 1519 3305 5089 6874 784CIP2C 101 4481 1519 3305 5089 6875 784CIP2C 101 4481 1519 3305 5089 6877 784CIP2C 101 4481 1523 3309 5085 6881 784CIP2C 110 4481 1524 3310 5096 6882 784CIP2C 110 4481 1523 3309 5085 6891 784CIP2C 110 4481 1524 3310 5096 6882 784CIP2C 110 4481 1523 3309 5085 6878 784CIP2C 110 4481 1524 3310 5096 6882 784CIP2C 110 4485 1526 3311 5097 6883 784CIP2C 110 4485 1526 3311 5097 6883 784CIP2C 110 4485 1526 3311 5097 6883 784CIP2C 110 4485 1528 3311 5097 6883 784CIP2C 110 4485 1528 3311 5097 6889 784CIP2C 110 4485 1528 3311 5096 6889 784CIP2C 110 4485 1528 3311 5096 6889 784CIP2C			5063	6849	784CIP2C_80	3989
1494   3280   5066   6852   784CIP2C   83   4360     1495   3281   5067   6853   784CIP2C   84   4362     1496   3282   5068   6854   784CIP2C   86   4371     1497   3283   5069   6855   784CIP2C   86   4373     1498   3284   5070   6856   784CIP2C   86   4373     1499   3285   5071   6857   784CIP2C   89   4378     1500   3286   5072   6858   784CIP2C   99   4378     1501   3287   5073   6859   784CIP2C   90   4382     1501   3287   5073   6859   784CIP2C   91   4409     1502   3288   5074   6860   784CIP2C   92   4421     1503   3289   5075   6861   784CIP2C   92   4421     1504   3290   5076   6862   784CIP2C   94   4426     1505   3291   5077   6863   784CIP2C   94   4426     1506   3292   5078   6864   784CIP2C   96   4435     1507   3293   5079   6865   784CIP2C   97   4436     1508   3294   5080   6866   784CIP2C   98   4439     1509   3295   5081   6867   784CIP2C   99   4440     1511   3297   5083   6869   784CIP2C   99   4440     1511   3297   5083   6869   784CIP2C   99   4440     1512   3298   5084   6870   784CIP2C   101   4442     1513   3299   5085   6867   784CIP2C   101   4442     1514   3300   5086   6872   784CIP2C   102   4455     1515   3301   5087   6869   784CIP2C   103   4462     1516   3302   5088   6877   784CIP2C   104   4466     1516   3302   5088   6877   784CIP2C   104   4466     1516   3302   5088   6877   784CIP2C   107   4481     1518   3304   5090   6876   784CIP2C   108   4483     1520   3306   5095   6876   784CIP2C   108   4483     1521   3307   5093   6879   784CIP2C   107   4481     1521   3307   5093   6879   784CIP2C   107   4481     1522   3308   5095   6876   784CIP2C   108   4483     1523   3309   5095   6881   784CIP2C   108   4483     1524   3310   5096   6882   784CIP2C   108   4483     1524   3310   5096   6882   784CIP2C   108     1525   3311   5097   6883   784CIP2C   115     1526   3312   5098   6884   784CIP2C   115     1526   3314   5100   6886   784CIP2C   115     1527   3313   5101   6897   784CIP2C   115     1531   3317   5103   6899   784CIP2C   125   4		1.	5064	6850	784CIP2C_81	4295
1495 3281 5367 6853 784CIP2C_84 4362 1496 3282 5068 6854 784CIP2C_85 4371 1497 3283 5069 6855 784CIP2C_86 4373 1498 3284 5070 6856 784CIP2C_87 4376 1498 3285 5071 6857 784CIP2C_87 4376 1499 3285 5071 6857 784CIP2C_87 4376 1500 3286 5072 6858 784CIP2C_90 4382 1501 3287 5073 6859 784CIP2C_90 4382 1502 3288 5074 6860 784CIP2C_92 4421 1503 3289 5075 6861 784CIP2C_92 4421 1504 3290 5076 6862 784CIP2C_92 4421 1505 3291 5077 6863 784CIP2C_94 4426 1505 3291 5077 6863 784CIP2C_95 4430 1506 3292 5078 6864 784CIP2C_95 4430 1507 3293 5079 6865 784CIP2C_95 4430 1508 3294 5080 6866 784CIP2C_98 4435 1509 3295 5081 6866 784CIP2C_98 4436 1510 3296 5082 6866 784CIP2C_98 4430 1510 3296 5082 6868 784CIP2C_98 4440 1511 3297 5083 6869 784CIP2C_98 4440 1512 3298 5084 6870 784CIP2C_100 4441 1511 3297 5083 6869 784CIP2C_101 4442 1512 3298 5084 6870 784CIP2C_101 4442 1513 3299 5085 6871 784CIP2C_102 4455 1514 3300 5086 6872 784CIP2C_103 4466 1516 3302 5088 6874 784CIP2C_103 4466 1517 3303 5089 6873 784CIP2C_104 4466 1518 3304 5090 6877 784CIP2C_103 4466 1519 3305 5080 6877 784CIP2C_103 4466 1516 3302 5088 6874 784CIP2C_104 4481 1519 3303 5089 6873 784CIP2C_104 4469 1510 3296 5082 6888 784CIP2C_108 4481 1511 3307 5083 6897 784CIP2C_108 4481 1512 3298 5084 6870 784CIP2C_108 4481 1513 3303 5089 6873 784CIP2C_108 4481 1514 3300 5086 6872 784CIP2C_108 4481 1515 3303 5089 6874 784CIP2C_108 4481 1516 3302 5088 6874 784CIP2C_108 4481 1517 3303 5089 6878 784CIP2C_108 4481 1520 3306 5092 6878 784CIP2C_108 4481 1521 3307 5093 6889 784CIP2C_110 4486 1521 3307 5095 6881 784CIP2C_111 4499 1522 3308 5094 6880 784CIP2C_111 4499 1522 3308 5094 6880 784CIP2C_112 4499 1523 3319 5095 6881 784CIP2C_113 4506 1524 3311 5097 6883 784CIP2C_114 4596 1524 3312 5098 6884 784CIP2C_114 4596 1526 3312 5098 6884 784CIP2C_114 4596 1527 3313 5099 6885 784CIP2C_114 4596 1528 3314 5100 6886 784CIP2C_124 4591 1533 3319 5105 6891 784CIP2C_124 4591 1534 3320 55106 6892 784CIP2C_124 4559 1539 3315 5101 6897 784CIP2C_124 4559 1539 3315 5101 6899 784CIP2C_124 4559 1539 3315 510	1	1	5065	6851	784CIP2C_82	4300
1496   3282   5068   6854   784CIP2C   85   4371     1497   3283   5069   6855   784CIP2C   86   4373     1498   3284   5070   6856   784CIP2C   87   4376     1499   3285   5071   6857   784CIP2C   89   4378     1500   3286   5072   6858   784CIP2C   89   4378     1501   3287   5073   6859   784CIP2C   91   4409     1502   3288   5074   6860   784CIP2C   92   4421     1503   3288   5075   6861   784CIP2C   92   4421     1504   3290   5076   6862   784CIP2C   94   4426     1505   3291   5077   6863   784CIP2C   94   4426     1506   3292   5078   6864   784CIP2C   96   4435     1507   3293   5079   6865   784CIP2C   96   4435     1508   3294   5080   6866   784CIP2C   97   4436     1509   3295   5081   6867   784CIP2C   99   4440     1510   3296   5082   6868   784CIP2C   99   4440     1511   3297   5083   6869   784CIP2C   99   4440     1512   3298   5084   6869   784CIP2C   101   4442     1513   3299   5086   6869   784CIP2C   101   4442     1514   3300   5086   6877   784CIP2C   101   4442     1515   3301   5087   6869   784CIP2C   102   4466     1515   3301   5087   6873   784CIP2C   102   4466     1516   3302   5088   6871   784CIP2C   103   4466     1517   3303   5089   6874   784CIP2C   104   4466     1518   3304   5090   6876   784CIP2C   104   4466     1519   3305   5081   6867   784CIP2C   104   4466     1510   3305   5089   6874   784CIP2C   104   4466     1512   3309   5088   6874   784CIP2C   104   4466     1513   3301   5087   6873   784CIP2C   104   4466     1514   3300   5086   6877   784CIP2C   104   4466     1515   3301   5087   6873   784CIP2C   107   4481     1519   3305   5091   6876   784CIP2C   108   4483     1520   3306   5095   6876   784CIP2C   107   4481     1521   3307   5093   6876   784CIP2C   107   4481     1522   3308   5095   6876   784CIP2C   107   4481     1523   3311   5097   6883   784CIP2C   116     1524   3312   5098   6884   784CIP2C   116     1526   3314   5100   6886   784CIP2C   116     1526   3314   5100   6886   784CIP2C   120     1523   3318   5101   6897   784CIP2C			L	6852		4360
1497   3283   5069   6555   764CIP2C_86   4373     1498   3284   5070   6556   764CIP2C_87   3376     1499   3285   5071   6557   764CIP2C_87   3376     1500   3286   5072   6558   764CIP2C_90   4382     1501   3287   5073   6659   764CIP2C_92   4421     1502   3288   5074   6860   784CIP2C_93   4421     1503   3289   5075   6661   784CIP2C_93   4421     1504   3290   5076   6682   784CIP2C_93   4421     1505   3291   5077   6663   764CIP2C_95   4430     1506   3292   5078   6664   764CIP2C_95   4430     1507   3293   5079   6664   764CIP2C_95   4430     1508   3294   5080   6666   784CIP2C_98   4439     1510   3296   5082   6666   784CIP2C_98   4439     1511   3297   5083   6666   784CIP2C_98   4439     1512   3298   5084   6670   784CIP2C_100   4441     1511   3297   5083   6668   784CIP2C_100   4441     1514   3300   5086   6671   784CIP2C_102   4455     1515   3301   5087   6673   784CIP2C_103   4466     1516   3300   5086   6672   784CIP2C_103   4466     1517   3303   5089   6675   784CIP2C_105   4469     1518   3304   5080   6670   784CIP2C_105   4469     1519   3305   5087   6673   784CIP2C_105   4469     1519   3305   5087   6673   784CIP2C_105   4469     1519   3305   5091   6676   784CIP2C_106   4481     1519   3305   5091   6677   784CIP2C_107   4481     1520   3306   5092   6678   784CIP2C_108   4483     1521   3307   5093   6676   784CIP2C_108   4483     1520   3306   5092   6678   784CIP2C_108   4483     1521   3307   5093   6676   784CIP2C_108   4483     1521   3307   5093   6676   784CIP2C_108   4483     1521   3307   5093   6676   784CIP2C_108   4483     1521   3307   5093   6676   784CIP2C_110   4486     1521   3307   5093   6676   784CIP2C_110   4486     1521   3307   5093   6676   784CIP2C_111   4499     1522   3308   5094   6880   784CIP2C_112   4499     1523   3311   5097   6681   784CIP2C_121   4596     1526   3311   5097   6683   784CIP2C_112   4593     1536   3322   5108   6694   784CIP2C_122   4529     1531   3315   5101   6897   784CIP2C_122   4529     1531   3315   5101   6897   78		1	1	6853	784CIP2C_84	4362
1498   3284   5070   6856   784CIPZC_87   4376     1499   3285   5071   6857   784CIPZC_89   4378     1500   3286   5072   6858   784CIPZC_90   4382     1501   3287   5073   6859   784CIPZC_91   4409     1502   3288   5074   6850   784CIPZC_92   4421     1503   3289   5075   6861   784CIPZC_93   4421     1504   3290   5076   6862   784CIPZC_93   4421     1505   3291   5077   6863   784CIPZC_94   4426     1506   3292   5078   6864   784CIPZC_96   4435     1506   3292   5078   6864   784CIPZC_96   4435     1508   3294   5080   6866   784CIPZC_97   4436     1508   3294   5080   6866   784CIPZC_99   4440     1510   3296   5082   6868   784CIPZC_99   4440     1511   3297   5083   6869   784CIPZC_99   4440     1511   3297   5083   6869   784CIPZC_101   4442     1512   3298   5084   6870   784CIPZC_102   4466     1513   3299   5086   6872   784CIPZC_102   4466     1516   3300   5086   6872   784CIPZC_104   4466     1516   3301   5087   6873   784CIPZC_106   4477     1517   3303   5089   6875   784CIPZC_107   4481     1518   3304   5090   6877   784CIPZC_108   4481     1519   3305   5091   6877   784CIPZC_107   4481     1519   3305   5091   6877   784CIPZC_108   4481     1520   3306   5092   6878   784CIPZC_109   4484     1521   3307   5093   6879   784CIPZC_107   4481     1522   3308   5094   6880   784CIPZC_109   4484     1523   3309   5095   6877   784CIPZC_101   4499     1523   3309   5095   6879   784CIPZC_111   4490     1524   3310   5096   6887   784CIPZC_111   4490     1525   3311   5097   6883   784CIPZC_111   4490     1528   3314   5100   6886   784CIPZC_112   4499     1529   3316   5092   6878   784CIPZC_114   4506     1526   3312   5098   6887   784CIPZC_114   4506     1526   3312   5098   6887   784CIPZC_114   4506     1526   3312   5098   6887   784CIPZC_114   4506     1526   3315   5000   6886   784CIPZC_114   4506     1526   3311   5097   6883   784CIPZC_114   4508     1526   3312   5098   6884   784CIPZC_117   4516     1526   3315   5000   6886   784CIPZC_121   4528     1531   3317   5103   6899   78		l		<del></del>		4371
1499   3285   5071   6857   784CIP2C 89   4378     1500   3286   5072   6858   784CIP2C 90   4382     1501   3287   5073   6859   784CIP2C 91   4409     1502   3288   5074   6860   784CIP2C 92   4421     1503   3289   5075   6861   784CIP2C 93   4421     1504   3290   5076   6862   784CIP2C 93   4421     1505   3291   5077   6863   784CIP2C 93   4421     1506   3292   5078   6864   784CIP2C 95   4430     1507   3293   5079   6865   784CIP2C 97   4436     1508   3294   5080   6866   784CIP2C 98   4439     1509   3295   5081   6867   784CIP2C 98   4439     1510   3296   5082   6868   784CIP2C 98   4449     1511   3297   5083   6866   784CIP2C 100   4441     1511   3297   5083   6867   784CIP2C 102   4455     1514   3300   5086   6872   784CIP2C 103   4466     1514   3300   5086   6872   784CIP2C 103   4466     1516   3329   5088   6871   784CIP2C 105   4469     1516   3302   5088   6874   784CIP2C 107   4481     1519   3303   5089   6875   784CIP2C 107   4481     1519   3305   5089   6876   784CIP2C 107   4481     1519   3305   5091   6877   784CIP2C 107   4481     1519   3305   5091   6877   784CIP2C 108   4469     1520   3306   5092   6878   784CIP2C 107   4481     1521   3307   5093   6876   784CIP2C 108   4483     1522   3308   5094   6880   784CIP2C 108   4483     1523   3309   5095   6878   784CIP2C 108   4483     1524   3310   5096   6876   784CIP2C 108   4486     1521   3307   5093   6876   784CIP2C 108   4486     1522   3308   5094   6880   784CIP2C 110   4486     1523   3309   5095   6881   784CIP2C 110   4486     1524   3310   5096   6882   784CIP2C 110   4486     1523   3307   5093   6877   784CIP2C 110   4486     1524   3310   5096   6882   784CIP2C 110   4486     1523   3308   5094   6880   784CIP2C 110   4486     1524   3310   5096   6882   784CIP2C 110   4486     1526   3311   5097   6883   784CIP2C 115   4509     1526   3311   5097   6883   784CIP2C 115   4509     1526   3311   5097   6883   784CIP2C 120   4527     1531   3317   5103   6896   784CIP2C 122   4529     1531   3317   5103   6896				.1		4373
1500   3286   5072   6858   784CIP2C 90   4382     1501   3287   5073   6859   784CIP2C 91   4409     1502   3288   5074   6860   784CIP2C 92   4421     1503   3289   5075   6861   784CIP2C 93   4421     1504   3290   5076   6862   784CIP2C 95   4430     1505   3291   5077   6863   784CIP2C 95   4430     1506   3292   5078   6864   784CIP2C 96   4435     1507   3293   5079   6865   784CIP2C 97   4436     1508   3294   5080   6866   784CIP2C 97   4436     1509   3295   5081   6867   784CIP2C 98   4439     1500   3295   5081   6867   784CIP2C 99   4440     1510   3296   5082   6868   784CIP2C 99   4440     1511   3297   5083   6869   784CIP2C 100   4441     1512   3298   5084   6870   784CIP2C 101   4442     1513   3299   5085   6971   784CIP2C 102   4455     1514   3300   5086   6872   784CIP2C 103   4462     1515   3301   5087   6873   784CIP2C 104   4466     1516   3302   5088   6874   784CIP2C 105   4469     1517   3303   5089   6875   784CIP2C 109   4481     1518   3304   5090   6876   784CIP2C 100   4481     1519   3305   5091   6877   784CIP2C 101   4481     1520   3308   5091   6877   784CIP2C 101   4481     1521   3309   5085   6871   784CIP2C 104   4466     1521   3301   5087   6873   784CIP2C 105   4469     1516   3302   5088   6874   784CIP2C 107   4481     1529   3305   5091   6877   784CIP2C 101   4486     1520   3306   5092   6878   784CIP2C 101   4486     1521   3307   5093   6879   784CIP2C 110   4486     1521   3307   5093   6879   784CIP2C 111   4490     1522   3311   5097   6881   784CIP2C 115   4503     1526   3312   5098   6882   784CIP2C 115   4503     1526   3312   5098   6881   784CIP2C 115   4503     1526   3313   5099   6885   784CIP2C 114   4506     1528   3314   5100   6886   784CIP2C 115   4528     1530   3316   5102   6888   784CIP2C 115   4528     1531   3317   5103   6899   784CIP2C 124   4537     1536   3322   5108   6894   784CIP2C 127   4528     1536   3322   5108   6894   784CIP2C 120   4557     1536   3326   5106   6892   784CIP2C 123   4532     1536   3326   5106   6895					· —	4376
1501   3287   5073   6859   784CIP2C   51   4409     1503   3288   5074   6860   784CIP2C   52   4421     1503   3289   5075   6861   784CIP2C   53   4421     1504   3290   5076   6862   784CIP2C   54   4426     1505   3291   5077   6863   784CIP2C   54   4426     1506   3292   5078   6864   784CIP2C   56   4435     1507   3293   5079   6865   784CIP2C   56   4435     1508   3294   5080   6866   784CIP2C   57   4436     1509   3295   5081   6867   784CIP2C   59   4440     1510   3296   5082   6868   784CIP2C   59   4440     1511   3297   5083   6867   784CIP2C   69   4441     1511   3297   5083   6869   784CIP2C   101   4442     1512   3298   5084   6870   784CIP2C   101   4442     1514   3300   5086   6872   784CIP2C   102   4455     1515   3301   5087   6873   784CIP2C   104   4466     1516   3302   5088   6873   784CIP2C   104   4466     1516   3302   5088   6873   784CIP2C   104   4466     1518   3304   5090   6876   784CIP2C   107   4481     1519   3305   5091   6877   784CIP2C   107   4481     1520   3306   5092   6378   784CIP2C   109   4484     1520   3306   5092   6378   784CIP2C   109   4484     1521   3307   5093   6379   784CIP2C   101   4486     1521   3307   5093   6379   784CIP2C   107   4481     1522   3308   5094   6880   784CIP2C   107   4481     1520   3306   5092   6378   784CIP2C   108   4488     1521   3307   5093   6379   784CIP2C   111   4490     1522   3308   5094   6880   784CIP2C   114   4506     1523   3309   5095   6881   784CIP2C   114   4506     1524   3310   5096   6882   784CIP2C   114   4506     1525   3311   5097   6883   784CIP2C   115   4509     1526   3312   5098   6884   784CIP2C   114   4506     1526   3312   5098   6884   784CIP2C   114   4506     1527   3313   5099   6885   784CIP2C   114   4506     1528   3314   5100   6886   784CIP2C   115   4509     1530   3316   5102   6888   784CIP2C   115   4509     1531   3317   5103   6889   784CIP2C   127   4512     1531   3317   5103   6889   784CIP2C   127   4512     1533   3319   5106   6892   784CIP2C   128   4557     153		<u>.                                      </u>	L	I		1
1502   3288   5074   6880   784CIP2C_52   4421   1503   3289   5075   6861   784CIP2C_93   4421   1504   3290   5076   6862   784CIP2C_94   4426   1505   3291   5077   6863   784CIP2C_95   4430   1506   3292   5078   6864   784CIP2C_95   4430   1507   3293   5079   6865   784CIP2C_96   4435   1507   3293   5079   6865   784CIP2C_97   4436   1508   3294   5080   6866   784CIP2C_97   4436   1509   3295   5081   6867   784CIP2C_98   4439   1500   3296   5082   6868   784CIP2C_99   4440   1510   3296   5082   6868   784CIP2C_100   4441   1511   3297   5083   6869   784CIP2C_101   4442   1511   3298   5084   6870   784CIP2C_102   4455   1513   3298   5084   6870   784CIP2C_103   4462   1514   3300   5086   6872   784CIP2C_103   4462   1515   3301   5087   6873   784CIP2C_104   4466   1516   3302   5088   6874   784CIP2C_105   4469   1518   3304   5090   6876   784CIP2C_106   4477   1518   3304   5090   6876   784CIP2C_109   4481   1520   3306   5092   6875   784CIP2C_109   4484   1521   3307   5093   6877   784CIP2C_109   4484   1521   3307   5093   6877   784CIP2C_109   4484   1521   3307   5093   6877   784CIP2C_109   4484   1521   3307   5093   6877   784CIP2C_109   4484   1521   3307   5093   6877   784CIP2C_110   4486   1522   3308   5094   6880   784CIP2C_111   4490   1522   3308   5094   6880   784CIP2C_112   4499   1523   3311   5096   6882   784CIP2C_113   4506   1526   3312   5098   6881   784CIP2C_115   4506   1527   3313   5099   6885   784CIP2C_116   4514   1528   3314   5100   6886   784CIP2C_116   4528   1529   3315   5101   6887   784CIP2C_120   4527   1530   3316   5102   6888   784CIP2C_121   4528   1529   3315   5101   6887   784CIP2C_121   4528   1530   3316   5102   6888   784CIP2C_121   4528   1531   3317   5103   6889   784CIP2C_121   4528   1533   3319   5105   6891   784CIP2C_122   4529   1533   3319   5105   6891   784CIP2C_122   4529   1538   3324   5110   6896   784CIP2C_123   4525   1539   3325   5111   6897   784CIP2C_123   4555   1542   3328   5114   6900   784CIP2C_133   4552				L		
1503   3289   5075   6861   784CIP2C_93   4421     1504   3290   5076   6862   784CIP2C_94   4426     1505   3291   5077   6863   784CIP2C_95   4430     1506   3292   5078   6864   784CIP2C_95   4435     1507   3293   5079   6865   784CIP2C_96   4435     1508   3294   5080   6866   784CIP2C_97   4436     1509   3295   5081   6867   784CIP2C_98   4439     1509   3295   5081   6867   784CIP2C_98   4439     1510   3296   5082   6868   784CIP2C_99   4440     1511   3297   5083   6869   784CIP2C_100   4441     1512   3298   5084   6870   784CIP2C_101   4442     1513   3299   5085   6971   784CIP2C_102   4455     1514   3300   5086   6872   784CIP2C_104   4466     1516   3302   5588   6874   784CIP2C_105   4469     1516   3302   5588   6874   784CIP2C_105   4469     1517   3303   5089   6875   784CIP2C_106   4477     1518   3304   5090   6076   784CIP2C_109   4481     1520   3306   5092   6878   784CIP2C_109   4486     1520   3306   5092   6878   784CIP2C_109   4486     1521   3307   5093   6877   784CIP2C_101   4496     1522   3308   5094   6880   784CIP2C_110   4486     1523   3309   5095   6878   784CIP2C_110   4486     1524   3310   5096   6882   784CIP2C_111   4490     1525   3311   5097   6883   784CIP2C_112   4499     1526   3312   5098   6884   784CIP2C_115   4506     1528   3314   5100   6886   784CIP2C_116   4514     1528   3314   5100   6886   784CIP2C_117   4516     1528   3315   5101   6887   784CIP2C_121   4528     1530   3316   5102   6888   784CIP2C_121   4528     1531   3307   5103   6889   784CIP2C_121   4528     1533   3319   5104   6890   784CIP2C_122   4539     1536   3322   5106   6892   784CIP2C_123   4532     1536   3322   5106   6892   784CIP2C_124   4537     1539   3325   5106   6892   784CIP2C_124   4537     1531   3327   5103   6899   784CIP2C_124   4537     1534   3320   5106   6892   784CIP2C_124   4537     1535   3321   5107   6893   784CIP2C_124   4537     1536   3322   5106   6892   784CIP2C_123   4532     1537   3323   5106   6896   784CIP2C_124   4537     1539   3326   5114   6896						
1504   3290   5076   6862   784CIP2C_94   4426     1505   3291   5077   6863   784CIP2C_95   4430     1506   3292   5078   6864   784CIP2C_96   6435     1507   3293   5079   6865   784CIP2C_97   4436     1508   3294   5080   6866   784CIP2C_98   4439     1509   3295   5081   6867   784CIP2C_99   4440     1510   3296   5082   6868   784CIP2C_100   4441     1511   3297   5083   6869   784CIP2C_100   4441     1512   3298   5084   6870   784CIP2C_101   4442     1513   3299   5085   6871   784CIP2C_102   4455     1514   3300   5086   6872   784CIP2C_103   4462     1515   3301   5087   6873   784CIP2C_105   4469     1516   3302   5088   6874   784CIP2C_106   4477     1518   3304   5089   6875   784CIP2C_106   4477     1519   3305   5091   6877   784CIP2C_109   4484     1519   3305   5091   6877   784CIP2C_109   4486     1521   3307   5093   6878   784CIP2C_109   4486     1522   3308   5094   6880   784CIP2C_110   4486     1522   3308   5094   6880   784CIP2C_110   4486     1523   3309   5095   6877   784CIP2C_110   4486     1524   3307   5093   6878   784CIP2C_110   4486     1525   3311   5097   6881   784CIP2C_111   4490     1526   3312   5098   6884   784CIP2C_114   4506     1528   3314   5100   6886   784CIP2C_117   4516     1529   3315   5101   6887   784CIP2C_117   4516     1529   3316   5102   6888   784CIP2C_118   4522     1531   3317   5103   6889   784CIP2C_112   4528     1532   3318   5104   6890   784CIP2C_112   4528     1533   3319   5105   6881   784CIP2C_122   4529     1533   3319   5105   6881   784CIP2C_122   4529     1533   3320   5106   6892   784CIP2C_122   4529     1536   3322   5108   6894   784CIP2C_122   4529     1536   3322   5108   6894   784CIP2C_124   4537     1536   3326   5106   6892   784CIP2C_124   4537     1536   3326   5106   6892   784CIP2C_124   4537     1536   3326   5106   6892   784CIP2C_124   4537     1537   3323   5109   6895   784CIP2C_124   4537     1538   3324   5100   6896   784CIP2C_125   4538     1536   3322   5108   6894   784CIP2C_126   4551     1537   3323   5109   6	1		l			1
1505   3291   5077   6863   784CIP2C_95   4430     1506   3292   5078   6864   784CIP2C_96   4435     1507   3293   5079   6865   784CIP2C_97   4436     1508   3294   5080   6866   784CIP2C_98   4439     1509   3295   5081   6867   784CIP2C_99   4440     1510   3296   5082   6868   784CIP2C_100   4441     1511   3297   5083   6869   784CIP2C_101   4442     1512   3298   5084   6870   784CIP2C_101   4442     1513   3299   5085   6871   784CIP2C_102   4455     1514   3300   5086   6872   784CIP2C_103   4466     1515   3301   5087   6873   784CIP2C_105   4469     1516   3302   5088   6874   784CIP2C_105   4469     1517   3303   5089   6875   784CIP2C_106   4477     1518   3304   5090   6876   784CIP2C_108   4483     1519   3305   5091   6877   784CIP2C_108   4483     1520   3306   5092   6878   784CIP2C_110   4486     1521   3307   5093   6879   784CIP2C_110   4486     1521   3307   5093   6879   784CIP2C_110   4486     1521   3307   5093   6879   784CIP2C_110   4486     1522   3308   5094   6880   784CIP2C_110   4486     1523   3309   5095   6881   784CIP2C_111   4499     1524   3310   5096   6882   784CIP2C_111   4499     1525   3311   5097   6883   784CIP2C_113   4503     1526   3312   5098   6884   784CIP2C_116   4514     1529   3315   5101   6887   784CIP2C_117   4516     1529   3315   5101   6887   784CIP2C_117   4516     1529   3315   5101   6887   784CIP2C_117   4516     1529   3315   5101   6887   784CIP2C_112   4528     1530   3316   5102   6888   784CIP2C_121   4528     1531   3317   5103   6890   784CIP2C_122   4529     1533   3319   5105   6891   784CIP2C_122   4529     1531   3317   5103   6890   784CIP2C_122   4529     1533   3319   5105   6891   784CIP2C_124   4527     1538   3324   5100   6896   784CIP2C_124   4527     1531   3317   5103   6890   784CIP2C_124   4527     1533   3318   5104   6890   784CIP2C_124   4527     1536   3322   5108   6894   784CIP2C_124   4527     1538   3324   5100   6896   784CIP2C_126   4551     1530   3326   5112   6898   784CIP2C_129   4567     1542   3328   5114					_i <del></del>	
1506   3292   5078   6864   784CIP2C 96   4435     1507   3293   5079   6865   784CIP2C 97   4436     1508   3294   5080   6866   784CIP2C 98   4439     1509   3295   5081   6867   784CIP2C 99   4440     1510   3296   5082   6868   784CIP2C 100   4441     1511   3297   5083   6869   784CIP2C 101   4442     1512   3298   5084   6870   784CIP2C 102   4455     1513   3299   5085   6871   784CIP2C 102   4455     1514   3300   5086   6872   784CIP2C 103   4466     1515   3301   5087   6873   784CIP2C 105   4469     1516   3302   5088   6874   784CIP2C 105   4469     1517   3303   5089   6875   784CIP2C 107   4481     1518   3304   5090   6876   784CIP2C 108   4483     1520   3306   5092   6878   784CIP2C 109   4484     1520   3306   5092   6878   784CIP2C 101   4490     1521   3307   5093   6879   784CIP2C 110   4486     1521   3307   5093   6879   784CIP2C 110   4486     1522   3308   5094   6880   784CIP2C 111   4490     1523   3309   5095   6881   784CIP2C 111   4490     1524   3310   5096   6882   784CIP2C 111   4490     1525   3311   5097   6883   784CIP2C 114   4506     1526   3312   5098   6884   784CIP2C 114   4506     1529   3315   5101   6887   784CIP2C 116   4514     1529   3315   5100   6886   784CIP2C 120   4527     1530   3316   5102   6888   784CIP2C 121   4528     1531   3327   5103   6899   784CIP2C 121   4528     1533   3319   5105   6891   784CIP2C 121   4528     1534   3320   5106   6892   784CIP2C 124   4527     1535   3321   5107   6893   784CIP2C 124   4527     1536   3322   5108   6894   784CIP2C 124   4528     1536   3322   5108   6894   784CIP2C 124   4529     1538   3324   5100   6866   784CIP2C 124   4528     1536   3322   5108   6894   784CIP2C 124   4527     1537   3323   5109   6895   784CIP2C 124   4528     1538   3324   5100   6869   784CIP2C 124   4529     1531   3327   5103   6899   784CIP2C 124   4529     1532   3318   5104   6890   784CIP2C 124   4529     1533   3326   5106   6893   784CIP2C 125   4529     1536   3322   5108   6894   784CIP2C 126   4551     1536   3326   5112						
1507   3293   5079   6865   784CIP2C 97   4436     1508   3294   5080   6866   784CIP2C 98   4439     1509   3295   5081   6867   784CIP2C 99   4440     1510   3296   5082   6868   784CIP2C 100   4441     1511   3297   5083   6869   784CIP2C 101   4442     1512   3298   5084   6870   784CIP2C 102   4455     1513   3299   5085   6971   784CIP2C 103   4462     1514   3300   5086   6872   784CIP2C 104   4466     1515   3301   5067   6873   784CIP2C 105   4469     1516   3302   5088   6874   784CIP2C 106   4477     1517   3303   5089   6875   784CIP2C 107   4481     1518   3304   5090   6876   784CIP2C 108   4483     1519   3305   5091   6877   784CIP2C 109   4486     1520   3306   5092   6878   784CIP2C 110   4486     1521   3307   5093   6879   784CIP2C 110   4486     1522   3308   5094   6880   784CIP2C 111   4490     1522   3308   5094   6880   784CIP2C 112   4499     1523   3309   5095   6881   784CIP2C 113   4503     1524   3310   5096   6882   784CIP2C 114   4506     1525   3311   5097   6883   784CIP2C 116   4514     1528   3314   5100   6886   784CIP2C 116   4514     1529   3315   5101   6887   784CIP2C 117   4516     1529   3316   5102   6888   784CIP2C 12   4529     1531   3317   5103   6889   784CIP2C 12   4528     1531   3317   5103   6889   784CIP2C 12   4528     1533   3319   5105   6891   784CIP2C 12   4528     1534   3320   5106   6889   784CIP2C 12   4528     1535   3318   5104   6690   784CIP2C 12   4528     1536   3322   5108   6894   784CIP2C 12   4528     1538   3324   5107   6693   784CIP2C 12   4528     1538   3324   5107   6693   784CIP2C 12   4528     1538   3324   5107   6693   784CIP2C 12   4528     1538   3325   5111   6897   784CIP2C 129   4567     1542   3326   5112   6698   784CIP2C 129   4567     1542   3328   5114   6900   784CIP2C 133   4592     1542   3328   5114   6900   784CIP2C 133   4592     1542   3328   5114   6900   784CIP2C 133   4592     1542   3328   5114   6900   784CIP2C 133   4592     1542   3328   5114   6900   784CIP2C 133   4592     1542   3328   5114   6900   7						
1508   3294   5080   6866   784CIP2C_98   4439   1509   3295   5081   6867   784CIP2C_98   4440   1510   3296   5082   6868   784CIP2C_100   4441   1511   3297   5083   6869   784CIP2C_101   4441   1512   3298   5084   6870   784CIP2C_102   4455   1513   3299   5085   6971   784CIP2C_103   4462   1514   3300   5086   6872   784CIP2C_103   4462   1515   3301   5087   6873   784CIP2C_105   4469   1516   3302   5088   6874   784CIP2C_105   4469   1516   3302   5088   6874   784CIP2C_105   4469   1516   3302   5088   6874   784CIP2C_106   4477   1517   3303   5089   6875   784CIP2C_107   4481   1518   3304   5090   6876   784CIP2C_108   4483   1519   3305   5091   6877   784CIP2C_109   4484   1520   3306   5092   6878   784CIP2C_109   4484   1520   3306   5092   6878   784CIP2C_110   4486   1521   3307   5093   6879   784CIP2C_111   4499   1522   3308   5094   6880   784CIP2C_111   4499   1522   3308   5094   6880   784CIP2C_111   4499   1524   3310   5096   6682   784CIP2C_112   4499   1526   3312   5096   6688   784CIP2C_114   4506   1525   3311   5097   6883   784CIP2C_115   4509   1526   3312   5099   6886   784CIP2C_116   4514   1527   3313   5099   6886   784CIP2C_117   4516   1529   3315   5101   6887   784CIP2C_118   4522   1530   3316   5102   6888   784CIP2C_12   19   4525   1530   3316   5102   6889   784CIP2C_12   14452   1524   3317   5103   6889   784CIP2C_12   14452   1531   3317   5103   6889   784CIP2C_12   14452   1534   3320   5106   6692   784CIP2C_12   14452   1534   3320   5106   6693   784CIP2C_12   14453   1534   3320   5106   6693   784CIP2C_12   14453   1534   3320   5106   6693   784CIP2C_12   1452   1534   3320   5106   6693   784CIP2C_12   1452   1534   3320   5106   6693   784CIP2C_12   1452   1534   3320   5106   6693   784CIP2C_12   4529   1534   3320   5106   6693   784CIP2C_12   4529   1534   3320   5106   6693   784CIP2C_12   4529   1534   3326   5106   6693   784CIP2C_12   4529   1534   3326   5106   6693   784CIP2C_12   4529   1534   3326   5106   6693   784CIP2C_12   4529   1				l		
1509   3295   5081   6867   784CIP2C_99   4440     1510   3296   5082   6868   784CIP2C_100   4441     1511   3297   5083   6869   784CIP2C_101   4442     1511   3298   5084   6870   784CIP2C_101   4442     1512   3298   5084   6870   784CIP2C_102   4455     1513   3299   5085   6871   784CIP2C_103   4462     1514   3300   5086   6872   784CIP2C_104   4466     1515   3301   5087   6873   784CIP2C_105   4469     1516   3302   5088   6874   784CIP2C_106   4477     1517   3303   5089   6875   784CIP2C_107   4481     1518   3304   5090   6876   784CIP2C_107   4481     1519   3305   5091   6877   784CIP2C_109   4484     1520   3306   5092   6878   784CIP2C_109   4486     1521   3307   5093   6879   784CIP2C_110   4486     1522   3308   5094   6880   784CIP2C_111   4490     1523   3309   5095   6881   784CIP2C_111   4490     1524   3310   5096   6882   784CIP2C_114   4506     1525   3311   5097   6883   784CIP2C_114   4506     1526   3312   5098   6884   784CIP2C_116   4514     1527   3313   5099   6885   784CIP2C_116   4514     1528   3314   5100   6886   784CIP2C_117   4516     1529   3316   5101   6887   784CIP2C_119   4525     1530   3316   5102   6888   784CIP2C_119   4528     1531   3317   5103   6889   784CIP2C_122   4529     1533   3319   5105   6891   784CIP2C_122   4529     1534   3320   5106   6892   784CIP2C_124   4537     1535   3321   5107   6893   784CIP2C_121   4528     1536   3322   5108   6894   784CIP2C_124   4537     1538   3324   5110   6896   784CIP2C_127   4552     1538   3324   5110   6897   784CIP2C_126   4551     1538   3324   5110   6896   784CIP2C_127   4552     1539   3325   5111   6897   784CIP2C_129   4567     1540   3326   5112   6698   784CIP2C_129   4567     1541   3327   5113   6899   784CIP2C_129   4567     1541   3327   5113   6899   784CIP2C_133   4592     1542   3328   5114   6900   784CIP2C_133   4592     1542   3328   5114   6900   784CIP2C_133   4592     1542   3328   5114   6900   784CIP2C_133   4592     1542   3328   5114   6900   784CIP2C_133   4592		L		1		
1510   3296   5082   6868   784CIP2C_100   4441     1511   3297   5083   6869   784CIP2C_101   4442     1512   3298   5084   6870   784CIP2C_102   4455     1513   3299   5085   6871   784CIP2C_103   4462     1514   3300   5086   6872   784CIP2C_105   4466     1515   3301   5087   6873   784CIP2C_105   4469     1516   3302   5088   6874   784CIP2C_105   4467     1517   3303   5089   6875   784CIP2C_106   4477     1518   3304   5090   6876   784CIP2C_107   4481     1518   3304   5090   6876   784CIP2C_109   4484     1519   3305   5091   6877   784CIP2C_109   4484     1520   3306   5092   6878   784CIP2C_109   4484     1521   3307   5093   6879   784CIP2C_110   4486     1521   3307   5093   6879   784CIP2C_111   4490     1522   3308   5094   6880   784CIP2C_111   4490     1523   3309   5095   6861   784CIP2C_112   4499     1524   3310   5096   6882   784CIP2C_113   4503     1526   3311   5097   6883   784CIP2C_114   4506     1527   3313   5099   6885   784CIP2C_116   4514     1528   3314   5100   6886   784CIP2C_116   4514     1529   3315   5101   6887   784CIP2C_120   4527     1531   3317   5103   6889   784CIP2C_120   4528     1532   3318   5104   6890   784CIP2C_121   4528     1533   3316   5105   6891   784CIP2C_121   4528     1534   3320   5106   6892   784CIP2C_121   4528     1535   3321   5107   6893   784CIP2C_125   4538     1536   3322   5108   6894   784CIP2C_125   4538     1537   3323   5109   6895   784CIP2C_125   4538     1538   3324   5110   6896   784CIP2C_126   4557     1538   3324   5110   6896   784CIP2C_127   4552     1539   3325   5111   6897   784CIP2C_129   4567     1540   3326   5112   6898   784CIP2C_129   4567     1541   3327   5113   6899   784CIP2C_121   4528     1541   3327   5113   6899   784CIP2C_133   4592     1542   3328   5114   6900   784CIP2C_133   4592     1542   3328   5114   6900   784CIP2C_133   4592     1542   3328   5114   6900   784CIP2C_133   4592     1542   3328   5114   6900   784CIP2C_133   4592     1542   3328   5114   6900   784CIP2C_133   4592						1
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1512   3298   5084   6870   784CIP2C_102   4455	L					
1513   3299   5085   6871   784CIP2C_103   4462						
1514   3300   5086   6872   784CIP2C 104   4466     1515   3301   5087   6873   784CIP2C 105   4469     1516   3302   5088   6374   784CIP2C 106   4477     1517   3303   5089   6875   784CIP2C 107   4481     1518   3304   5090   6876   784CIP2C 108   4483     1519   3305   5091   6877   784CIP2C 109   4484     1520   3306   5092   6378   784CIP2C 109   4484     1521   3307   5093   6379   784CIP2C 110   4486     1521   3307   5093   6379   784CIP2C 111   4490     1522   3308   5094   6880   784CIP2C 112   4499     1523   3309   5095   6881   784CIP2C 112   4499     1524   3310   5096   6882   784CIP2C 114   4506     1525   3311   5097   6883   784CIP2C 115   4509     1526   3312   5098   6884   784CIP2C 115   4509     1528   3314   5100   6886   784CIP2C 117   4516     1529   3315   5101   6887   784CIP2C 119   4525     1529   3315   5101   6887   784CIP2C 119   4525     1530   3316   5102   6888   784CIP2C 120   4527     1531   3317   5103   6889   784CIP2C 121   4528     1532   3318   5104   6890   784CIP2C 122   4529     1533   3319   5105   6891   784CIP2C 123   4528     1534   3320   5106   6892   784CIP2C 123   4532     1535   3321   5107   6893   784CIP2C 124   4537     1536   3322   5108   6894   784CIP2C 125   4538     1537   3323   5109   6895   784CIP2C 127   4552     1538   3324   5110   6896   784CIP2C 127   4552     1539   3325   5111   6897   784CIP2C 128   4559     1530   3326   5112   6898   784CIP2C 129   4567     1540   3326   5112   6898   784CIP2C 129   4567     1540   3326   5112   6898   784CIP2C 133   4592     1542   3328   5114   6900   784CIP2C 133   4592						
1515   3301   5087   6873   784CIP2C_105   4469     1516   3302   5088   6874   784CIP2C_106   4477     1517   3303   5089   6875   784CIP2C_107   4481     1518   3304   5090   6876   784CIP2C_108   4483     1519   3305   5091   6877   784CIP2C_109   4484     1520   3306   5092   6878   784CIP2C_109   4486     1521   3307   5093   6879   784CIP2C_110   4486     1521   3307   5093   6879   784CIP2C_111   4490     1522   3308   5094   6880   784CIP2C_112   4499     1523   3309   5095   6881   784CIP2C_113   4553     1524   3310   5096   6882   784CIP2C_113   4506     1525   3311   5097   6883   784CIP2C_115   4509     1526   3312   5098   6884   784CIP2C_116   4514     1527   3313   5099   6885   784CIP2C_117   4516     1528   3314   5100   6886   784CIP2C_118   4522     1529   3315   5101   6887   784CIP2C_119   4525     1530   3316   5102   6888   784CIP2C_119   4525     1531   3317   5103   6889   784CIP2C_121   4528     1532   3318   5104   6890   784CIP2C_121   4528     1533   3319   5105   6891   784CIP2C_122   4528     1534   3320   5106   6892   784CIP2C_123   4532     1535   3321   5107   6893   784CIP2C_124   4537     1535   3321   5107   6893   784CIP2C_126   4551     1536   3322   5108   6894   784CIP2C_126   4551     1537   3323   5109   6895   784CIP2C_126   4551     1538   3324   5110   6896   784CIP2C_128   4559     1539   3325   5111   6897   784CIP2C_128   4559     1530   3326   5112   6898   784CIP2C_128   4559     1530   3326   5112   6898   784CIP2C_130   4568     1541   3327   5113   6899   784CIP2C_131   4585     1542   3328   5114   6900   784CIP2C_133   4592				L		
1516   3302   5088   6874   784CIP2C   106   4477     1517   3303   5089   6875   784CIP2C   107   4481     1518   3304   5090   6876   784CIP2C   108   4483     1519   3305   5091   6877   784CIP2C   109   4484     1520   3306   5092   6878   784CIP2C   110   4486     1521   3307   5093   6879   784CIP2C   111   4490     1522   3308   5094   6880   784CIP2C   112   4499     1523   3309   5095   6881   784CIP2C   113   4503     1524   3310   5096   6882   784CIP2C   114   4506     1525   3311   5097   6883   784CIP2C   114   4506     1526   3312   5098   6884   784CIP2C   116   4514     1527   3313   5099   6885   784CIP2C   117   4516     1528   3314   5100   6886   784CIP2C   118   4522     1530   3316   5102   6888   784CIP2C   119   4525     1530   3316   5102   6888   784CIP2C   120   4527     1531   3317   5103   6889   784CIP2C   121   4528     1532   3318   5104   6890   784CIP2C   121   4528     1533   3319   5105   6891   784CIP2C   124   4537     1534   3320   5106   6892   784CIP2C   124   4537     1535   3321   5107   6893   784CIP2C   124   4537     1536   3322   5108   6894   784CIP2C   124   4537     1537   3323   5109   6895   784CIP2C   124   4537     1539   3325   5111   6897   784CIP2C   128   4559     1530   3326   5112   6898   784CIP2C   129   4567     1540   3326   5112   6898   784CIP2C   133   4592     1542   3328   5114   6900   784CIP2C   133   4592						1
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1683   3469   5255   7041   784CTP2D_31   5012     1684   3470   5256   7042   784CTP2D_32   5013     1685   3471   5257   7043   784CTP2D_33   5025     1686   3472   5258   7044   784CTP2D_34   5053     1687   3473   5259   7045   784CTP2D_35   5054     1688   3474   5260   7046   784CTP2D_36   5054     1689   3475   5261   7047   784CTP2D_37   5054     1689   3475   5261   7047   784CTP2D_37   5113     1690   3476   5262   7048   784CTP2D_38   9134     1691   3477   5263   7049   784CTP2D_39   9152     1692   3478   5264   7050   784CTP2D_40   9152     1693   3478   5264   7050   784CTP2D_40   9152     1694   3480   5266   7051   784CTP2D_41   9211     1695   3481   5267   7053   784CTP2D_42   9223     1695   3481   5267   7053   784CTP2D_44   9231     1697   3483   5268   7054   784CTP2D_45   9236     1698   3484   5270   7056   784CTP2D_45   9236     1699   3485   5271   7057   784CTP2D_47   9236     1699   3486   5272   7058   784CTP2D_48   9236     1699   3488   5274   7060   784CTP2D_48   9303     1700   3486   5272   7058   784CTP2D_48   9303     1701   3489   5273   7059   784CTP2D_59   9314     1702   3489   5275   7061   784CTP2D_51   9314     1703   3489   5275   7061   784CTP2D_51   9314     1704   3490   3276   7062   784CTP2D_52   9348     1705   3491   5277   7063   784CTP2D_52   9348     1706   3492   5278   7066   784CTP2D_52   9348     1707   3493   5279   7065   784CTP2D_52   9348     1708   3494   5280   7066   784CTP2D_52   9348     1709   3495   5281   7067   784CTP2D_52   9348     1701   3496   5282   7068   784CTP2D_52   9348     1701   3496   5282   7068   784CTP2D_54   9362     1703   3499   5281   7067   784CTP2D_56   9569     1714   3500   5286   7072   784CTP2D_56   9551     1716   3492   5281   7067   784CTP2D_56   9569     1716   3502   5288   7074   784CTP2D_56   9569     1716   3502   5288   7074   784CTP2D_56   9569     1716   3503   5299   7061   784CTP2D_66   9581     1716   3504   5290   7076   784CTP2D_66   9581     1717   3503   5299   7061   784CTP2D_66   9581     1720			t _			
1684   3470   5256   7042   784CIP2D_32   3013   1685   3471   5257   7043   784CIP2D_34   3025   3686   3472   5258   7044   784CIP2D_34   3053   1687   3473   5259   7045   784CIP2D_35   3055   1687   3474   5260   7046   784CIP2D_35   3054   1688   3474   5260   7046   784CIP2D_35   3054   1688   3474   5260   7046   784CIP2D_35   3054   1689   3475   5261   7047   784CIP2D_37   3113   1690   3476   5262   7048   784CIP2D_38   3134   1691   3477   5263   7049   784CIP2D_38   3134   1691   3477   5263   7049   784CIP2D_39   3152   1693   3478   5264   7050   784CIP2D_40   0 9152   1693   3479   5265   7051   784CIP2D_40   0 9152   1693   3479   5265   7051   784CIP2D_41   2211   1694   3480   5266   7052   784CIP2D_42   2 9223   1696   3482   5268   7054   784CIP2D_44   2331   1697   3483   5269   7055   784CIP2D_44   3231   1697   3483   5269   7055   784CIP2D_45   2236   1698   3484   5270   7056   784CIP2D_45   2236   1699   3485   5271   7057   784CIP2D_45   2236   1699   3485   5271   7057   784CIP2D_46   3236   1699   3485   5272   7058   784CIP2D_47   3003   1700   3486   5272   7058   784CIP2D_47   3039   1700   3488   5272   7058   784CIP2D_47   3039   1700   3498   5275   7061   784CIP2D_50   3326   1703   3499   5275   7061   784CIP2D_50   3326   1704   3490   5276   7062   784CIP2D_50   3326   1704   3492   5279   7065   784CIP2D_50   3326   1707   3493   5279   7065   784CIP2D_50   3326   1707   3493   5279   7065   784CIP2D_50   3326   1707   3493   5279   7065   784CIP2D_50   3326   1707   3493   5279   7065   784CIP2D_50   3326   1707   3493   5279   7065   784CIP2D_50   3949   1700   3496   5282   7068   784CIP2D_50   3949   1700   3496   5282   7068   784CIP2D_50   3949   1700   3495   5281   7067   784CIP2D_50   3949   1700   3495   5281   7067   784CIP2D_50   3949   1700   3496   5282   7068   784CIP2D_50   3949   1700   3496   5282   7068   784CIP2D_50   3949   1700   3496   5282   7068   784CIP2D_50   3949   1700   3496   5282   7068   784CIP2D_50   3950   1706   3492   5295   7068   7				I		
1685   3471   5257   7043   784CIP2D_33   3025     1686   3472   3258   7044   784CIP2D_34   9053     1687   3473   5259   7045   784CIP2D_35   9054     1688   3474   5260   7046   784CIP2D_35   9054     1689   3475   5261   7047   784CIP2D_37   9054     1690   3476   5262   7048   784CIP2D_37   9113     1690   3476   5262   7048   784CIP2D_38   9134     1691   3477   5263   7049   784CIP2D_39   9152     1692   3478   5264   7050   784CIP2D_40   9152     1693   3479   5265   7051   784CIP2D_40   9152     1694   3480   5266   7052   784CIP2D_40   9152     1695   3481   5267   7053   784CIP2D_41   9211     1696   3482   5268   7053   784CIP2D_41   9223     1695   3481   5267   7053   784CIP2D_41   9231     1697   3483   5269   7055   784CIP2D_46   9231     1698   3484   5270   7056   784CIP2D_46   9236     1699   3485   5271   7057   784CIP2D_46   9236     1699   3485   5271   7057   784CIP2D_46   9236     1699   3486   5272   7058   784CIP2D_48   9309     1701   3487   5273   7059   784CIP2D_49   9314     1702   3488   5274   7060   784CIP2D_50   9326     1703   3489   5275   7061   784CIP2D_51   9319     1704   3490   5276   7062   784CIP2D_51   9319     1705   3491   5277   7063   784CIP2D_51   9319     1706   3492   5278   7064   784CIP2D_52   9348     1707   3439   5279   7065   784CIP2D_54   9382     1708   3494   5280   7066   784CIP2D_54   9382     1709   3495   5281   7067   784CIP2D_55   9407     1709   3495   5281   7067   784CIP2D_56   9382     1701   3496   5282   7068   784CIP2D_56   9568     1710   3496   5282   7068   784CIP2D_56   9568     1711   3497   5283   7069   784CIP2D_56   9511     1712   3498   5281   7067   784CIP2D_56   9591     1714   3500   5286   7072   784CIP2D_56   9591     1716   3502   5288   7074   784CIP2D_56   9568     1716   3502   5288   7074   784CIP2D_56   9568     1716   3502   5288   7074   784CIP2D_56   9568     1716   3502   5288   7077   784CIP2D_56   9568     1716   3505   5297   7063   784CIP2D_66   9588     1716   3506   5292   7068   784CIP2D_76   9597     1720					<u> </u>	l .
1686   3472   5258   7044   784CIP2D_34   9053     1687   3473   5259   7045   784CIP2D_35   9054     1688   3474   5260   7046   784CIP2D_35   9054     1689   3475   5261   7047   784CIP2D_37   9113     1690   3476   5262   7048   784CIP2D_37   9113     1691   3477   5263   7049   784CIP2D_39   9152     1691   3477   5263   7049   784CIP2D_39   9152     1692   3478   5264   7050   784CIP2D_40   9152     1693   3479   5265   7051   784CIP2D_40   9152     1694   3480   5266   7052   784CIP2D_41   9211     1695   3481   5267   7053   784CIP2D_42   9223     1696   3482   5268   7054   784CIP2D_44   9231     1697   3483   5269   7055   784CIP2D_44   9231     1698   3484   5270   7056   784CIP2D_45   9236     1698   3484   5270   7056   784CIP2D_47   9303     1700   3486   5271   7057   784CIP2D_47   9303     1701   3487   5273   7059   784CIP2D_49   9314     1702   3488   5274   7050   784CIP2D_51   9326     1703   3489   5275   7051   784CIP2D_51   9326     1704   3490   5276   7052   784CIP2D_51   9326     1705   3491   5277   7062   784CIP2D_51   9326     1706   3492   5278   7060   784CIP2D_52   9348     1705   3491   5277   7062   784CIP2D_52   9348     1706   3492   5278   7064   784CIP2D_52   9348     1707   3493   5279   7065   784CIP2D_54   9312     1708   3494   5280   7066   784CIP2D_55   9414     1709   3495   5281   7067   784CIP2D_55   9415     1701   3496   5282   7068   784CIP2D_56   9415     1701   3496   5282   7068   784CIP2D_56   9459     1701   3496   5282   7068   784CIP2D_56   9459     1701   3496   5281   7067   784CIP2D_57   9435     1701   3496   5282   7068   784CIP2D_56   9459     1701   3496   5281   7067   784CIP2D_57   9435     1701   3499   5265   7071   784CIP2D_57   9435     1701   3496   5282   7068   784CIP2D_56   9459     1701   3496   5280   7066   784CIP2D_56   9459     1701   3496   5280   7066   784CIP2D_56   9459     1701   3496   5280   7066   784CIP2D_56   9568     1701   3503   5286   7071   784CIP2D_66   9588     1701   3503   5286   7072   784CIP2D_66   9588     1701		<b></b>		L		I
1687 3473 5259 7045 784CIP2D_35 9054 1688 3474 5260 7046 784CIP2D_36 9054 1689 3475 5261 7047 784CIP2D_37 9054 1690 3476 5262 7048 784CIP2D_37 9113 1690 3476 5262 7048 784CIP2D_38 9134 1691 3477 5263 7049 784CIP2D_39 9152 1692 3478 5264 7050 784CIP2D_40 9152 1693 3479 5265 7051 784CIP2D_40 9152 1694 3480 5266 7052 784CIP2D_40 9211 1695 3481 5267 7053 784CIP2D_42 9223 1695 3481 5267 7053 784CIP2D_43 9231 1697 3483 5269 7055 784CIP2D_44 9231 1699 3485 5270 7056 784CIP2D_46 9236 1699 3485 5271 7057 784CIP2D_48 9303 1700 3486 5272 7058 784CIP2D_48 9309 1701 3487 5273 7059 784CIP2D_48 9309 1701 3487 5273 7059 784CIP2D_50 9314 1702 3488 5274 7060 784CIP2D_50 9314 1703 3489 5275 7061 784CIP2D_50 9326 1704 3490 5276 7062 784CIP2D_51 9339 1706 3491 5277 7063 784CIP2D_53 9319 1707 3493 5276 7062 784CIP2D_53 9319 1708 3494 5280 7066 784CIP2D_53 9319 1709 3495 5275 7061 784CIP2D_53 9319 1700 3496 5272 7058 784CIP2D_50 9326 1703 3491 5277 7063 784CIP2D_53 9319 1704 3490 5276 7062 784CIP2D_53 9319 1705 3491 5277 7063 784CIP2D_53 9319 1706 3492 5278 7066 784CIP2D_55 9348 1707 3493 5279 7065 784CIP2D_55 9348 1708 3494 5280 7066 784CIP2D_55 9349 1709 3495 5280 7066 784CIP2D_56 9414 1709 3495 5280 7066 784CIP2D_56 9414 1709 3495 5282 7068 784CIP2D_58 9465 1711 3497 5283 7069 784CIP2D_58 9465 1711 3497 5283 7069 784CIP2D_58 9465 1711 3497 5283 7069 784CIP2D_58 9465 1711 3498 5280 7066 784CIP2D_58 9465 1711 3498 5280 7066 784CIP2D_58 9465 1711 3498 5280 7066 784CIP2D_58 9465 1711 3498 5280 7066 784CIP2D_58 9465 1711 3503 5287 7077 784CIP2D_66 9588 1719 3505 5281 7077 784CIP2D_66 9588 1719 3505 5281 7077 784CIP2D_67 9557 1716 3504 5296 7078 784CIP2D_67 9557 1717 3503 5289 7075 784CIP2D_68 9612 1718 3500 5286 7071 784CIP2D_67 9557 1718 3501 5287 7078 784CIP2D_68 9612 1724 3510 5297 7088 784CIP2D_68 9612 1725 3511 5297 7088 784CIP2D_68 9612 1726 3512 5298 7088 784CIP2D_79 9649 1727 3513 5299 7085 784CIP2D_70 9649 1728 3513 5299 7085 784CIP2D_76 9777 1729 3513 5296 7088 784CIP2D_79 9622 1727 3513 5299 7088 784CIP2D_79 9642 1728 3513 5	L					
1688				4 · · · · · · · · · · · · · · · · · · ·		l
1689   3475   5261   7047   784CIP2D 37   9113     1690   3476   5262   7048   784CIP2D 38   9134     1691   3477   5263   7049   784CIP2D 38   9152     1692   3478   5264   7050   784CIP2D 40     1693   3479   5265   7051   784CIP2D 40     9152   1693   3479   5265   7051   784CIP2D 40     9152   1694   3480   5266   7052   784CIP2D 42     1694   3480   5266   7052   784CIP2D 42     1695   3481   5267   7053   784CIP2D 43     1696   3482   5268   7054   784CIP2D 43     1697   3483   5269   7055   784CIP2D 45     1699   3485   5270   7056   784CIP2D 45     1699   3485   5271   7057   784CIP2D 48     1699   3486   5272   7058   784CIP2D 48     1700   3486   5272   7058   784CIP2D 48     1701   3487   5273   7059   784CIP2D 48     1702   3488   5274   7060   784CIP2D 50     3339   1704   3490   5276   7061   784CIP2D 50     3349   5275   7061   784CIP2D 50     3349   5277   7063   784CIP2D 50     3349   5277   7063   784CIP2D 50     3349   5276   7062   784CIP2D 50     3349   5276   7062   784CIP2D 50     3349   5276   7062   784CIP2D 50     3349   5276   7062   784CIP2D 50     3349   5276   7062   784CIP2D 50     3349   5278   7064   784CIP2D 53     3376   1706   3492   5278   7064   784CIP2D 53     3376   1707   3493   5279   7065   784CIP2D 55     3401   1707   3493   5279   7065   784CIP2D 56     3491   5277   7066   784CIP2D 57   9439     1710   3496   5282   7066   784CIP2D 58   9485     1711   3497   5283   7067   784CIP2D 58   9485     1711   3498   5284   7007   784CIP2D 58   9485     1711   3498   5284   7007   784CIP2D 60   9501     1712   3498   5284   7007   784CIP2D 60   9501     1713   3499   5285   7071   784CIP2D 60   9501     1714   3500   5286   7072   784CIP2D 60   9501     1715   3501   5287   7073   784CIP2D 60   9501     1716   3502   5288   7074   784CIP2D 60   9501     1716   3502   5288   7074   784CIP2D 60   9501     1716   3502   5288   7074   784CIP2D 60   9501     1716   3502   5288   7074   784CIP2D 60   9501     1716   3502   5288   7074   784CIP2D 60   9526     1716   3500   529						
1690 3476 5262 7048 784CIP2D_38 9134 1691 3477 5263 7049 784CIP2D_39 9152 1692 3478 5264 7050 784CIP2D_39 9152 1693 3478 5264 7050 784CIP2D_40 9152 1693 3479 5265 7051 784CIP2D_41 9211 1694 3480 5266 7052 784CIP2D_42 9223 1695 3481 5267 7053 784CIP2D_43 9223 1696 3482 5268 7054 784CIP2D_44 9231 1697 3483 5269 7055 784CIP2D_45 9236 1698 3484 5270 7056 784CIP2D_46 9236 1698 3484 5270 7056 784CIP2D_46 9236 1699 3485 5271 7057 784CIP2D_47 9303 1700 3486 5272 7058 784CIP2D_47 9303 1701 3487 5273 7059 784CIP2D_49 9314 1702 3488 5274 70560 784CIP2D_51 9339 1703 3489 5275 7061 784CIP2D_51 9339 1704 3490 5276 7062 784CIP2D_52 9348 1705 3491 5277 7063 784CIP2D_52 9348 1706 3492 5278 7064 784CIP2D_54 9326 1707 3493 5279 7065 784CIP2D_54 9302 1708 3494 5280 7066 784CIP2D_55 9407 1708 3494 5280 7066 784CIP2D_56 9414 1709 3495 5281 7067 784CIP2D_57 9439 1710 3496 5282 7068 784CIP2D_57 9439 1711 3497 5283 7069 784CIP2D_57 9439 1712 3498 5284 7067 784CIP2D_57 9439 1713 3499 5285 7061 784CIP2D_57 9439 1710 3496 5282 7068 784CIP2D_57 9439 1711 3497 5283 7069 784CIP2D_57 9439 1712 3498 5284 7067 784CIP2D_57 9439 1713 3499 5285 7071 784CIP2D_57 9439 1714 3500 5286 7072 784CIP2D_56 9414 1709 3495 5281 7067 784CIP2D_57 9439 1711 3497 5283 7069 784CIP2D_56 9414 1709 3495 5281 7067 784CIP2D_57 9439 1711 3497 5283 7069 784CIP2D_56 9414 1709 3495 5281 7067 784CIP2D_56 9451 1711 3497 5283 7069 784CIP2D_56 9451 1711 3497 5283 7069 784CIP2D_66 9551 1712 3498 5284 7070 784CIP2D_66 9551 1714 3500 5286 7072 784CIP2D_66 9551 1716 3504 5290 7076 784CIP2D_66 9551 1718 3504 5290 7079 784CIP2D_66 9551 1718 3501 5287 7079 784CIP2D_66 9551 1718 3504 5290 7079 784CIP2D_66 9558 1719 3505 5291 7079 784CIP2D_66 9556 1718 3504 5290 7079 784CIP2D_66 9551 1718 3504 5290 7079 784CIP2D_66 9558 1719 3505 5291 7079 784CIP2D_66 9556 1718 3507 5293 7079 784CIP2D_67 9597 1720 3508 5295 7081 784CIP2D_67 9597 1721 3507 5293 7079 784CIP2D_67 9597 1722 3513 5299 7085 784CIP2D_77 9669 1724 3513 5299 7085 784CIP2D_79 9669 1724 3515 5301 7087 784CIP2D_79 9669			ł			
1691   3478   5263   7049   784CIP2D 39   9152     1692   3478   5264   7050   784CIP2D 40   9152     1693   3479   5265   7051   784CIP2D 40   9152     1694   3480   5266   7052   764CIP2D 42   9223     1695   3481   5267   7053   784CIP2D 42   9223     1696   3482   5268   7054   784CIP2D 44   9231     1697   3483   5269   7055   784CIP2D 45   9236     1698   3484   5270   7056   784CIP2D 45   9236     1699   3485   5271   7057   784CIP2D 47   9303     1700   3486   5272   7058   784CIP2D 49   9314     1701   3487   5273   7059   784CIP2D 50   9326     1703   3489   5274   7060   784CIP2D 50   9326     1704   3490   5276   7062   784CIP2D 52   9348     1705   3491   5277   7063   784CIP2D 52   9348     1706   3492   5278   7064   784CIP2D 53   9376     1708   3494   5280   7066   784CIP2D 55   9376     1709   3495   5281   7067   784CIP2D 55   9376     1709   3496   5282   7066   784CIP2D 55   9376     1709   3496   5282   7066   784CIP2D 55   9376     1709   3496   5282   7066   784CIP2D 55   9376     1701   3493   5279   7065   784CIP2D 55   9407     1709   3495   5281   7067   784CIP2D 55   9407     1709   3496   5282   7066   784CIP2D 55   9407     1710   3498   5281   7067   784CIP2D 55   9407     1711   3497   5283   7068   784CIP2D 56   9414     1709   3496   5282   7068   784CIP2D 56   9415     1711   3498   5284   7007   784CIP2D 60   9501     1712   3498   5284   7070   784CIP2D 60   9501     1713   3499   5285   7071   784CIP2D 60   9501     1714   3500   5286   7072   784CIP2D 66   9588     1716   3502   5288   7074   784CIP2D 66   9588     1717   3503   5289   7075   784CIP2D 66   9588     1718   3504   5290   7076   784CIP2D 66   9588     1719   3505   5291   7077   784CIP2D 67   9597     1720   3506   5292   7078   784CIP2D 67   9597     1721   3507   5293   7079   784CIP2D 67   9597     1722   3508   5294   7080   784CIP2D 67   9597     1723   3509   5295   7081   784CIP2D 67   9597     1724   3510   5296   7082   784CIP2D 70   9649     1725   3511   5297   7083   784CIP2D 70   9649     1721						
1692 3478 5264 7050 784CIP2D 40 9152 1693 3479 5265 7051 784CIP2D 41 9211 1694 3480 5266 7052 784CIP2D 42 9223 1695 3481 5267 7053 784CIP2D 43 9223 1695 3482 5268 7054 784CIP2D 44 9231 1697 3483 5269 7055 784CIP2D 45 9236 1697 3483 5269 7055 784CIP2D 46 9236 1698 3484 5270 7056 784CIP2D 46 9236 1699 3485 5271 7057 784CIP2D 48 9309 1700 3486 5272 7058 784CIP2D 48 9309 1701 3487 5273 7059 784CIP2D 49 9314 1702 3488 5274 7060 784CIP2D 50 9326 1703 3489 5275 7061 784CIP2D 51 9339 1704 3490 5276 7082 784CIP2D 51 9339 1705 3491 5277 7063 784CIP2D 52 9376 1706 3492 5278 7064 784CIP2D 54 9382 1707 3493 5279 7065 784CIP2D 54 9382 1707 3493 5279 7065 784CIP2D 55 9376 1708 3494 5280 7066 784CIP2D 56 9414 1709 3495 5281 7067 784CIP2D 56 9414 1709 3496 5282 7068 784CIP2D 57 9439 1710 3496 5282 7068 784CIP2D 56 9414 1709 3495 5281 7067 784CIP2D 57 9439 1710 3496 5282 7068 784CIP2D 57 9439 1711 3497 5283 7069 784CIP2D 59 9493 1712 3498 5284 7070 784CIP2D 59 9493 1713 3499 5285 7071 784CIP2D 60 9501 1713 3499 5285 7071 784CIP2D 60 9501 1714 3500 5286 7072 784CIP2D 62 9526 1715 3501 5287 7073 784CIP2D 62 9526 1716 3502 5288 7074 784CIP2D 64 9557 1717 3503 5289 7075 784CIP2D 66 9551 1718 3504 5290 7076 784CIP2D 66 9551 1719 3505 5291 7077 784CIP2D 66 9551 1710 3506 5292 7078 784CIP2D 67 9557 1710 3508 5291 7077 784CIP2D 67 9557 1717 3503 5289 7075 784CIP2D 67 9557 1718 3504 5290 7076 784CIP2D 66 9588 1719 3505 5291 7077 784CIP2D 67 9557 1710 3506 5292 7078 784CIP2D 67 9557 1717 3503 5289 7075 784CIP2D 67 9557 1718 3504 5290 7076 784CIP2D 67 9557 1719 3505 5291 7079 784CIP2D 67 9569 1712 3508 5291 7077 784CIP2D 67 9557 1716 3504 5290 7076 784CIP2D 67 9557 1717 3503 5289 7075 784CIP2D 67 9597 1720 3506 5292 7078 784CIP2D 67 9597 1721 3507 5293 7079 784CIP2D 67 9597 1722 3508 5291 7077 784CIP2D 67 9597 1724 3510 5296 7082 784CIP2D 79 9649 1724 3510 5296 7082 784CIP2D 79 9649 1723 3509 5296 7086 784CIP2D 70 9649 1724 3511 5297 7088 784CIP2D 79 9649 1724 3513 5299 7085 784CIP2D 79 9787 1729 3515 5301 7087 784CIP2D 79 9787			L			9134
1693 3479 5265 7051 784CIP2D_41 9211 1694 3480 5266 7052 784CIP2D_42 9223 1695 3481 5267 7053 784CIP2D_43 9223 1696 3482 5268 7054 784CIP2D_44 9231 1697 3483 5269 7055 784CIP2D_45 9226 1698 3484 5270 7056 784CIP2D_46 9236 1698 3484 5270 7056 784CIP2D_47 9303 1700 3486 5272 7058 784CIP2D_47 9303 1701 3487 5273 7059 784CIP2D_49 9314 1702 3488 5274 7060 784CIP2D_49 9314 1703 3489 5274 7060 784CIP2D_50 9326 1704 3490 5276 7082 784CIP2D_52 9348 1706 3492 5278 7064 784CIP2D_52 9348 1707 3493 5279 7065 784CIP2D_55 9312 1708 3494 5280 7066 784CIP2D_55 9312 1709 3495 5281 7067 784CIP2D_55 9407 1709 3496 5280 7066 784CIP2D_55 9414 1709 3495 5281 7067 784CIP2D_55 9419 1701 3497 5283 7069 784CIP2D_56 9419 1707 3493 5279 7065 784CIP2D_57 9439 1710 3496 5280 7066 784CIP2D_56 9414 1709 3495 5281 7067 784CIP2D_57 9439 1711 3497 5283 7069 784CIP2D_57 9439 1711 3498 5280 7066 784CIP2D_56 9419 1711 3498 5280 7067 784CIP2D_56 9419 1714 3500 5286 7072 784CIP2D_56 9419 1714 3500 5286 7072 784CIP2D_66 9561 1715 3501 5287 7073 784CIP2D_66 9561 1716 3502 5288 7074 784CIP2D_66 9568 1718 3500 5287 7073 784CIP2D_66 9568 1718 3500 5286 7072 784CIP2D_66 9568 1718 3500 5286 7072 784CIP2D_66 9568 1718 3500 5286 7072 784CIP2D_66 9588 1718 3500 5286 7072 784CIP2D_66 9568 1718 3500 5286 7072 784CIP2D_66 9568 1718 3500 5280 7076 784CIP2D_66 9568 1718 3500 5286 7072 784CIP2D_66 9568 1719 3503 5289 7075 784CIP2D_66 9568 1719 3503 5289 7075 784CIP2D_66 9568 1719 3503 5289 7075 784CIP2D_66 9568 1719 3503 5289 7076 784CIP2D_66 9568 1718 3500 5296 7082 784CIP2D_69 9628 1720 3506 5292 7078 784CIP2D_79 9660 1721 3507 5293 7079 784CIP2D_79 9660 1722 3508 5294 7080 784CIP2D_79 9660 1723 3509 5296 7081 784CIP2D_79 9660 1724 3513 5299 7085 784CIP2D_79 9660 1725 3511 5297 7083 784CIP2D_79 9662 1726 3512 5298 7084 788CIP2D_79 9660 1727 3513 5299 7085 784CIP2D_79 9787 1728 3514 5300 7086 784CIP2D_79 9787 1730 3516 5302 7088 784CIP2D_79 9787 1731 3516 5302 7088 784CIP2D_79 9842 1732 3518 5304 7099 784CIP2D_80 9842				1 .	784CIP2D_39	9152
1694 3480 5266 7052 784CTP2D_42 9223 1695 3481 5267 7053 784CTP2D_43 9223 1696 3482 5268 7054 784CTP2D_44 9231 1697 3483 5269 7055 784CTP2D_45 9236 1698 3484 5270 7056 784CTP2D_45 9236 1698 3484 5270 7056 784CTP2D_46 9236 1699 3485 5271 7057 784CTP2D_47 9303 1700 3486 5272 7058 784CTP2D_48 9309 1701 3487 5273 7059 784CTP2D_48 9309 1702 3488 5274 7060 784CTP2D_50 9326 1703 3489 5275 7061 784CTP2D_50 9326 1703 3489 5275 7061 784CTP2D_51 9339 1704 3490 5276 7062 784CTP2D_51 9339 1705 3491 5277 7063 784CTP2D_53 9376 1706 3492 5278 7064 784CTP2D_53 9376 1708 3494 5280 7066 784CTP2D_55 9407 1708 3495 5281 7067 784CTP2D_55 9407 1709 3495 5281 7067 784CTP2D_55 9407 1709 3495 5281 7067 784CTP2D_55 9414 1709 3495 5281 7067 784CTP2D_56 9414 1710 3496 5282 7068 784CTP2D_57 9439 1711 3497 5283 7069 784CTP2D_58 9485 1711 3497 5283 7069 784CTP2D_57 9439 1712 3498 5284 7070 784CTP2D_58 9485 1711 3499 5285 7071 784CTP2D_59 9493 1712 3498 5284 7070 784CTP2D_58 9485 1711 3500 5286 7072 784CTP2D_59 9493 1712 3501 5287 7073 784CTP2D_69 9501 1716 3502 5288 7074 784CTP2D_69 9501 1717 3503 5289 7075 784CTP2D_69 9557 1716 3502 5288 7074 784CTP2D_69 9557 1717 3503 5289 7075 784CTP2D_69 9557 1718 3501 5287 7073 784CTP2D_66 9557 1719 3503 5289 7075 784CTP2D_66 9557 1710 3508 5291 7077 784CTP2D_66 9557 1712 3509 5296 7079 784CTP2D_69 9501 1713 3509 5296 7079 784CTP2D_69 9501 1712 3509 5296 7079 784CTP2D_69 9562 1715 3501 5287 7073 784CTP2D_69 9557 1716 3500 5296 7079 784CTP2D_69 9562 1717 3503 5289 7075 784CTP2D_69 9562 1718 3507 5293 7079 784CTP2D_69 9562 1719 3506 5291 7077 784CTP2D_67 9567 1720 3606 5292 7078 784CTP2D_79 9669 1722 3508 5294 7080 784CTP2D_79 9662 1723 3513 5299 7085 784CTP2D_79 9662 1724 3510 5296 7082 784CTP2D_79 9662 1725 3511 5297 7083 784CTP2D_79 9662 1726 3511 5297 7083 784CTP2D_79 9787 1729 3513 5299 7085 784CTP2D_79 9787 1729 3515 5301 7087 784CTP2D_79 9787 1730 3516 5302 7088 784CTP2D_79 9787 1731 3513 5299 7085 784CTP2D_79 9842 1732 3518 5304 7090 784CTP2D_79 9842				7050	784CIP2D_40	9152
1695 3481 5267 7053 784CIP2D 43 9223 1696 3482 5268 7054 784CIP2D 44 9231 1697 3483 5269 7055 784CIP2D 45 9236 1698 3484 5270 7056 784CIP2D 45 9236 1698 3484 5270 7056 784CIP2D 46 9236 1699 3485 5271 7057 784CIP2D 48 9309 1700 3486 5272 7058 784CIP2D 49 9314 1701 3487 5273 7059 784CIP2D 49 9314 1702 3488 5274 7060 784CIP2D 59 9326 1703 3489 5274 7060 784CIP2D 50 9326 1704 3490 5276 7061 784CIP2D 51 9339 1706 3491 5277 7063 784CIP2D 52 9348 1707 3493 5276 7062 784CIP2D 52 9348 1708 3494 5280 7066 784CIP2D 55 9376 1708 3494 5280 7066 784CIP2D 55 9407 1709 3495 5281 7067 784CIP2D 55 9414 1709 3495 5281 7067 784CIP2D 55 9414 1709 3496 5282 7068 784CIP2D 55 9483 1711 3497 5283 7069 784CIP2D 57 9439 1712 3498 5284 7070 784CIP2D 58 9485 1711 3497 5283 7069 784CIP2D 60 9501 1714 3500 5286 7072 784CIP2D 60 9501 1715 3501 5287 7073 784CIP2D 62 9526 1716 3502 5288 7074 784CIP2D 62 9526 1717 3503 5289 7075 784CIP2D 63 9539 1718 3500 5286 7072 784CIP2D 62 9526 1719 3503 5289 7075 784CIP2D 63 9531 1718 3500 5286 7072 784CIP2D 63 9531 1718 3500 5286 7072 784CIP2D 63 9531 1719 3503 5289 7075 784CIP2D 63 9551 1716 3502 5288 7074 784CIP2D 63 9551 1717 3503 5289 7075 784CIP2D 66 9588 1719 3505 5291 7075 784CIP2D 66 9588 1719 3505 5291 7077 784CIP2D 66 9588 1719 3505 5291 7077 784CIP2D 66 9588 1719 3505 5291 7077 784CIP2D 66 9588 1719 3505 5291 7077 784CIP2D 66 9588 1719 3505 5291 7077 784CIP2D 66 9588 1719 3505 5291 7077 784CIP2D 66 9588 1719 3507 5293 7079 784CIP2D 68 9615 1720 3506 5292 7078 784CIP2D 68 9615 1721 3507 5293 7079 784CIP2D 70 9649 1722 3508 5294 7080 784CIP2D 70 9649 1723 3509 5295 7081 784CIP2D 71 9652 1724 3513 5299 7085 784CIP2D 77 9787 1729 3513 5299 7085 784CIP2D 77 9787 1729 3513 5299 7085 784CIP2D 77 9787 1729 3515 5301 7087 784CIP2D 77 9787 1729 3515 5301 7087 784CIP2D 77 9787 1730 3516 5302 7088 784CIP2D 79 9842 1731 3517 5303 7089 784CIP2D 79 9842	£ 1		5265	7051	784CIP2D_41	9211
1696   3482   5268   7054   784CIP2D 44   9231   1697   3483   5269   7055   784CIP2D 45   9236   1698   3484   5270   7056   784CIP2D 45   9236   1699   3485   5271   7057   784CIP2D 47   9303   1700   3486   5272   7058   784CIP2D 49   9314   1702   3488   5274   7060   784CIP2D 49   9314   1702   3489   5275   7061   784CIP2D 50   9326   1703   3489   5276   7062   784CIP2D 50   9326   1704   3490   5276   7062   784CIP2D 52   9348   1705   3491   5277   7063   784CIP2D 52   9348   1706   3492   5278   7064   784CIP2D 53   9376   1707   3493   5279   7065   784CIP2D 55   9407   1708   3494   5280   7066   784CIP2D 55   9407   1709   3495   5281   7067   784CIP2D 56   9414   1709   3496   5282   7068   784CIP2D 58   9485   1711   3497   5283   7069   784CIP2D 58   9485   1711   3498   5284   7070   784CIP2D 60   9501   1714   3500   5286   7072   784CIP2D 61   9526   1714   3501   5287   7075   784CIP2D 61   9526   1716   3502   5288   7074   784CIP2D 64   9557   1716   3502   5288   7074   784CIP2D 64   9557   1719   3496   5290   7076   784CIP2D 65   9568   1711   3503   5289   7075   784CIP2D 65   9568   1712   3503   5289   7075   784CIP2D 64   9557   1716   3502   5288   7074   784CIP2D 64   9557   1717   3503   5289   7075   784CIP2D 67   9597   1720   3506   5292   7078   784CIP2D 67   9597   1720   3506   5292   7078   784CIP2D 67   9597   1720   3506   5292   7078   784CIP2D 70   9649   1721   3503   5289   7075   784CIP2D 67   9597   1720   3506   5292   7078   784CIP2D 70   9649   1721   3503   5296   7082   784CIP2D 70   9649   1722   3508   5294   7080   784CIP2D 70   9649   1723   3509   5295   7081   784CIP2D 70   9649   1724   3510   5296   7082   784CIP2D 70   9649   1725   3511   5297   7083   784CIP2D 70   9649   1726   3512   5298   7084   784CIP2D 70   9649   1728   3514   5300   7086   784CIP2D 70   9649   1729   3515   5301   7087   784CIP2D 70   9777   1729   3515   5301   7087   784CIP2D 79   9842   1732   3518   5304   7090   784CIP2D 79   9842		3480	5266	7052	784CIP2D_42	9223
1697         3483         5269         7055         784CIP2D 45         9236           1698         3484         5270         7056         784CIP2D 46         9236           1699         3485         5271         7057         784CIP2D 48         9309           1700         3486         5272         7058         784CIP2D 48         9309           1701         3487         5273         7059         784CIP2D 49         9314           1702         3488         5274         7060         784CIP2D 50         9326           1703         3489         5275         7061         784CIP2D 51         9339           1704         3490         5276         7062         784CIP2D 52         9348           1705         3491         5277         7063         784CIP2D 53         9376           1706         3492         5278         7064         784CIP2D 54         9382           1707         3493         5279         7065         784CIP2D 55         9407           1708         3494         5280         7066         784CIP2D 55         9407           1709         3495         5281         7067         784CIP2D 56         9414		3481	5267	7053	784CIP2D_43	9223
1698		3482	5268	7054	784CIP2D 44	9231
1699   3485   5271   7057   784CIP2D_47   9303     1700   3486   5272   7058   784CIP2D_48   9309     1701   3487   5273   7059   784CIP2D_48   9314     1702   3498   5274   7060   784CIP2D_50   9326     1703   3489   5275   7061   784CIP2D_50   9326     1704   3490   5276   7062   784CIP2D_51   9339     1705   3491   5277   7063   784CIP2D_53   93376     1706   3492   5278   7064   784CIP2D_53   9376     1706   3492   5278   7064   784CIP2D_54   9382     1707   3493   5279   7065   784CIP2D_55   9407     1708   3494   5280   7066   784CIP2D_55   9407     1709   3495   5281   7067   784CIP2D_57   9439     1710   3496   5282   7068   784CIP2D_57   9439     1711   3497   5283   7069   784CIP2D_58   9485     1711   3499   5285   7071   784CIP2D_50   9493     1712   3498   5284   7070   784CIP2D_50   9501     1714   3500   5286   7072   784CIP2D_60   9501     1715   3501   5287   7073   784CIP2D_62   9526     1716   3502   5288   7074   784CIP2D_62   9526     1718   3504   5289   7075   784CIP2D_65   9568     1719   3505   5291   7077   784CIP2D_65   9568     1719   3505   5291   7077   784CIP2D_66   9597     1720   3506   5292   7078   784CIP2D_66   9615     1721   3507   5283   7079   784CIP2D_66   9615     1722   3508   5291   7077   784CIP2D_67   9597     1723   3509   5295   7081   784CIP2D_67   9597     1724   3500   5295   7078   784CIP2D_67   9597     1725   3511   5297   7083   784CIP2D_79   9660     1724   3510   5296   7082   784CIP2D_79   9660     1725   3511   5297   7083   784CIP2D_79   9660     1726   3512   5298   7084   784CIP2D_79   9660     1727   3513   5299   7085   784CIP2D_79   9660     1728   3514   5300   7086   784CIP2D_79   9674     1729   3515   5301   7087   784CIP2D_79   9842     1732   3518   5304   7090   784CIP2D_79   9842     1732   3518   5304   7090   784CIP2D_80   9842     1732   3518   5304   7090   784CIP2D_80   9842     1732   3518   5304   7090   784CIP2D_80   9842     1732   3518   5304   7090   784CIP2D_80   9842     1732   3518   5304   7090   784CIP2D_80   9842     173	1697	3483	5269	7055	784CIP2D 45	9236
1700   3486   5272   7058   784CIP2D_48   9309     1701   3487   5273   7059   784CIP2D_49   9314     1702   3488   5274   7060   784CIP2D_50   9326     1703   3489   5275   7061   784CIP2D_51   9339     1704   3490   5276   7062   784CIP2D_52   9348     1705   3491   5277   7063   784CIP2D_52   9348     1706   3492   5278   7064   784CIP2D_54   9382     1707   3493   5279   7065   784CIP2D_55   9407     1708   3494   5280   7066   784CIP2D_56   9414     1709   3495   5281   7067   784CIP2D_58   9485     1710   3496   5282   7068   784CIP2D_58   9485     1711   3497   5283   7069   784CIP2D_59   9493     1712   3498   5284   7070   784CIP2D_60   9501     1713   3499   5285   7071   784CIP2D_62   9526     1714   3500   5286   7072   784CIP2D_62   9526     1716   3502   5288   7074   784CIP2D_63   9551     1716   3503   5289   7075   784CIP2D_66   9588     1719   3505   5291   7077   784CIP2D_66   9588     1719   3505   5291   7077   784CIP2D_66   9588     1719   3505   5291   7077   784CIP2D_66   9588     1719   3505   5291   7077   784CIP2D_66   9588     1719   3505   5291   7077   784CIP2D_66   9588     1719   3505   5291   7077   784CIP2D_66   9588     1719   3505   5291   7077   784CIP2D_66   9588     1710   3508   5290   7076   784CIP2D_66   9588     1712   3509   5295   7081   784CIP2D_69   9628     1721   3507   5293   7079   784CIP2D_69   9628     1722   3508   5294   7080   784CIP2D_79   9649     1723   3509   5295   7081   784CIP2D_79   9629     1724   3510   5296   7082   784CIP2D_79   9662     1725   3511   5297   7083   784CIP2D_79   9622     1726   3512   5298   7084   784CIP2D_79   9725     1728   3514   5300   7086   784CIP2D_79   9787     1729   3515   5301   7087   784CIP2D_79   9787     1729   3515   5301   7087   784CIP2D_79   9787     1721   3513   5299   7085   784CIP2D_79   9787     1722   3513   5299   7085   784CIP2D_79   9787     1723   3516   5302   7088   784CIP2D_79   9787     1731   3517   5303   7089   784CIP2D_79   9786     1732   3518   5304   7090   784CIP2D_80   9842     1732	1698	3484	5270	7056	784CIP2D 46	9236
1701   3487   5273   7059   784CTP2D 49   9314     1702   3488   5274   7060   784CTP2D 50   9326     1703   3489   5275   7061   784CTP2D 50   9326     1704   3490   5276   7062   784CTP2D 52   9348     1705   3491   5277   7063   784CTP2D 52   9348     1706   3492   5278   7064   784CTP2D 54   9382     1707   3493   5279   7065   784CTP2D 54   9382     1707   3493   5279   7065   784CTP2D 55   9407     1708   3494   5280   7066   784CTP2D 56   9414     1709   3495   5281   7067   784CTP2D 57   9439     1710   3496   5282   7068   784CTP2D 57   9439     1711   3497   5283   7069   784CTP2D 59   9493     1712   3498   5284   7070   784CTP2D 60   9501     1713   3499   5285   7071   784CTP2D 61   9526     1714   3500   5286   7072   784CTP2D 62   9526     1715   3501   5287   7073   784CTP2D 63   9551     1716   3502   5288   7074   784CTP2D 64   9557     1717   3503   5289   7075   784CTP2D 66   9568     1718   3504   5290   7076   784CTP2D 66   9588     1719   3505   5291   7077   784CTP2D 66   9588     1719   3505   5291   7077   784CTP2D 66   9588     1710   3508   5292   7078   784CTP2D 68   9615     1721   3507   5293   7079   784CTP2D 68   9615     1722   3508   5291   7077   784CTP2D 68   9628     1723   3509   5295   7081   784CTP2D 69   9628     1724   3550   5292   7078   784CTP2D 69   9628     1725   3511   5297   7083   784CTP2D 70   9649     1727   3513   5296   7082   784CTP2D 71   9652     1728   3514   5300   7086   784CTP2D 72   9660     1725   3515   5301   7087   784CTP2D 75   9746     1728   3516   5302   7088   784CTP2D 75   9746     1729   3515   5301   7087   784CTP2D 75   9746     1729   3515   5301   7087   784CTP2D 75   9746     1729   3515   5301   7087   784CTP2D 75   9746     1729   3515   5301   7087   784CTP2D 75   9746     1729   3515   5301   7087   784CTP2D 75   9746     1729   3515   5301   7087   784CTP2D 75   9746     1729   3515   5301   7087   784CTP2D 75   9746     1729   3515   5301   7087   784CTP2D 75   9746     1729   3515   5301   7087   784CTP2D 75   9746     1732	1699	3485	5271	7057	784CIP2D 47	9303
1702   3488   5274   7060   784CIP2D_50   9326     1703   3489   5275   7061   784CIP2D_51   9339     1704   3490   5276   7062   784CIP2D_52   9348     1705   3491   5277   7063   784CIP2D_52   9348     1706   3492   5278   7064   784CIP2D_54   9382     1707   3493   5279   7065   784CIP2D_55   9407     1708   3494   5280   7066   784CIP2D_56   9414     1709   3495   5281   7067   784CIP2D_56   9414     1709   3496   5282   7068   784CIP2D_59   9439     1710   3496   5282   7068   784CIP2D_59   9493     1711   3497   5283   7069   784CIP2D_59   9493     1712   3498   5284   7070   784CIP2D_60   9501     1713   3499   5285   7071   784CIP2D_61   9526     1714   3500   5286   7072   784CIP2D_61   9526     1715   3501   5287   7073   784CIP2D_63   9551     1716   3502   5288   7074   784CIP2D_63   9551     1716   3502   5288   7074   784CIP2D_65   9588     1719   3503   5289   7075   784CIP2D_65   9568     1719   3505   5291   7077   784CIP2D_66   9588     1719   3505   5291   7077   784CIP2D_66   9588     1719   3505   5291   7077   784CIP2D_67   9597     1720   3506   5292   7078   784CIP2D_69   9628     1721   3507   5293   7079   784CIP2D_69   9628     1722   3508   5294   7080   784CIP2D_69   9628     1723   3509   5296   7081   784CIP2D_71   9652     1724   3510   5296   7081   784CIP2D_72   9660     1725   3511   5297   7083   784CIP2D_72   9660     1726   3512   5298   7084   784CIP2D_72   9660     1727   3513   5299   7085   784CIP2D_75   9746     1728   3514   5300   7086   784CIP2D_75   9746     1729   3515   5301   7087   784CIP2D_76   9777     1729   3515   5301   7087   784CIP2D_76   9777     1729   3515   5301   7087   784CIP2D_76   9777     1729   3515   5301   7087   784CIP2D_76   9777     1729   3515   5301   7087   784CIP2D_76   9777     1731   3517   5303   7089   784CIP2D_76   9777     1732   3518   5304   7090   784CIP2D_78   9790     1731   3517   5303   7089   784CIP2D_78   9790     1732   3518   5304   7090   784CIP2D_80   9842     1732   3518   5304   7090   784CIP2D_80   9842     1732	1700	3486	5272	7058	784CIP2D 48	9309
1703   3489   5275   7061   784CIP2D_51   9339     1704   3490   5276   7062   784CIP2D_52   9348     1705   3491   5277   7063   784CIP2D_53   9376     1706   3492   5278   7064   784CIP2D_53   9376     1707   3493   5279   7065   784CIP2D_55   9407     1708   3494   5280   7066   784CIP2D_55   9407     1709   3495   5281   7067   784CIP2D_56   9414     1709   3495   5281   7067   784CIP2D_57   9439     1710   3496   5282   7068   784CIP2D_57   9439     1711   3497   5283   7069   784CIP2D_59   9493     1712   3498   5284   7070   784CIP2D_60   9501     1713   3499   5285   7071   784CIP2D_60   9501     1714   3500   5286   7072   784CIP2D_62   9526     1715   3501   5287   7073   784CIP2D_62   9526     1716   3502   5288   7074   784CIP2D_63   9551     1716   3502   5288   7074   784CIP2D_65   9568     1719   3505   5291   7077   784CIP2D_65   9588     1719   3505   5291   7077   784CIP2D_66   9598     1719   3505   5291   7077   784CIP2D_66   9588     1712   3507   5293   7079   784CIP2D_66   9527     1720   3506   5292   7078   784CIP2D_68   9628     1721   3507   5293   7079   784CIP2D_69   9628     1722   3508   5294   7080   784CIP2D_70   9649     1723   3509   5295   7081   784CIP2D_70   9649     1724   3510   5296   7082   784CIP2D_71   9652     1725   3511   5297   7083   784CIP2D_71   9652     1726   3512   5298   7084   784CIP2D_71   9652     1727   3513   5299   7085   784CIP2D_71   9725     1728   3514   5300   7086   784CIP2D_76   9777     1728   3515   5301   7087   784CIP2D_78   9790     1731   3517   5303   7089   784CIP2D_79   9842     1732   3518   5304   7090   784CIP2D_79   9842     1733   3518   5304   7090   784CIP2D_79   9842     1733   3518   5304   7090   784CIP2D_79   9842     1733   3518   5304   7090   784CIP2D_79   9842     1733   3518   5304   7090   784CIP2D_80   9842     1733   3518   5304   7090   784CIP2D_80   9842     1733   3518   5304   7090   784CIP2D_80   9842     1733   3518   5304   7090   784CIP2D_80   9842     1733   3518   5304   7090   784CIP2D_80   9842     1733	1701	3487	5273	7059	784CIP2D 49	9314
1703 3489 5275 7061 784CIP2D_51 9339 1704 3490 5276 7062 784CIP2D_52 9348 1705 3491 5277 7063 784CIP2D_52 9348 1706 3492 5278 7064 784CIP2D_54 9382 1707 3493 5279 7065 784CIP2D_55 9407 1708 3494 5280 7066 784CIP2D_55 9407 1709 3495 5281 7067 784CIP2D_56 9414 1709 3495 5281 7067 784CIP2D_57 9439 1710 3496 5282 7068 784CIP2D_58 9485 1711 3497 5283 7069 784CIP2D_59 9493 1712 3498 5284 7070 784CIP2D_60 9501 1713 3499 5285 7071 784CIP2D_61 9526 1714 3500 5286 7072 784CIP2D_61 9526 1715 3501 5287 7073 784CIP2D_63 9551 1716 3502 5288 7074 784CIP2D_64 9557 1717 3503 5289 7075 784CIP2D_66 9568 1718 3504 5290 7076 784CIP2D_66 9568 1719 3505 5291 7077 784CIP2D_66 9588 1719 3505 5291 7077 784CIP2D_66 9588 1719 3505 5291 7077 784CIP2D_66 9588 1712 3507 5293 7079 784CIP2D_66 9589 1721 3507 5293 7079 784CIP2D_66 9649 1722 3508 5294 7080 784CIP2D_69 9628 1723 3509 5295 7081 784CIP2D_70 9649 1724 3510 5296 7080 784CIP2D_70 9649 1725 3511 5297 7083 784CIP2D_70 9649 1726 3512 5298 7081 784CIP2D_70 9660 1727 3513 5299 7080 784CIP2D_71 9652 1728 3514 5300 7086 784CIP2D_73 9660 1728 3514 5300 7086 784CIP2D_76 9777 1729 3515 5301 7087 784CIP2D_76 9777 1729 3515 5301 7087 784CIP2D_77 97660 1731 3517 5303 7089 784CIP2D_76 9777 1729 3515 5301 7086 784CIP2D_76 9777 1729 3515 5301 7086 784CIP2D_76 9777 1729 3515 5301 7087 784CIP2D_77 9786	1702	3488	5274	7060	784CIP2D 50	9326
1705         3491         5277         7063         784CIP2D_53         9376           1706         3492         5278         7064         784CIP2D_54         9382           1707         3493         5279         7065         784CIP2D_55         9407           1708         3494         5280         7066         784CIP2D_56         9414           1709         3495         5281         7067         784CIP2D_57         9439           1710         3496         5282         7068         784CIP2D_58         9485           1711         3497         5283         7069         784CIP2D_59         9493           1712         3498         5284         7070         784CIP2D_60         9501           1713         3499         5285         7071         784CIP2D_60         9501           1713         3499         5286         7072         784CIP2D_62         9526           1714         3500         5286         7072         784CIP2D_62         9526           1715         3501         5287         7073         784CIP2D_64         9557           1717         3503         5288         7074         784CIP2D_64         9558	1703	3489	5275	7061	784CIP2D 51	
1706	1704	3490	5276	7062	784CIP2D 52	9348
1707   3493   5279   7065   784CIP2D 55   9407	1705	3491	5277	7063	784CIP2D 53	9376
1708         3494         5280         7066         784CIP2D_56         9414           1709         3495         5281         7067         784CIP2D_57         9439           1710         3496         5282         7068         784CIP2D_58         9485           1711         3497         5283         7069         784CIP2D_59         9493           1712         3498         5284         7070         784CIP2D_60         9501           1713         3499         5285         7071         784CIP2D_61         9526           1714         3500         5286         7072         784CIP2D_62         9526           1715         3501         5287         7073         784CIP2D_63         9551           1716         3502         5288         7074         784CIP2D_63         9551           1717         3503         5289         7075         784CIP2D_65         9568           1718         3504         5290         7076         784CIP2D_65         9588           1719         3505         5291         7077         784CIP2D_66         9588           1720         3506         5292         7078         784CIP2D_69         9628		3492	5278	7064	784CIP2D 54	9382
1709         3495         5281         7067         784CIP2D 57         9439           1710         3496         5282         7068         784CIP2D 58         9485           1711         3497         5283         7069         784CIP2D 59         9493           1712         3498         5284         7070         784CIP2D 60         9501           1713         3499         5285         7071         784CIP2D 61         9526           1714         3500         5286         7072         784CIP2D 62         9526           1715         3501         5287         7073         784CIP2D 63         9551           1716         3502         5288         7074         784CIP2D 64         9557           1717         3503         5289         7075         784CIP2D 65         9568           1718         3504         5290         7076         784CIP2D 66         9588           1719         3505         5291         7077         784CIP2D 66         9588           1719         3506         5292         7078         784CIP2D 68         9615           1721         3507         5293         7079         784CIP2D 68         9615	1707	3493	5279	7065	784CIP2D 55	9407
1710         3496         5282         7068         784CIP2D 58         9485           1711         3497         5283         7069         784CIP2D 59         9493           1712         3498         5284         7070         784CIP2D 60         9501           1713         3499         5285         7071         784CIP2D 61         9526           1714         3500         5286         7072         784CIP2D 62         9526           1715         3501         5287         7073         784CIP2D 63         9551           1716         3502         5288         7074         784CIP2D 63         9551           1717         3503         5289         7075         784CIP2D 64         9557           1717         3503         5289         7075         784CIP2D 65         9588           1718         3504         5290         7076         784CIP2D 66         9588           1719         3505         5291         7077         784CIP2D 67         9597           1720         3506         5292         7078         784CIP2D 68         9615           1721         3507         5293         7079         784CIP2D 69         9628	1708	3494	5280	7066	784CIP2D 56	9414
1711       3497       5283       7069       784CIP2D 59       9493         1712       3498       5284       7070       784CIP2D 60       9501         1713       3499       5285       7071       784CIP2D 61       9526         1714       3500       5286       7072       784CIP2D 62       9526         1715       3501       5287       7073       784CIP2D 63       9551         1716       3502       5288       7074       784CIP2D 64       9557         1717       3503       5289       7075       784CIP2D 65       9568         1718       3504       5290       7076       784CIP2D 66       9588         1719       3505       5291       7077       784CIP2D 67       9597         1720       3506       5292       7078       784CIP2D 68       9615         1721       3507       5293       7079       784CIP2D 69       9628         1722       3508       5294       7080       784CIP2D 70       9649         1723       3509       5295       7081       784CIP2D 71       9652         1724       3510       5296       7082       784CIP2D 72       9660	1709	3495	. 5281	7067	784CIP2D 57	9439
1711         3497         5283         7069         784CIP2D_59         9493           1712         3498         5284         7070         784CIP2D_60         9501           1713         3499         5285         7071         784CIP2D_61         9526           1714         3500         5286         7072         784CIP2D_62         9526           1715         3501         5287         7073         784CIP2D_63         9551           1716         3502         5288         7074         784CIP2D_64         9557           1717         3503         5289         7075         784CIP2D_65         9568           1718         3504         5290         7076         784CIP2D_66         9588           1719         3505         5291         7077         784CIP2D_67         9597           1720         3506         5292         7078         784CIP2D_69         9628           1721         3507         5293         7079         784CIP2D_69         9628           1722         3508         5294         7080         784CIP2D_70         9649           1723         3509         5295         7081         784CIP2D_70         9649	1710	3496	5282	7068	784CIP2D 58	9485
1712         3498         5284         7070         784CIP2D_60         9501           1713         3499         5285         7071         784CIP2D_61         9526           1714         3500         5286         7072         784CIP2D_62         9526           1715         3501         5287         7073         784CIP2D_63         9551           1716         3502         5288         7074         784CIP2D_64         9557           1717         3503         5289         7075         784CIP2D_65         9568           1718         3504         5290         7076         784CIP2D_66         9588           1719         3505         5291         7077         784CIP2D_67         9597           1720         3506         5292         7078         784CIP2D_68         9615           1721         3507         5293         7079         784CIP2D_69         9628           1722         3508         5294         7080         784CIP2D_70         9649           1723         3509         5295         7081         784CIP2D_71         9652           1724         3510         5296         7082         784CIP2D_72         9660	1711	3497	5283	7069		
1713         3499         5285         7071         784CIP2D_61         9526           1714         3500         5286         7072         784CIP2D_62         9526           1715         3501         5287         7073         784CIP2D_63         9551           1716         3502         5288         7074         784CIP2D_64         9557           1717         3503         5289         7075         784CIP2D_65         9568           1718         3504         5290         7076         784CIP2D_66         9588           1719         3505         5291         7077         784CIP2D_67         9597           1720         3506         5292         7078         784CIP2D_68         9615           1721         3507         5293         7079         784CIP2D_69         9628           1722         3508         5294         7080         784CIP2D_70         9649           1723         3509         5295         7081         784CIP2D_71         9652           1724         3510         5296         7082         784CIP2D_71         9652           1724         3511         5297         7083         784CIP2D_72         9660	1712	3498	5284	7070	784CIP2D 60	9501
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1716         3502         5288         7074         784CIP2D_64         9557           1717         3503         5289         7075         784CIP2D_65         9568           1718         3504         5290         7076         784CIP2D_66         9588           1719         3505         5291         7077         784CIP2D_67         9597           1720         3506         5292         7078         784CIP2D_68         9615           1721         3507         5293         7079         784CIP2D_69         9628           1722         3508         5294         7080         784CIP2D_70         9649           1723         3509         5295         7081         784CIP2D_70         9649           1723         3510         5296         7082         784CIP2D_71         9652           1724         3510         5296         7082         784CIP2D_72         9660           1725         3511         5297         7083         784CIP2D_73         9662           1726         3513         5299         7085         784CIP2D_75         9746           1728         3514         5300         7086         784CIP2D_76         9777	1715	3501	5287			
1717         3503         5289         7075         784CIP2D 65         9568           1718         3504         5290         7076         784CIP2D 66         9588           1719         3505         5291         7077         784CIP2D 67         9597           1720         3506         5292         7078         784CIP2D 68         9615           1721         3507         5293         7079         784CIP2D 69         9628           1722         3508         5294         7080         784CIP2D 70         9649           1723         3509         5295         7081         784CIP2D 70         9649           1724         3510         5296         7082         784CIP2D 71         9652           1724         3511         5297         7083         784CIP2D 72         9660           1725         3511         5297         7083         784CIP2D 73         9662           1726         3512         5298         7084         784CIP2D 74         9725           1727         3513         5299         7085         784CIP2D 75         9746           1728         3514         5300         7086         784CIP2D 76         9777	1716	3502				
1718         3504         5290         7076         784CIP2D 66         9588           1719         3505         5291         7077         784CIP2D 67         9597           1720         3506         5292         7078         784CIP2D 68         9615           1721         3507         5293         7079         784CIP2D 69         9628           1722         3508         5294         7080         784CIP2D 70         9649           1723         3509         5295         7081         784CIP2D 71         9652           1724         3510         5296         7082         784CIP2D 72         9660           1725         3511         5297         7083         784CIP2D 73         9662           1726         3512         5298         7084         784CIP2D 74         9725           1727         3513         5299         7085         784CIP2D 75         9746           1728         3514         5300         7086         784CIP2D 76         9777           1729         3515         5301         7087         784CIP2D 77         9787           1730         3516         5302         7088         784CIP2D 79         9842	1717	3503				
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1721         3507         5293         7079         784CIP2D 69         9628           1722         3508         5294         7080         784CIP2D 70         9649           1723         3509         5295         7081         784CIP2D 71         9652           1724         3510         5296         7082         784CIP2D 72         9660           1725         3511         5297         7083         784CIP2D 73         9662           1726         3512         5298         7084         784CIP2D 74         9725           1727         3513         5299         7085         784CIP2D 75         9746           1728         3514         5300         7086         784CIP2D 76         9777           1729         3515         5301         7087         784CIP2D 77         9787           1730         3516         5302         7088         784CIP2D 78         9790           1731         3517         5303         7089         784CIP2D 79         9842           1732         3518         5304         7090         784CIP2D 80         9842						
1722         3508         5294         7080         784CIP2D_70         9649           1723         3509         5295         7081         784CIP2D_71         9652           1724         3510         5296         7082         784CIP2D_72         9660           1725         3511         5297         7083         784CIP2D_73         9662           1726         3512         5298         7084         784CIP2D_74         9725           1727         3513         5299         7085         784CIP2D_75         9746           1728         3514         5300         7086         784CIP2D_76         9777           1729         3515         5301         7087         784CIP2D_77         9787           1730         3516         5302         7088         784CIP2D_78         9790           1731         3517         5303         7089         784CIP2D_79         9642           1732         3518         5304         7090         784CIP2D_80         9842						
1723         3509         5295         7081         784CIP2D_71         9652           1724         3510         5296         7082         784CIP2D_72         9660           1725         3511         5297         7083         784CIP2D_73         9662           1726         3512         5298         7084         784CIP2D_74         9725           1727         3513         5299         7085         784CIP2D_75         9746           1728         3514         5300         7086         784CIP2D_76         9777           1729         3515         5301         7087         784CIP2D_77         9787           1730         3516         5302         7088         784CIP2D_78         9790           1731         3517         5303         7089         784CIP2D_79         9842           1732         3518         5304         7090         784CIP2D_80         9842						
1724         3510         5296         7082         784CIP2D_72         9660           1725         3511         5297         7083         784CIP2D_73         9662           1726         3512         5298         7084         784CIP2D_74         9725           1727         3513         5299         7085         784CIP2D_75         9746           1728         3514         5300         7086         784CIP2D_76         9777           1729         3515         5301         7087         784CIP2D_77         9787           1730         3516         5302         7088         784CIP2D_78         9790           1731         3517         5303         7089         784CIP2D_79         9842           1732         3518         5304         7090         784CIP2D_80         9842						
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1726         3512         5298         7084         784CIP2D_74         9725           1727         3513         5299         7085         784CIP2D_75         9746           1728         3514         5300         7086         784CIP2D_76         9777           1729         3515         5301         7087         784CIP2D_77         9787           1730         3516         5302         7088         784CIP2D_78         9790           1731         3517         5303         7089         784CIP2D_79         9842           1732         3518         5304         7090         784CIP2D_80         9842						
1727         3513         5299         7085         784CIP2D 75         9746           1728         3514         5300         7086         784CIP2D 76         9777           1729         3515         5301         7087         784CIP2D 77         9787           1730         3516         5302         7088         784CIP2D 78         9790           1731         3517         5303         7089         784CIP2D 79         9842           1732         3518         5304         7090         784CIP2D 80         9842						
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1730         3516         5302         7088         784CIP2D 78         9790           1731         3517         5303         7089         784CIP2D 79         9642           1732         3518         5304         7090         784CIP2D 80         9842						
1731 3517 5303 7089 784CIP2D 79 9842 1732 3518 5304 7090 784CIP2D 80 9842						
1732 3518 5304 7090 784CIP2D_80 9842		(				
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	1/33	3519	5305	7091	784CIP2D_81	9848

Seq 10 Not   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of full-   Not of	SEQ ID NO:	7 656 75	1 600 TE 100	1 222		
Length   nucleotide sequence		SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
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1748 3534 5320 7106 784CTP2E 4 3673 1749 3535 5321 7107 784CTP2E 5 4018 1750 3536 5322 7108 784CTP2E 6 4467 1751 3537 5323 7109 784CTP2E 7 4865 1752 3538 5324 7110 784CTP2E 8 4916 1753 3539 5325 7111 784CTP2E 8 4916 1753 3539 5325 7111 784CTP2E 9 4923 1754 3540 5326 7112 784CTP2E 10 4926 1755 3541 5327 7113 784CTP2E 11 4962 1756 3542 5328 7114 784CTP2E 12 4963 1757 3543 5329 7115 784CTP2E 13 4964 1759 3545 5331 7117 784CTP2E 13 4964 1759 3545 5331 7117 784CTP2E 13 4964 1756 3546 5332 7118 784CTP2E 14 6983 1759 3545 5331 7117 784CTP2E 15 5835 1760 3546 5332 7118 784CTP2E 16 7682 1761 3547 5333 7119 784CTP2E 18 7689 1762 3548 5334 7120 784CTP2E 18 7689 1763 3549 5335 7121 784CTP2E 19 7707 1764 3550 5336 7122 784CTP2E 19 7707 1764 3550 5336 7122 784CTP2E 20 7707 1765 3551 5337 7123 784CTP2E 20 7707 1766 3552 5338 7122 784CTP2E 21 7752 1766 3552 5338 7124 784CTP2E 21 7752 1766 3553 5339 7125 784CTP2E 21 752 1767 3553 5339 7125 784CTP2E 22 8357 1769 3555 5341 7127 784CTP2E 21 7752 1767 3553 5339 7125 784CTP2E 21 7752 1767 3553 5339 7122 784CTP2E 21 7752 1767 3553 5339 7125 784CTP2E 21 752 1767 3553 5339 7125 784CTP2E 21 752 1767 3553 5339 7125 784CTP2E 21 752 1767 3553 5339 7127 784CTP2E 21 752 1767 3553 5339 7127 784CTP2E 21 752 1767 3553 5339 7127 784CTP2E 21 752 1767 3553 5339 7127 784CTP2E 21 752 1767 3553 5349 7123 784CTP2E 21 752 1767 3553 5349 7125 784CTP2E 21 752 1767 3556 5342 7128 784CTP2E 2 3559 1771 3557 5343 7129 784CTP2E 2 3559 1771 3557 5343 7129 784CTP2E 3 4021 1772 3558 5344 7130 784CTP2E 3 4021 1773 3559 5345 7131 784CTP2F 5 4566 1775 3563 5349 7135 784CTP2F 1 5008 1778 3566 5352 7348 7139 784CTP2F 1 5008 1778 3566 5352 7349 7135 784CTP2F 1 5008 1778 3566 5352 7349 7135 784CTP2F 1 5008 1778 3566 5352 7349 7135 784CTP2F 1 5008 1778 3569 5355 7341 737 784CTP2F 1 5008 1778 3569 5357 7143 784CTP2F 1 5005 1778 3569 5357 7143 784CTP2F 1 5005 1788 3569 5357 7143 784CTP2F 1 5005			L	7104		3121
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1750		3534	5320	7106	784CIP2E_4	3673
1751 3537 5323 7109 784CIP2E 7 4865 1752 3538 5324 7110 784CIP2E 8 4916 1753 3538 5324 7110 784CIP2E 8 4916 1753 3539 S325 7111 784CIP2E 9 4923 1754 3540 5326 7112 784CIP2E 10 4926 1755 3541 5327 7113 784CIP2E 11 4962 1755 3541 5327 7113 784CIP2E 11 4962 1755 3541 5327 7113 784CIP2E 11 4962 1757 3543 5329 7115 784CIP2E 13 4964 1758 3544 5330 7116 784CIP2E 13 4964 1759 3545 5331 7117 784CIP2E 14 4988 1759 3545 5331 7117 784CIP2E 16 7682 1760 3546 5332 7118 784CIP2E 16 7682 1761 3547 5333 7119 784CIP2E 16 7682 1762 3548 5334 7120 784CIP2E 17 7682 1763 3549 5335 7121 784CIP2E 19 7707 1764 3550 5336 7122 784CIP2E 19 7707 1765 3551 5337 7123 784CIP2E 10 7702 1766 3552 5338 7124 784CIP2E 20 7707 1766 3552 5338 7124 784CIP2E 22 8357 1767 3553 5339 7125 784CIP2E 23 9065 1768 3554 5340 7126 784CIP2E 23 9065 1769 3555 5341 7127 784CIP2E 23 9065 1769 3555 5341 7127 784CIP2E 24 9324 1769 3556 5342 7128 784CIP2E 24 9324 1769 3555 5341 7127 784CIP2E 2 3559 1771 3557 5343 7129 784CIP2E 2 3559 1771 3557 5343 7129 784CIP2E 3 4021 1772 3558 5344 7130 784CIP2E 2 3559 1771 3557 5343 7129 784CIP2E 3 4021 1772 3558 5344 7130 784CIP2E 3 4021 1773 3559 5345 7131 784CIP2E 3 4021 1773 3559 5345 7131 784CIP2E 9 5008 1774 3560 5366 5362 5348 7134 784CIP2E 9 5008 1778 3563 5359 7355 7136 784CIP2E 9 5008 1778 3563 5359 7355 7136 784CIP2E 9 5008 1779 3565 5367 7135 784CIP2E 9 5008 1779 3563 5359 7355 7136 784CIP2E 9 5008 1779 3563 5359 7355 7136 784CIP2E 1 5015 1790 3566 5352 7138 784CIP2E 1 5015 1791 3567 5353 7139 784CIP2E 1 5015 1791 3567 5353 7139 784CIP2E 1 5015 1791 3567 5353 7139 784CIP2E 1 5015 1793 3569 5355 7141 784CIP2E 15 8828 1794 3569 5355 7141 784CIP2E 15 8828 1798 3569 5355 7141 784CIP2E 15 8828 1798 3569 5355 7141 784CIP2E 15 8828 1798 3569 5355 7141 784CIP2E 15 8828 1785 3571 5357 7143 784CIP2E 15 8830 1785 3571 5357 7143 784CIP2E 17 9739	1749	3535	5321	7107	784CIP2E 5	4018
1752   3538   5324   7110   784CIP2E 8   4916     1753   3539   5325   7111   784CIP2E 9   4923     1754   3540   5326   7112   784CIP2E 10   4926     1755   3541   5327   7113   784CIP2E 11   4962     1756   3542   5328   7114   784CIP2E 11   4962     1757   3543   5329   7115   784CIP2E 12   4963     1757   3543   5329   7115   784CIP2E 13   4964     1758   3544   5330   7116   784CIP2E 14   4988     1759   3545   5331   7117   784CIP2E 15   5835     1760   3546   5332   7118   784CIP2E 16   7682     1761   3547   5333   7119   784CIP2E 16   7682     1762   3548   5334   7120   784CIP2E 18   7699     1763   3549   5335   7121   784CIP2E 19   7707     1764   3550   5336   7122   784CIP2E 19   7707     1765   3551   5337   7123   784CIP2E 20   7707     1766   3552   5338   7124   784CIP2E 22   8357     1767   3553   5339   7125   784CIP2E 22   8357     1768   3554   5340   7126   784CIP2E 24   9324     1769   3555   5341   7127   784CIP2E 24   9324     1769   3555   5341   7127   784CIP2E 24   9324     1769   3555   5341   7127   784CIP2E 24   9324     1770   3556   5342   7128   784CIP2E 24   9324     1771   3557   5343   7129   784CIP2E 3   5559     1771   3557   5343   7129   784CIP2E 3   4021     1772   3558   5344   7130   784CIP2E 3   4021     1773   3559   5345   7131   784CIP2E 3   4021     1774   3560   5346   7132   784CIP2E 3   4021     1777   3563   5349   7135   784CIP2E 3   4021     1778   3565   5349   7135   784CIP2E 6   4705     1779   3565   5349   7135   784CIP2E 7   4707     1776   3565   5349   7135   784CIP2E 10   5009     1778   3566   5352   7138   784CIP2E 11   5018     1781   3557   5353   7139   784CIP2E 11   5018     1781   3569   5355   7141   784CIP2E 14   7725     1782   3568   5354   7140   784CIP2E 15   8828     1785   3571   5357   7143   784CIP2E 17   9739	1750	3536	5322	7108	784CIP2E 6	4467
1753 3539 5325 7111 784CIP2E 9 4923 1754 3540 5326 7112 784CIP2E 10 4926 1755 3541 5327 7113 784CIP2E 11 4962 1755 3541 5327 7113 784CIP2E 11 4962 1755 3542 5328 7114 784CIP2E 12 4963 1757 3543 5329 7115 784CIP2E 13 4964 1758 3544 5330 7116 784CIP2E 14 4988 1759 3545 5331 7117 784CIP2E 15 5835 1760 3546 5332 7118 784CIP2E 16 7682 1761 3547 5333 7119 784CIP2E 16 7682 1762 3548 5334 7120 784CIP2E 17 7682 1763 3549 5335 7121 784CIP2E 18 7699 1763 3549 5335 7121 784CIP2E 19 7707 1764 3550 5336 7122 784CIP2E 19 7707 1765 3551 5337 7123 784CIP2E 19 7707 1766 3552 5338 7124 784CIP2E 20 7707 1767 3553 5339 7125 784CIP2E 21 7752 1769 3555 5341 7127 784CIP2E 23 9065 1769 3555 5341 7127 784CIP2E 24 9324 1769 3555 5341 7127 784CIP2E 23 9065 1768 3554 5340 7126 784CIP2E 24 9324 1769 3555 5341 7127 784CIP2E 23 9065 1768 3554 5340 7126 784CIP2E 24 9324 1769 3555 5341 7127 784CIP2E 2 3559 1771 3557 5343 7129 784CIP2E 3 4021 1772 3558 5344 7130 784CIP2E 3 4021 1773 3558 5344 7130 784CIP2E 3 4021 1773 3559 5345 7131 784CIP2E 3 4021 1773 3556 5342 7128 784CIP2E 3 4021 1773 3556 5342 7128 784CIP2E 3 4021 1773 3556 5343 7129 784CIP2E 3 4021 1773 3556 5346 7131 784CIP2E 3 4021 1773 3556 5346 7131 784CIP2E 5 4566 1774 3560 5346 7132 784CIP2E 5 5068 1778 3561 5347 7133 784CIP2E 9 5008 1778 3563 5349 7135 784CIP2E 9 5008 1778 3563 5349 7135 784CIP2E 9 5008 1779 3563 5349 7135 784CIP2E 9 5008 1778 3569 5355 7137 784CIP2E 10 5009 1779 3563 5349 7135 784CIP2E 1 5015 1780 3566 5352 7138 784CIP2E 1 5015 1781 3567 5353 7139 784CIP2E 1 5015 1780 3568 5354 7140 784CIP2E 15 8828 1784 3570 5355 7141 784CIP2E 15 8828 1784 3570 5355 7141 784CIP2E 15 8828 1785 3571 5357 7143 784CIP2E 17 9739	1751	3537	5323	7109	784CIP2E 7	4865
1753	1752	3538	5324	7110	784CIP2E 8	4916
1754   3540   5326   7112   784CIP2E_10   4926   1755   3541   5327   7113   784CIP2E_11   4962   1756   3542   5328   7114   784CIP2E_12   4963   1757   3543   5329   7115   784CIP2E_13   4964   1758   3544   5330   7116   784CIP2E_14   4988   1759   3545   5331   7117   784CIP2E_15   5835   1760   3546   5332   7118   784CIP2E_16   5835   1760   3546   5332   7118   784CIP2E_17   7682   1761   3547   5333   7119   784CIP2E_17   7682   1761   3548   5334   7120   784CIP2E_18   7699   1763   3549   5335   7121   784CIP2E_19   7707   1764   3550   5336   7122   784CIP2E_20   7707   1765   3551   5337   7123   784CIP2E_21   7752   1766   3552   5338   7124   784CIP2E_22   8357   1767   3553   5339   7125   784CIP2E_23   9065   1768   3554   5340   7126   784CIP2E_24   9324   1769   3555   5341   7127   784CIP2E_24   9324   1769   3555   5342   7128   784CIP2E_24   9324   1769   3556   5342   7128   784CIP2E_24   9324   1770   3556   5342   7128   784CIP2E_3   3065   1771   3557   5343   7129   784CIP2E_3   3559   1771   3558   5344   7130   784CIP2E_3   4021   1772   3558   5344   7130   784CIP2E_3   4021   1773   3559   5346   7131   784CIP2E_5   4476   1776   3560   5346   7132   784CIP2E_5   4470   1776   3560   5346   7132   784CIP2E_5   4666   1774   3560   5346   7132   784CIP2E_6   4705   1776   3563   5349   7135   784CIP2E_6   4705   1776   3563   5349   7135   784CIP2E_1   5008   1778   3564   5359   7136   784CIP2E_1   5008   1778   3564   5359   7136   784CIP2E_1   5008   1778   3564   5359   5355   7137   784CIP2E_1   5015   1780   3566   5352   7138   784CIP2E_1   5015   1780   3566   5352   7138   784CIP2E_1   5015   1781   3567   5353   7139   784CIP2E_1   5015   1781   3569   5355   7141   784CIP2E_1   5015   1781   3569   5355   7141   784CIP2E_1   5015   1781   3569   5355   7141   784CIP2E_1   5015   1781   3569   5355   7142   784CIP2E_1   5015   1781   3569   5355   7141   784CIP2E_1   5015   1784   3560   5355   7142   784CIP2E_1   5015   1784   3560   5355   7142   784CIP2E_1   5015   17	1753	3539	5325	7111		
1755   3541   5327   7113   784CIP2E 11   4962     1756	1754	3540	5326	7112		4
1756	1755	3541	5327		<u> </u>	
1757 3543 5329 7115 784CIP2E_13 4964 1758 3544 5330 7116 784CIP2E_14 4988 1759 3545 5331 7117 784CIP2E_15 5835 1760 3546 5332 7118 784CIP2E_16 7682 1761 3547 5333 7119 784CIP2E_16 7682 1762 3548 5334 7120 784CIP2E_18 7699 1763 3549 5335 7121 784CIP2E_18 7699 1764 3550 5336 7122 784CIP2E_20 7707 1765 3551 5337 7123 784CIP2E_21 7752 1766 3552 5338 7124 784CIP2E_21 7752 1766 3552 5338 7124 784CIP2E_22 8357 1767 3553 5339 7125 784CIP2E_23 9065 1768 3554 5340 7126 784CIP2E_24 9324 1769 3555 5341 7127 784CIP2E_2 4 9324 1769 3555 5341 7127 784CIP2E_2 4 9324 1769 3556 5342 7128 784CIP2E_2 3 3559 1771 3557 5343 7129 784CIP2E_2 4 9324 1772 3558 5344 7130 784CIP2E_3 4021 1772 3558 5344 7130 784CIP2E_4 4474 1773 3559 5345 7131 784CIP2E_5 4566 1774 3560 5346 7132 784CIP2E_6 4705 1775 3561 5347 7133 784CIP2E_6 4705 1776 3563 5349 7135 784CIP2E_6 4705 1777 3563 5349 7135 784CIP2E_8 4712 1777 3563 5349 7135 784CIP2E_8 4712 1777 3563 5349 7135 784CIP2E_8 4712 1777 3563 5349 7135 784CIP2E_8 4712 1777 3563 5349 7135 784CIP2E_1 5008 1778 3564 5350 7136 784CIP2E_1 5008 1779 3565 5351 7137 784CIP2E_1 5008 1779 3565 5351 7137 784CIP2E_1 5008 1779 3563 5349 7135 784CIP2E_1 5008 1779 3563 5349 7135 784CIP2E_1 5008 1779 3565 5351 7137 784CIP2E_1 5008 1779 3565 5351 7137 784CIP2E_1 5005 1780 3566 5352 7138 784CIP2E_1 5005 1780 3566 5352 7138 784CIP2E_1 5005 1780 3568 5354 7140 784CIP2E_1 1 5015 1781 3567 5355 7141 784CIP2E_1 16 8830 1784 3570 5356 7142 784CIP2E_1 16 8830 1785 3571 5357 7143 784CIP2E_1 16 8830	1756	3542				
1758         3544         5330         7116         784CIP2E_14         4988           1759         3545         5331         7117         784CIP2E_15         5835           1760         3546         5332         7118         784CIP2E_16         7682           1761         3547         5333         7119         784CIP2E_17         7682           1762         3548         5334         7120         784CIP2E_18         7699           1763         3549         5335         7121         784CIP2E_19         7707           1764         3550         5336         7122         784CIP2E_20         7707           1765         3551         5337         7123         784CIP2E_21         7752           1766         3552         5338         7124         784CIP2E_21         7752           1767         3553         5339         7125         784CIP2E_22         8357           1767         3553         5339         7125         784CIP2E_22         8357           1768         3554         5340         7126         784CIP2E_22         8357           1769         3555         5341         7127         784CIP2E_1         2976	1757					
1759         3545         5331         7117         784CIP2E 15         5835           1760         3546         5332         7118         784CIP2E 16         7682           1761         3547         5333         7119         784CIP2E 17         7682           1762         3548         5334         7120         784CIP2E 18         7699           1763         3549         5335         7121         784CIP2E 19         7707           1764         3550         5336         7122         784CIP2E 20         7707           1765         3551         5337         7123         784CIP2E 21         7752           1766         3552         5338         7124         784CIP2E 22         8357           1767         3553         5339         7125         784CIP2E 23         9065           1768         3554         5340         7126         784CIP2E 23         9065           1768         3555         5341         7127         784CIP2E 24         9324           1769         3555         5341         7127         784CIP2F 1         2976           1770         3556         5342         7128         784CIP2F 2         3559	1758					
1760         3546         5332         7118         784CIPZE_16         7682           1761         3547         5333         7119         784CIPZE_17         7682           1762         3548         5334         7120         784CIPZE_18         7699           1763         3549         5335         7121         784CIPZE_19         7707           1764         3550         5336         7122         784CIPZE_20         7707           1765         3551         5337         7123         784CIPZE_21         7752           1766         3552         5338         7124         784CIPZE_22         8357           1767         3553         5339         7125         784CIPZE_22         8357           1767         3553         5339         7125         784CIPZE_22         8357           1768         3554         5340         7126         784CIPZE_23         9065           1768         3555         5341         7127         784CIPZE_24         9324           1769         3555         5341         7127         784CIPZE_24         9324           1769         3555         5341         7127         784CIPZE_2         3559	1759					L
1761     3547     5333     7119     784CIP2E 17     7682       1762     3548     5334     7120     784CIP2E 18     7699       1763     3549     5335     7121     784CIP2E 19     7707       1764     3550     5336     7122     784CIP2E 20     7707       1765     3551     5337     7123     784CIP2E 21     7752       1766     3552     5338     7124     784CIP2E 23     9065       1767     3553     5339     7125     784CIP2E 23     9065       1768     3554     5340     7126     784CIP2E 24     9324       1769     3555     5341     7127     784CIP2F 1     2976       1770     3556     5342     7128     784CIP2F 2     3559       1771     3557     5343     7129     784CIP2F 3     4021       1772     3558     5344     7130     784CIP2F 3     4021       1772     3558     5345     7131     784CIP2F 5     4566       1771     3550     5345     7131     784CIP2F 5     4566       1774     3560     5346     7132     784CIP2F 5     4705       1775     3561     5347     7133     784CIP2F 6 <td>1760</td> <td>3546</td> <td></td> <td></td> <td></td> <td></td>	1760	3546				
1762         3548         5334         7120         784CIP2E 18         7699           1763         3549         5335         7121         784CIP2E 19         7707           1764         3550         5336         7122         784CIP2E 20         7707           1765         3551         5337         7123         784CIP2E 21         7752           1766         3552         5338         7124         784CIP2E 23         9065           1767         3553         5339         7125         784CIP2E 23         9065           1768         3554         5340         7126         784CIP2E 23         9065           1769         3555         5341         7127         784CIP2E 1         2976           1770         3556         5342         7128         784CIP2F 1         2976           1771         3557         5343         7129         784CIP2F 3         4021           1771         3558         5344         7130         784CIP2F 3         4021           1771         3558         5344         7130         784CIP2F 3         4021           1771         3559         5345         7131         784CIP2F 5         4566 </td <td>1761</td> <td>3547</td> <td></td> <td></td> <td></td> <td></td>	1761	3547				
1763     3549     5335     7121     784CIP2E 19     7707       1764     3550     5336     7122     784CIP2E 20     7707       1765     3551     5337     7123     784CIP2E 21     7752       1766     3552     5338     7124     784CIP2E 22     8357       1767     3553     5339     7125     784CIP2E 23     9065       1768     3554     5340     7126     784CIP2E 24     9324       1769     3555     5341     7127     784CIP2E 1     2976       1770     3556     5342     7128     784CIP2F 2     3559       1771     3557     5343     7129     784CIP2F 3     4021       1772     3558     5344     7130     784CIP2F 3     4021       1773     3559     5345     7131     784CIP2F 5     4566       1774     3560     5346     7132     784CIP2F 5     4705       1775     3561     5347     7133     784CIP2F 6     4705       1775     3561     5347     7133     784CIP2F 7     4707       1776     3562     5348     7134     784CIP2F 10     5008       1777     3563     5349     7135     784CIP2F 10 <td>1762</td> <td></td> <td></td> <td></td> <td></td> <td></td>	1762					
1764         3550         5336         7122         784CIP2E 20         7707           1765         3551         5337         7123         784CIP2E 21         7752           1766         3552         5338         7124         784CIP2E 22         8357           1767         3553         5339         7125         784CIP2E 23         9065           1768         3554         5340         7126         784CIP2E 24         9324           1769         3555         5341         7127         784CIP2E 1         2976           1770         3556         5342         7128         784CIP2F 1         2976           1771         3557         5343         7129         784CIP2F 1         2976           1771         3558         5344         7130         784CIP2F 3         4021           1772         3558         5344         7130         784CIP2F 4         4474           1773         3559         5345         7131         784CIP2F 5         4566           1774         3560         5346         7132         784CIP2F 6         4705           1775         3561         5347         7133         784CIP2F 7         4707 <td>1763</td> <td>3549</td> <td></td> <td></td> <td></td> <td></td>	1763	3549				
1765         3551         5337         7123         784CIP2E 21         7752           1766         3552         5338         7124         784CIP2E 22         8357           1767         3553         5339         7125         784CIP2E 23         9065           1768         3554         5340         7126         784CIP2E 24         9324           1769         3555         5341         7127         784CIP2F 1         2976           1770         3556         5342         7128         784CIP2F 2         3559           1771         3557         5343         7129         784CIP2F 3         4021           1772         3558         5344         7130         784CIP2F 3         4021           1772         3558         5344         7130         784CIP2F 4         4474           1773         3559         5345         7131         784CIP2F 5         4566           1774         3560         5346         7132         784CIP2F 5         4705           1775         3561         5347         7133         784CIP2F 7         4707           1776         3562         5348         7134         784CIP2F 9         5008	1764					
1766         3552         5338         7124         784CIP2E_22         8357           1767         3553         5339         7125         784CIP2E_23         9065           1768         3554         5340         7126         784CIP2E_24         9324           1769         3555         5341         7127         784CIP2F_1         2976           1770         3556         5342         7128         784CIP2F_2         3559           1771         3557         5343         7129         784CIP2F_3         4021           1772         3558         5344         7130         784CIP2F_3         4021           1773         3559         5345         7131         784CIP2F_5         4566           1774         3560         5346         7132         784CIP2F_5         4566           1774         3560         5346         7132         784CIP2F_6         4705           1775         3561         5347         7133         784CIP2F_7         4707           1776         3562         5348         7134         784CIP2F_8         4712           1777         3563         5349         7135         784CIP2F_10         5009	1765					
1767         3553         5339         7125         784CIP2E 23         9065           1768         3554         5340         7126         784CIP2E 24         9324           1769         3555         5341         7127         784CIP2F 1         2976           1770         3556         5342         7128         784CIP2F 2         3559           1771         3557         5343         7129         784CIP2F 3         4021           1772         3558         5344         7130         784CIP2F 3         4021           1772         3558         5344         7130         784CIP2F 3         4021           1773         3559         5345         7131         784CIP2F 5         4566           1774         3560         5346         7132         784CIP2F 5         4566           1774         3560         5346         7132         784CIP2F 6         4705           1775         3561         5347         7133         784CIP2F 7         4707           1776         3562         5348         7134         784CIP2F 8         4712           1777         3563         5349         7135         784CIP2F 10         5009	1766					
1768         3554         5340         7126         784CIP2E 24         9324           1769         3555         5341         7127         784CIP2F 1         2976           1770         3556         5342         7128         784CIP2F 2         3559           1771         3557         5343         7129         784CIP2F 3         4021           1772         3558         5344         7130         784CIP2F 4         4474           1773         3559         5345         7131         784CIP2F 5         4566           1774         3560         5346         7132         784CIP2F 5         4566           1774         3561         5347         7133         784CIP2F 6         4705           1775         3561         5347         7133         784CIP2F 7         4707           1776         3562         5348         7134         784CIP2F 8         4712           1777         3563         5349         7135         784CIP2F 9         5008           1778         3564         5350         7136         784CIP2F 10         5009           1779         3565         5351         7137         784CIP2F 11         5015	1767					
1769         3555         5341         7127         784CIP2F         1         2976           1770         3556         5342         7128         784CIP2F         2         3559           1771         3557         5343         7129         784CIP2F         3         4021           1772         3558         5344         7130         784CIP2F         4         4474           1773         3559         5345         7131         784CIP2F         5         4566           1774         3560         5346         7132         784CIP2F         6         4705           1775         3561         5347         7133         784CIP2F         6         4705           1776         3562         5348         7134         784CIP2F         7         4707           1776         3563         5349         7135         784CIP2F         9         5008           1778         3564         5350         7136         784CIP2F         9         5008           1778         3565         5351         7137         784CIP2F         10         5009           1779         3565         5351         7137         784CIP2F						
1770         3556         5342         7128         784CIP2F         2         3559           1771         3557         5343         7129         784CIP2F         3         4021           1772         3558         5344         7130         784CIP2F         4         4474           1773         3559         5345         7131         784CIP2F         5         4566           1774         3560         5346         7132         784CIP2F         6         4705           1775         3561         5347         7133         784CIP2F         7         4707           1776         3562         5348         7134         784CIP2F         8         4712           1777         3563         5349         7135         784CIP2F         9         5008           1778         3564         5350         7136         784CIP2F         10         5009           1779         3565         5351         7137         784CIP2F         10         5009           1779         3565         5351         7137         784CIP2F         11         5015           1780         3566         5352         7138         784CIP2F	1769	3555				
1771         3557         5343         7129         784CIP2F 3         4021           1772         3558         5344         7130         784CIP2F 4         4474           1773         3559         5345         7131         784CIP2F 5         4566           1774         3560         5346         7132         784CIP2F 6         4705           1775         3561         5347         7133         784CIP2F 7         4707           1776         3562         5348         7134         784CIP2F 8         4712           1777         3563         5349         7135         784CIP2F 9         5008           1778         3564         5350         7136         784CIP2F 10         5009           1779         3565         5351         7137         784CIP2F 11         5015           1780         3566         5352         7138         784CIP2F 12         5015           1781         3567         5353         7139         784CIP2F 13         7724           1782         3568         5354         7140         784CIP2F 14         7725           1783         3569         5355         7141         784CIP2F 15         8828 <td>1770</td> <td></td> <td></td> <td></td> <td></td> <td></td>	1770					
1772     3558     5344     7130     784CIP2F 4     4474       1773     3559     5345     7131     784CIP2F 5     4566       1774     3560     5346     7132     784CIP2F 6     4705       1775     3561     5347     7133     784CIP2F 7     4707       1776     3562     5348     7134     784CIP2F 8     4712       1777     3563     5349     7135     784CIP2F 9     5008       1778     3564     5350     7136     784CIP2F 10     5009       1779     3565     5351     7137     784CIP2F 11     5015       1780     3566     5352     7138     784CIP2F 12     5015       1781     3567     5353     7139     784CIP2F 13     7724       1782     3568     5354     7140     784CIP2F 14     7725       1783     3569     5355     7141     784CIP2F 15     8828       1784     3570     5356     7142     784CIP2F 16     8830       1785     3571     5357     7143     784CIP2F 17     9739						
1773         3559         5345         7131         784CIP2F 5         4566           1774         3560         5346         7132         784CIP2F 6         4705           1775         3561         5347         7133         784CIP2F 7         4707           1776         3562         5348         7134         784CIP2F 8         4712           1777         3563         5349         7135         784CIP2F 9         5008           1778         3564         5350         7136         784CIP2F 10         5009           1779         3565         5351         7137         784CIP2F 11         5015           1780         3566         5352         7138         784CIP2F 12         5015           1781         3567         5353         7139         784CIP2F 13         7724           1782         3568         5354         7140         784CIP2F 14         7725           1783         3569         5355         7141         784CIP2F 15         8828           1784         3570         5356         7142         784CIP2F 16         8830           1785         3571         5357         7143         784CIP2F 17         9739     <						
1774         3560         5346         7132         784CIP2F 6         4705           1775         3561         5347         7133         784CIP2F 7         4707           1776         3562         5348         7134         784CIP2F 8         4712           1777         3563         5349         7135         784CIP2F 9         5008           1778         3564         5350         7136         784CIP2F 10         5009           1779         3565         5351         7137         784CIP2F 11         5015           1780         3566         5352         7138         784CIP2F 12         5015           1781         3567         5353         7139         784CIP2F 13         7724           1782         3568         5354         7140         784CIP2F 14         7725           1783         3569         5355         7141         784CIP2F 15         8828           1784         3570         5356         7142         784CIP2F 16         8830           1785         3571         5357         7143         784CIP2F 17         9739						
1775         3561         5347         7133         784CIP2F 7         4707           1776         3562         5348         7134         784CIP2F 8         4712           1777         3563         5349         7135         784CIP2F 9         5008           1778         3564         5350         7136         784CIP2F 10         5009           1779         3565         5351         7137         784CIP2F 11         5015           1780         3566         5352         7138         784CIP2F 12         5015           1781         3567         5353         7139         784CIP2F 13         7724           1782         3568         5354         7140         784CIP2F 14         7725           1783         3569         5355         7141         784CIP2F 15         8828           1784         3570         5356         7142         784CIP2F 16         8830           1785         3571         5357         7143         784CIP2F 17         9739						
1776         3562         5348         7134         784CIP2F 8         4712           1777         3563         5349         7135         784CIP2F 9         5008           1778         3564         5350         7136         784CIP2F 10         5009           1779         3565         5351         7137         784CIP2F 11         5015           1780         3566         5352         7138         784CIP2F 12         5015           1781         3567         5353         7139         784CIP2F 13         7724           1782         3568         5354         7140         784CIP2F 14         7725           1783         3569         5355         7141         784CIP2F 15         8828           1784         3570         5356         7142         784CIP2F 16         8830           1785         3571         5357         7143         784CIP2F 17         9739						
1777     3563     5349     7135     784CIP2F 9     5008       1778     3564     5350     7136     784CIP2F 10     5009       1779     3565     5351     7137     784CIP2F 11     5015       1780     3566     5352     7138     784CIP2F 12     5015       1781     3567     5353     7139     784CIP2F 13     7724       1782     3568     5354     7140     784CIP2F 14     7725       1783     3569     5355     7141     784CIP2F 15     8828       1784     3570     5356     7142     784CIP2F 16     8830       1785     3571     5357     7143     784CIP2F 17     9739						
1778     3564     5350     7136     784CIP2F 10     5009       1779     3565     5351     7137     784CIP2F 11     5015       1780     3566     5352     7138     784CIP2F 12     5015       1781     3567     5353     7139     784CIP2F 13     7724       1782     3568     5354     7140     784CIP2F 14     7725       1783     3569     5355     7141     784CIP2F 15     8828       1784     3570     5356     7142     784CIP2F 16     8830       1785     3571     5357     7143     784CIP2F 17     9739						
1779     3565     5351     7137     784CIP2F_11     5015       1780     3566     5352     7138     784CIP2F_12     5015       1781     3567     5353     7139     784CIP2F_13     7724       1782     3568     5354     7140     784CIP2F_14     7725       1783     3569     5355     7141     784CIP2F_15     8828       1784     3570     5356     7142     784CIP2F_16     8830       1785     3571     5357     7143     784CIP2F_17     9739						
1780         3566         5352         7138         784CIP2F_12         5015           1781         3567         5353         7139         784CIP2F_12         5015           1782         3568         5354         7140         784CIP2F_14         7725           1783         3569         5355         7141         784CIP2F_15         8828           1784         3570         5356         7142         784CIP2F_16         8830           1785         3571         5357         7143         784CIP2F_17         9739						*
1781     3567     5353     7139     784CIP2F_13     7724       1782     3568     5354     7140     784CIP2F_14     7725       1783     3569     5355     7141     784CIP2F_15     8828       1784     3570     5356     7142     784CIP2F_16     8830       1785     3571     5357     7143     784CIP2F_17     9739					· · · · · · · · · · · · · · · · · · ·	
1782     3568     5354     7140     784CIP2F_14     7725       1783     3569     5355     7141     784CIP2F_15     8828       1784     3570     5356     7142     784CIP2F_16     8830       1785     3571     5357     7143     784CIP2F_17     9739						
1783 3569 5355 7141 784CIP2F 15 8828 1784 3570 5356 7142 784CIP2F 16 8830 1785 3571 5357 7143 784CIP2F 17 9739				1		
1784         3570         5356         7142         784CIP2F 16         8830           1785         3571         5357         7143         784CIP2F 17         9739						
1785 3571 5357 7143 784CIP2F 17 9739						
355, /IIS / /UICITEX_I/						
1/86 3572 5358 7144 784CIP2F_18 9896						
	1786	3572	5358	7144	784CIP2F_18	9896

TRADOCS:1416247.1(%C\$701!.DOC)

TABLE 7

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	
ł		,	L-Leucine, M-Methionine, N-Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ì	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	Sequence	1.
			\=possible nucleotide insertion)
5359	337	1131	AHLSARLSALILDEVAILPAPQNLSVLSTNMKHLLMWSPVIAPG
			ETVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITA
İ	1		TVPYNLRVRATLGSQTS/CLEHP/VSIPLIETQPSLPDL/RMEI
1	•		TKDGFHLVIBLEDLGPQFEFLVAYWRREPGAEEHVKMVRSGGIP
1			
}	ł	f .	VHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPL
1			VLALFAFVGFMLILVVVPLFVWKMGRLLQ/YLLLPRGGSSQTPW
			KITQF
5360	2	1115	PRVRSSGGQEDPASQQWARPRFTQPSKMRRRVIARPVGSSVRLK
j	1		CVASGHPRPDITWMKDDQALTRPEAAEPRKKKWTLSLKNLRPED
Į.			
	ĺ	,	SGKYTCRVSNRAGAINATYKVDVIQRTRSKPVLTGTHPVNTTVD
}			FGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGGQKF
			VVLPTGDVWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYS
			FRSAFLTVLPDPKPPGPPVASSSSATSLPWPVVIGIPAGAVFIL
	<b>!</b>		GTLLLWLCQAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLPSL
1			AALSAGPGVGLCEEHGSPAAPQHLLGPGPVAGPKLYPKLYTGHS
1			
5361		^	TPHTYTHPPPSCQLNSSHS
330T	3	925	HEGSISSANILLDDQFQPKLTDFAMAHFRSHLEHQSCTINMTSS
			SSKHLWYMPERYIRQGKLSIKTDVYSFGIVIMEVLTGCRVVLDD
1			PKHIQLRDLLRELMEKRGLDSCLSFLDKKVPPCPRNFSAKLFCL
1			AGRCAATRAKLRPSMDEVLNTLESTOASLYFAEDPPTSLKSFRC
			PSPLFLENVPSIPVEDDESQNNNLLPSDEGLRIDRMTQKTPFEC
{			
1			SQSEVMFLSLDKKPESKRNEEACNMPSSSCEESWFPKYIVPSQD
			LRPYKVNIDPSSEAPGHSCRSRPVESSCSSKFSWDEYEQYKKE
5362	2	4879	SCQVEGCTRTYNSSQSIGKHMKTAHPDQYAAFKMQRKSKKGQKA
	ļ		NNLNTPNNGKFVYFLPSPVNSSNPFFTSQTKANGNPACSAQLQH
1 1			VSPPIFPAHLASVSTPLLSSMESVINPNITSQDKNEQGGMLCSO
ì			MENLPSTALPAQMEDLTKTVLPLNIDRGSDPFLSLPAESSSIDL
1 1	' t		FPSPADSGTNSVFSQLENNTNHYSSQIEGNTNSSFLKGGNGENA
}			LESEMOSCINS ALPOTENTINHIS POTECULINES L PROGUCENT
			VFPSQVNVANNFSSTNAQQSAPEKVKKDRGRGQTGKERKPKHNK
1 1			RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA
			RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA
-	·		RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA EIAQELLQSNGQPSLLASMILSTNAVNLQQPQQSTFNPEACFKD
			RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA EIAQELLQSNGQPSLLASMILSTNAVNLQQPQQSTFNPEACFKD PSFLQLLAENRSPAFLPNTFPRSGVTNFNTSVSQEGSEIIIQAL
	·		RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA EIAQELLQSNGQPSLLASMILSTNAVNLQQPQQSTFNPEACFKD PSFLQLLAENRSPAFLPNTFPRSGVTNFNTSVSQEGSEIIIQAL ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPLLH
-	·		RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA EIAQELLQSNGQPSLLASMILSTNAVNLQQPQQSTFNPEACFKD PSFLQLLAENRSPAFLPNTFPRSGVTNFNTSVSQEGSEIIIQAL ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPLLH TVCHPNTLLTNQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN
-	٠		RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA EIAQELLQSNGQPSLLASMILSTNAVNLQQPQQSTFNPEACFKD PSFLQLLAENRSPAFLPNTFPRSGVTNFNTSVSQEGSEIIIQAL ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPLLH TVCHPNTLLTNQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN GLCSSSFPNSGGPSQNFTSNSSRVSVISGPQNTRSSHLNKKGNS
	·	·	RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA EIAQELLQSNGQPSLLASMILSTNAVNLQQPQQSTFNPEACFKD PSFLQLLAENRSPAFLPNTFPRSGVTNFNTSVSQEGSEIIIQAL ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPLLH TVCHPNTLLTNQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN GLCSSSFPNSGPSQNFTSNSSRVSVISGPQNTRSSHLMKKGNS ASKRRKKVAPPLIAPNASQNLVTSDLTTMGLIAKSVEIPTTNLH
	·		RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA EIAQELLQSNGQPSLLASMILSTNAVNLQQPQQSTFNPEACFKD PSFLQLLAENRSPAFLPNTFPRSGVTNFNTSVSQEGSEIIIQAL ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPLLH TVCHPNTLLTNQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN GLCSSSFPNSGGPSQNFTSNSSRVSVISGPQNTRSSHLNKKGNS
	•		RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA EIAQELLQSNGQPSLLASMILSTNAVNLQQPQQSTFNPEACFKD PSFLQLLAENRSPAFLPNTFPRSGVTNFNTSVSQEGSEIIIQAL ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPLLH TVCHPNTLLTNQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN GLCSSSFPNSGPSQNFTSNSSRVSVISGPQNTRSSHLMKKGNS ASKRRKKVAPPLIAPNASQNLVTSDLTTMGLIAKSVEIPTTNLH
	•		RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA EIAQELLQSNGQPSLLASMILSTNAVNLQQPQQSTFNPEACFKD PSFLQLLAENRSPAFLPNTFPRSGVTNFNTSVSQEGSEIIIQAL ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPLLH TVCHPNTLLTNQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN GLCSSSFPNSGGPSQNFTSNSSRVSVISGPQNTRSSHLNKKGNS ASKRKKVAPPLIAPNASQNLVTSDLTTMGLIAKSVEIPTTNLH SNVIPTCEPQSLVENLTQKLNNVNNQLFMTDVKENFKTSLESHT VLAPLTLKTENGDSQMMALNSCTTSVNSDLQISEDNVIQNFEKT
	·		RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA EIAQEILQSNGQPSLLASMILSTNAVNLQQPQQSTFNPEACFKD PSFLQLLAENRSPAFLPNTFPRSGVINFINTSVSQEGSEIIIQAL ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPLLH TVCHPNTLLTNQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN GLCSSSFPNSGGPSQNFTSNSSRVSVISGPQNTRSSHLNKKGNS ASKRRKKVAPPLIAPNASQNLVTSDLTTMGLIAKSVEIPTTNLH SVNPTCEPQSLVENLTQKLNNVNNQLFMTDVKENFKTSLESHT VLAPLTLKTENGDSQMMALNSCTTSVNSDLQISEDNVIQNFEKT LEIIKTAMNSQILEVKSGSQGAGETSQNAQINYNIQLPSVNTVQ
	•		RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA EIAQEILQSNGQPSLLASMILSTNAVNLQQPQQSTFNPEACFKD PSFLQLLAENRSPAFLPNTFPRSGVTNFTTSVSQEGSEIIIQAL ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPPLH TVCHPNTLLTNQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN GLCSSSFPNSGGPSQNFTSNSSRVSVISGPQNTRSSHLNKKGNS ASKRRKKVAPPLIAPNASQNLVTSDLTTMGLIAKSVEIPTTNLH SNVIPTCEPQSLVENLTQKLMNVNNQLFMTDVKENFKTSLESHT VLAPLTLKTENGDSQMMALNSCTTSVNSDLQISEDNVIQNFEKT LEIIKTAMMSQILEVKSGSQGAGETSQNAQINYNIQLPSVNTVQ NNKLPDSSP\FSSFISVMPTESNIPQSE\VSHKEDQIQEILEGL
			RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA EIAQEILQSNGQPSLLASMILSTNAVNLQQPQQSTFNPEACFKD PSFLQLLAENRSPAFLPNTFPRSGYTNFNTSVSQEGSEIIIQAL ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPPLLH TVCHPNTLLTNQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN GLCSSSFPNSGGPSQNFTSNSSRVSVISGPQNTRSSHLNKKGNS ASKRRKVAPPLIAPNASQNLVTSDLTTMGLIAKSVEIPTTNLH SNVIPTCEPQSLVENLTQKLNNVNNQLFMTDVKENFKTSLESHT VLAPLTLKTENGDSQMMALNSCTTSVNSDLQISEDNVIQNFEKT LEIIKTAMNSQILEVKSGSQGAGETSQNAQINYNIQLPSVNTVQ NNKLPDSSP\FSSFISVMPTESNIPQSE\VSHKEDQIQBILEGL QKLKLENDLSTPASQCVLINTSVTLTPTPVKSTADITVIQPVSE
	·		RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA EIAQEILQSNGQPSLLASMILSTNAVNLQQPQQSTFNPEACFKD PSFLQLLAENRSPAFLPNTFPRSGVTNFNTSVSQEGSEIIIQAL ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPPLLH TVCHPNTLLTNQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN GLCSSSFPNSGGPSQNFTSNSSRVSVISGPQNTRSSHLMKKGNS ASKRRKKVAPPLIAPNASQNLVTSDLTTMGLIAKSVEIPTTNLH SNVIPTCEPQSLVENLTQKLMNVNNQLFMTDVKENFKTSLESHT VLAPLTLKTENGDSQMMALNSCTTSVNSDLQISEDNVIQNFEKT LEIIKTAMNSQILEVKSGSQCAGETSQNAQINYNIQLPSVNTVQ NNKLPDSSP\FSSFISVMPTESNIPQSE\VSHKEDQIQEILEGL QKLKLENDLSTPASQCVLINTSVTLTPTPVKSTADITVIQPVSE MINIQFNDKVNKPFVCQNQGCNYSAMTKDALFKHYGKIHQYTPE
			RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA EIAQEILQSNGQPSLLASMILSTNAVNLQQPQQSTFNPEACFKD PSFLQLLAENRSPAFLPNTFPRSGYTNFNTSVSQEGSEIIIQAL ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPPLLH TVCHPNTLLTNQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN GLCSSSFPNSGGPSQNFTSNSSRVSVISGPQNTRSSHLNKKGNS ASKRRKVAPPLIAPNASQNLVTSDLTTMGLIAKSVEIPTTNLH SNVIPTCEPQSLVENLTQKLNNVNNQLFMTDVKENFKTSLESHT VLAPLTLKTENGDSQMMALNSCTTSVNSDLQISEDNVIQNFEKT LEIIKTAMNSQILEVKSGSQGAGETSQNAQINYNIQLPSVNTVQ NNKLPDSSP\FSSFISVMPTESNIPQSE\VSHKEDQIQBILEGL QKLKLENDLSTPASQCVLINTSVTLTPTPVKSTADITVIQPVSE
			RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA EIAGELLQSNGQPSLLASMILSTNAVNLQQPQQSTFNPEACFKD PSFLQLLAENRSPAFLPNTFPRSGVINFNTSVSQEGSEIIIQAL ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPLLH TVCHPNTLLTNQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN GLCSSSFPNSGGPSQNFTSNSSRVSVISGPQNTRSSHLNKKGNS ASKRRKKVAPPLIAPNASQNLVTSDLTTMGLIAKSVEIPTTNLH SVNIPTCEPQSLVENLTQKLNNVNNQLFMTDVKENFKTSLESHT VLAPLTLKTENGDSQMMALNSCTTSVNSDLQISEDNVIQNFEKT LEIIKTAMNSQILEVKSGSQGAGETSQNAQINYNIQLPSVNTVQ NNKLPDSSP\FSSFISVMPTESNIPQSE\VSHKEDQIQEILEGL QKLKLENDLSTPASQCVLINTSVTLTPTPVKSTADITVIQPVSE MINIQFNDKVNKPFVCQNQGCNYSAMTKDALFKHYGKHQYTPE MILEIKKNQLKFAPFKCVVPTCTKTFTRNSNLRAHCQLVHHFTT EEMVKLKIKRPYGRKSQSENVPASRSTQVKKQLAMTEENKKESQ
	·		RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA EIAGELLQSNGQPSLLASMILSTNAVNLQQPQQSTFNPEACFKD PSFLQLLAENRSPAFLPNTFPRSGVINFNTSVSQEGSEIIIQAL ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPLLH TVCHPNTLLTNQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN GLCSSSFPNSGGPSQNFTSNSSRVSVISGPQNTRSSHLNKKGNS ASKRRKKVAPPLIAPNASQNLVTSDLTTMGLIAKSVEIPTTNLH SVNIPTCEPQSLVENLTQKLNNVNNQLFMTDVKENFKTSLESHT VLAPLTLKTENGDSQMMALNSCTTSVNSDLQISEDNVIQNFEKT LEIIKTAMNSQILEVKSGSQGAGETSQNAQINYNIQLPSVNTVQ NNKLPDSSP\FSSFISVMPTESNIPQSE\VSHKEDQIQEILEGL QKLKLENDLSTPASQCVLINTSVTLTPTPVKSTADITVIQPVSE MINIQFNDKVNKPFVCQNQGCNYSAMTKDALFKHYGKHQYTPE MILEIKKNQLKFAPFKCVVPTCTKTFTRNSNLRAHCQLVHHFTT EEMVKLKIKRPYGRKSQSENVPASRSTQVKKQLAMTEENKKESQ
			RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA EIAQEILQSNGQPSLLASMILSTNAVNLQQPQQSTFNPEACFKD PSFLQLLAENRSPAFLPNTFPRSGVTNFNTSVSQEGSEIIIQAL ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPPLLH TVCHPNTLLTNQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN GLCSSSFPNSGGPSQNFTSNSSRVSVISGPQNTRSSHLNKKGNS ASKRRKKVAPPLIAPNASQNLVTSDLTTMGLIAKSVEIPTTNLH SNVIPTCEPQSLVENLTQKLNNVNNQLFMTDVKENFKTSLESHT VLAPLTLKTENGDSQMMALNSCTTSVNSDLQISEDNVIQNFEKT LEILKTAMMSQILEVKSGSGCAGETSQNAQINYNIQLPSVNTVQ NNKLPDSSP\FSSFISVMPTESNIPQSE\VSHKEDQIQEILEGL QKLKLENDLSTPASQCVLINTSVTLTPTPVKSTADITVIQPVSE MINIQFNDKVNKPFVCQNQGCNYSAMTKDALFKHYGKLHQYTPT MILEIKKNQLKFAPFKCVVPTCTKTFTRNSNLRAHCQLVHHFTT EEMVKLKIRPYGRKSQSENVPASRSTQVKQLAMTEENKKESQ PALELRAETQNTHSNVAVIPEKQLIEKKSPDKTESSLQVITVTS
			RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA EIAQEILQSNGQPSLLASMILSTNAVNLQQPQQSTFNPEACFKD PSFLQLLAENRSPAFLPNTFPRSGYTNFTNTSVSQEGSEIIIQAL ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPPLH TVCHPNTLLTNQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN GLCSSSFPNSGGPSQNFTSNSSRVSVISGPQNTRSSHLNKKGNS ASKRRKKVAPPPLIAPNASQNLVTSDLTTMGLIAKSVEIPTTNLH SNVIPTCEPQSLVENLTQKLNNVNNQLFMTDVKENFKTSLESHT VLAPLTLKTENGDSQMMALNSCTTSVNSDLQISEDNVIQNFEKT LEIIKTAMNSQILEVKSGSQGAGETSQNAQINYNIQLPSVNTVQ NNKLPDSSP\FSSFISVMPTESNIPQSE\VSHKEDQIQEILEGL QKLKLENDLSTPASQCVLINTSVTLTPTPVKSTADITVIQPVSE MINIQFNDKVNKPFVCQNQGCNYSAMTKDALFKHYGKIHQYTPE MILEIKKNQLKFAPFKCVVPTCTKTFTRNSNLRAHCQLVHHFTT EEMVKLKIKRPYGRKSQSENVPASRSTQVKKQLAMTEENKKESQ PALELRAETQNTHSNVAVIPEKQLIEKKSPDKTESSLQVITVTS EQCNTNALTNTQTKGRKIRRHKKEKEEKKRKPVSQSLEFPTRY
			RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA EIAQEILQSNGQPSLLASMILSTNAVNLQQPQQSTFNPEACFKD PSFLQLLAENRSPAFLPNTFPRSGVTNFNTSVSQEGSEIIIQAL ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPPLLH TVCHPNTLLTRQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN GLCSSSFPNSGGPSQNFTSNSSRVSVISGPQNTRSSHLNKKGNS ASKRRKKVAPPLIAPNASQNLVTSDLTTMGLIAKSVEIPTTNLH SNVIPTCEPQSLVENLTQKLNNVNNQLFMTDVKENFKTSLESHT VLAPLTLKTENGDSQMMALNSCTTSVNSDLQISEDNVIQNFEKT LEIIKTAMNSQILEVKSGSQGAGETSQNAQINYNIQLPSVNTVQ NNKLPDSSP\FSSFISVMPTESNIPQSE\VSHKEDQIOBILEGL QKLKLENDLSTPASQCVLINTSVTLTPTPVKSTADITVIQPVSE MINIQFNDKVNKPFVCQNQGCNYSAMTKDALFKHYGKIHQYTPE MILEIKKNQLKFAPFKCVVPTCTKTFTRNSNLRAHCQLVHHFTT EEMVKLKIKRPYGRKSQSENVPASRSTQVKKQLAMTEENKKESQ PALELRAETQNTHSNVAVIPEKQLIEKKSPDKTESSLQVITVTS EQCNTNALTNTQTKGRKIRRHKKEKEEKKRKKPVSQSLEFPTRY SPYRPYRCVHQGCFAAFTIQQNLILHYQAVHKSDLPAFSAEVEE
			RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA EIAQEILQSNGQPSLLASMILSTNAVNLQQPQQSTFNPEACFKD PSFLQLLAENRSPAFLPNTFPRSGVTNFNTSVSQEGSEIIIQAL ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPLLH TVCHPNTLLTNQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN GLCSSSFPNSGGPSQNFTSNSSRVSVISGPQNTRSSHLMKKGNS ASKRRKKVAPPLIAPNASQNLVTSDLTTMGLIAKSVEIPTTNLH SNVIPTCEPQSLVENLTQKLNNVNNQLFMTDVKENFKTSLESHT VLAPLTLKTENGDSQMMALNSCTTSVNSDLQISEDNVIQNFEKT LEIIKTAMNSQILEVKSGSQCAGETSQNAQINYNIQLPSVNTVQ MNKLPDSSP\FSSFISVMPTESNIPQSE\VSHKEDQIQEILEGL QKLKLENDLSTPASQCVLINTSVTLTPTPVKSTADITVLQPVSZ MINIQFNDKVNKPFVCQNQGCNYSAMTKDALFKHYGKIHQYTPE MILEIKKNQLKFAPFKCVVPTCTKTFTRNSNLRAHCQLVHHFTT EEMVKLKIKRPYGRKSQSENVPASRSTQVKKQLAMTEENKKESQ PALELRAETQNTHSNVAVIPEKQLIEKKSPDKTESSLQVITVTS SPYRPYRCVHQGCFAAFTIQQNLILHYQAVHKSDLPAFSAEVEE ESEAGKESEETETKQTLKEFRCQVSDCSRIFQAITGLIQHYMKL
			RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA EIAGELLQSNGQPSLLASMILSTNAVNLQQPQQSTFNPEACFKD PSFLQLLAENRSPAFLPNTFPRSGVINFNTSVSQEGSEIIIQAL ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPLLH TVCHPNTLLTNQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN GLCSSSFPNSGGPSQNFTSNSSRVSVISGPQNTRSSHLNKKGNS ASKRRKKVAPPLIAPNASQNLVTSDLTTMGLIAKSVEIPTTNLH SNVIPTCEPQSLVENLTQKLNNVNNQLFMTDVKENFKTSLESHT VLAPLTLKTENGDSQMMALNSCTTSVNSDLQISEDNVIQNFEKT LEIIKTAMNSQILEVKSGSQGAGETSQNAQINYNIQLPSVNTVQ NNKLPDSSP\FSSFISVMPTESNIPQSE\VSHKEDQIQEILEGL QKLKLENDLSTPASQCVLINTSVTLTPTPVKSTADITVIQPVSZ MINIQFNDKVNKPFVCQNQGCNYSAMTKDALFKHYGKIHQYTPE MILEIKKNQLKFAPFKCVVPTCTKTFTRNSNLRAHCQLVHHFTT EEMVKLKIKRPYGRKSQSENVPASRSTQVKKQLAMTEENKKESQ PALELRAETQNTHSNVAVIPEKQLIEKKSPDKTESSLQVITVTS EQCNTNALTNTQTKGRKIRRHKEKEEKKRKKPVSQSLEFFTRY SPYRPYRCVHQGCFAAFTIQQNLILHYQAVHKSDLPAFSAEVEE ESEAGKESEETETKQTLKEFRCQVSDCSRIFQAITGLIQHYMKL HEMTPEEIESMTASVDVGKFPCDQLECKSSFTTYLNYVVHLEAD
			RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA EIAGELLQSNGGPSLLASMILSTNAVNLQQPQQSTFNPEACFKD PSFLQLLAENRSPAFLPNTFPRSGVINFNTSVSQEGSEIIIQAL ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPPLH TVCHPNTLLTNQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN GLCSSSFPNSGGPSQNFTSNSSRVSVISGPQNTRSSHLNKKGNS ASKRRKKVAPPLIAPNASQNLVTSDLTTMGLIAKSVEIPTTNLH SNVIPTCEPQSLVENLTQKLNNVNNQLFMTDVKENFKTSLESHT VLAPLTLKTENGDSQMMALNSCTTSVNSDLQISEDNVIQNFEKT LEILKTAMMSQILEVKSGSQGAGETSQNAQINYNIQLPSVNTVQ NNKLPDSSP\FSSFISVMPTESNIPQSE\VSHKEDQIQEILEGL QKLKLENDLSTPASQCVLINTSVTLTPTPVKSTADITVIQPVSE MINIQFNCKUNKPFVCQNQGCNYSAMTKDALFKHYGKHQYTPE MILEIKKNQLKFAPFKCVVPTCTKTFTRNSNLRAHCQLVHHFTT EEMVKLKIKRPYGRKSQSENVPASRSTQVKQLAMTEENKKESQ PALELRAETQNTHSNVAVIPEKQLIEKKSPDKTESSLQVITVTS EQCNTNALTNTQTKGRKIRRHKKEKEEKKRKKPVSQSLEFPTRY SPYRPYRCVHQGCFAAFTIQQNLILHYQAVHKSDLPAFSAEVEE ESAGKESEETETKQTLKEFRCQVSDCSRIFQAITGLIQHYMKL HEMTPEEISMTASVDVGKPPCDQLECKSSFTTYLNYVVHLEAD HGIGLRASKTEEDGVYKCDCEGCDRIYATRSNLLRHIFNKHNDK
	·		RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA EIAGELLQSNGGPSLLASMILSTNAVNLQQPQQSTFNPEACFKD PSFLQLLAENRSPAFLPNTFPRSGVINFNTSVSQEGSEIIIQAL ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPPLH TVCHPNTLLTNQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN GLCSSSFPNSGGPSQNFTSNSSRVSVISGPQNTRSSHLNKKGNS ASKRRKKVAPPLIAPNASQNLVTSDLTTMGLIAKSVEIPTTNLH SNVIPTCEPQSLVENLTQKLNNVNNQLFMTDVKENFKTSLESHT VLAPLTLKTENGDSQMMALNSCTTSVNSDLQISEDNVIQNFEKT LEILKTAMMSQILEVKSGSQGAGETSQNAQINYNIQLPSVNTVQ NNKLPDSSP\FSSFISVMPTESNIPQSE\VSHKEDQIQEILEGL QKLKLENDLSTPASQCVLINTSVTLTPTPVKSTADITVIQPVSE MINIQFNCKUNKPFVCQNQGCNYSAMTKDALFKHYGKHQYTPE MILEIKKNQLKFAPFKCVVPTCTKTFTRNSNLRAHCQLVHHFTT EEMVKLKIKRPYGRKSQSENVPASRSTQVKQLAMTEENKKESQ PALELRAETQNTHSNVAVIPEKQLIEKKSPDKTESSLQVITVTS EQCNTNALTNTQTKGRKIRRHKKEKEEKKRKKPVSQSLEFPTRY SPYRPYRCVHQGCFAAFTIQQNLILHYQAVHKSDLPAFSAEVEE ESAGKESEETETKQTLKEFRCQVSDCSRIFQAITGLIQHYMKL HEMTPEEISMTASVDVGKPPCDQLECKSSFTTYLNYVVHLEAD HGIGLRASKTEEDGVYKCDCEGCDRIYATRSNLLRHIFNKHNDK
			RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA EIAGELLQSNGGPSLLASMILSTNAVNLQOPQQSTFNPEACFKD PSFLQLLAENRSPAFLPNTFPRSGVTNFTNTSVSQEGSEIIIQAL ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPPLH TVCHPNTLLTNQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN GLCSSSFPNSGGPSQNFTSNSSRVSVISGPQNTRSSHLNKKGNS ASKRRKKVAPPLIAPNASQNLVTSDLTTMGLIAKSVEIPTTNLH SNVIPTCEPQSLVENLTQKLMNVNNQLFMTDVKENFKTSLESHT VLAPLTLKTENGDSQMMALNSCTTSVNSDLQISEDNVIQNFEKT LEILKTAMMSGILEVKSGSQGAGETSQNAQINYNIQLPSVNTVQ NNKLPDSSP\FSSFISVMPTESNIPQSE\VSHKEDQIQEILEGL QKLKLENDLSTPASQCVLINTSVTLTPTPVKSTADITVIQPVSE MINIQFNDKVNKPFVCQNQGCNYSAMTKDALFKHYGKKHQYTPE MILEIKKNQLKFAPFKCVVPTCTKTFTRNSNLRAHCQLVHHFTT EEMVKLKIKRPYGRKSQSENVPASRSTQVKKQLAMTEENKKESQ PALELRAETQNTHSNVAVIPEKQLIEKKSPDKTESSLQVITVTS EQCNTNALTNTQTKGRKIRRHKKEKEEKKRKPVSQSLEFPTRY SPYRPYRCYHGGCFAAFTIQQNLILHYQAVHKSDLPAFSAEVEE ESEAGKESEETETKQTLKEFRCQVSDCSRIFQAITGLIQHYMKL HEMTPEEIESMTASVDVGKFPCDQLECKSSFTTYLNYVVHLEAD HGIGLRASKTEEDGVYKCDCEGCDRIYATRSNLLRHIFNKHNDK HKAHLIRPRLTPGQENMSSKANQEKSKSKHRGTKHSRCGKEGI
			RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA EIAQEILQSNGQPSLLASMILSTNAVNLQQPQQSTFNPEACFKD PSFLQLLAENRSPAFLPNTFPRSGVTNFTNSVSQEGSEIIIQAL ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPPLLH TVCHPNTLLTRQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN GLCSSSFPNSGGPSQNFTSNSSRVSVISGPQNTRSSHLNKKGNS ASKRRKKVAPPLIAPNASQNLVTSDLTTMGLIAKSVEIPTTNLH SNVIPTCEPQSLVENLTQKLNNVNNQLFMTDVKENFKTSLESHT VLAPLTLKTENGDSQMMALNSCTTSVNSDLQISEDNVIQNFEKT LEIIKTAMNSQILEVKSGSQGAGETSQNAQINYNIQLPSVNTVQ NNKLPDSSP\FSSFISVMPTESNIPQSE\VSHKEDQIQEILEGL QKLKLENDLSTPASQCVLINTSVTLTPTPVKSTADITVIQPVSE MINIQFNDKVNKPFVCQNQGCNYSAMTKDALFKHYGKIHQYTPE MILEIKKNQLKFAPFKCVVPTCTKTFTRNSNLRAHCQLVHHHFTT EEMVKLKIKRPYGRKSQSENVPASRSTQVKKQLAMTEENKKESQ PALELRAETQNTHSNVAVIPEKQLIEKKSPDKTESSLQVITVTS EQCNTNALTNTQTKGRKIRRHKKEKEEKKRKPVSQSLEFPTRY SPYRPYRCVHQGCFAAFTIQQNLILHYQAVHKSDLPAFSAEVEE ESBAGKESEETETKQTLKEFFCQVSDCSRIFQAITGLIQHYMKL HEMTPEEIESMTASVDVGKPPCDQLECKSSFTTYLNYVVHLEAD HGIGLRASKTEEDGVYKCDCEGCDRIVATRSNLLRHIFNKHNDK HKAHLIRPRLTPGQENMSSKANQEKSKSKHRGTKHSRCGKEGI
	·		RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA EIAQEILQSNGQPSLLASMILSTNAVNLQQPQQSTFNPEACFKD PSFLQLLAENRSPAFLPNTFPRSGVTNFNTSVSQEGSEIIIQAL ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPPLLH TVCHPNTLLTRQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN GLCSSSFPNSGGPSQNFTSNSSRVSVISGPQNTRSSHLNKKGNS ASKRRKKVAPPLIAPNASQNLVTSDLTTMGLIAKSVEIPTTNLH SNVIPTCEPQSLVENLTQKLNNVNNQLFMTDVKENFKTSLESHT VLAPLTLKTENGDSQMMALNSCTTSVNSDLQISEDNVIQNFEKT LEIIKTAMNSQILEVKSGSQGAGETSQNAQINYNIQLPSVNTVQ NNKLPDSSP\FSSFISVMPTESNIPQSE\VSHKEDQIQBILEGL QKLKLENDLSTPASQCVLINTSVTLTPTPVKSTADITVIQPVSE MINIQFNDKVNKPFVCQNQGCNYSAMTKDALFKHYGKIHQYTPE MILEIKKNQLKFAPFKCVVPTCTKTFTRNSNLRAHCQLVHHFTT EEMVKLKIKRPYGRKSQSENVPASRSTQVKKQLAMTEENKKESQ PALELRAETQNTHSNVAVIPEKQLIEKKSPDKTESSLQVITVTS EQCNTNALTNTQTKGRKIRRHKKEKEEKKRKKVSQSLEFPTRY SPYRPYRCVHQGCFAAFTIQQNLILHYQAVHKSDLPAFSAEVEE ESEAGKESEETETKQTLKEFRCOVSDCSRIFQAITGLIQHYMKL HEMTPEEIESMTASVDVGKPPCDQLECKSSFTTYLNYVVHLEAD HGIGLRASKTEEDGVYKCDCEGCDRIYATRSNLLRHIFNKHNDK HKAHLIRPRRLTPGQENMSSKANQEKSKSKHRGTKMSRCGKEGI KMPKTKRKKKNNLENKNAKIVQIEENKPYSLKRGKHVYSIKARN DALSECTSRFVTQYPCMIKGCTSVVTSESNIIRHYKCHKLSKAF
			RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA EIAGELLQSNGGPSLLASMILSTNAVNLQQPQQSTFNPEACFKD PSFLQLLAENRSPAFLPNTFPRSGVINFNTSVSQEGSEIIIQAL ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPLLH TVCHPNTLLTNQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN GLCSSSFPNSGGPSQNFTSNSSRVSVISGPQNTRSSHLNKKGNS ASKRRKKVAPPLIAPNASQNLVTSDLTTMGLIAKSVEIPTTNLH SNVIPTCEPQSLVENLTQKLNNVNNQLFMTDVKENFKTSLESHT VLAPLTLKTENGDSQMMALNSCTTSVNSDLQISEDNVIQNFEKT LEIIKTAMNSQILEVKSGSQGAGETSQNAQINYNIQLPSVNTVQ NNKLPDSSP\FSSFISVMPTESNIPQSE\VSHKEDQIQEILEGL QKLKLENDLSTPASQCVLINTSVTLTPTPVKSTADITVIQPVSZ MINIQFNDKVNKPFVCQNQGCNYSAMTKDALFKHYGKIHQYTPE MILEIKKNQLKFAPFKCVVPTCTKTFTRNSNLRAHCQLVHHFTT EEMVKLKIKRPYGRKSQSENVPASRSTQVKKQLAMTEENKKESQ PALELRAETQNTHSNVAVIPEKQLIEKKSPDKTESSLQVITVTS EQCNTNALTNTQTKGRKIRHKKEKEEKKRKVPVSGSLEFFTRY SPYRPYRCVHQGCFAAFTIQQNLILHYQAVHKSDLPAFSAEVEE ESEAGKESETETTKQTLKEFRCQVSDCSRIFQAITGLIQHYMKL HEMTPEEIESMTASVDVGKFPCDQLECKSSFTTYLNYVVHLEAD HGIGLRASKTEEDGVYKCDCEGCDRIVATRSNLLRHIFNKHNDK HKAHLIRPRLTPGQENMSSKANQEKSKSKHRGTKRSRCGKEGI KMPKTKRKKNNLENKNAKIVQIEENKPYSLKRGKHVYSIKARN DALSECTSRFVTQYPCNIKGCTSVVTSESNIIRHYKCHKLSKAF TSQHRNLLIVFKRCCNSQVKETSEQEGAKNDVKDSDTCVSESND
			RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA EIAGELLQSNGGPSLLASMILSTNAVNLQQPQQSTFNPEACFKD PSFLQLLAENRSPAFLPNTFPRSGVTNFNTSVSQEGSEIIIQAL ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPPLLH TVCHPNTLLTNQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN GLCSSSFPNSGGPSQNFTSNSSRVSVISGPQNTRSSHLNKKGNS ASKRRKKVAPPLIAPNASQNLVTSDLTTMGLIAKSVEIPTTNLH SNVIPTCEPQSLVENLTQKLNNVNNQLFMTDVKENFKTSLESHT VLAPLTLKTENGDSQMMALNSCTTSVNSDLQISEDNVIQNFEKT LEILKTAMMSQILEVKSGSQGAGETSQNAQINYNIQLPSVNTVQ NNKLPDSSP\FSSFISVMPTESNIPQSE\VSHKEDQIQEILEGL QKLKLENDLSTPASQCVLINTSVTLTPTPVKSTADITVIQPVSZ MINIQFNCKUNKPFVCQNQGCNYSAMTKDALFKHYGKHQYTPE EMVKLKIKRPYGRKSQSZNVPASRSTQVKKQLAMTEENKKESQ PALELRAETQNTHSNVAVIPEKQLIEKKSPDKTESSLQVITVTS EQCNTNALTNTQTKGRKIRRHKKEKEEKKRKPVSQSLEFPTRY SPYRPYRCVHQGCFAAFTIQQNLILHYQAVHKSDLPAFSAEVEE ESEAGKESEETETKQTLKEFRCQVSDCSRIFQAITGLIQHYMKL HEMTPZEIESMTASVDVCKPPCDQLECKSSFTTYLNYVVHLEAD HGIGLRASKTEEDGVYKCDCEGCDRIYATRSNLLRHIFNKHNDK HKAHLIRPRRLTPGQENMSSKANQEKSKSKHRGTKHSRCGKEGI KMPKTKRKKKNNLENKNAKIVQIEENKPYSLKRGKHVYSIKARN DALSECTSRFVTQYPCMIKGCTSVVTSESNIIRHYKCHKLSKAF TSQHRNLLIVFKRCCNSQVKETSEQEGAKNDVKDSDTCVSESND NSRTTATVSQKEVBKNE*DEMDELTELFITKLINEDSTSVETQA
			RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA EIAGELLQSNGGPSLLASMILSTNAVNLQQPQQSTFNPEACFKD PSFLQLLAENRSPAFLPNTFPRSGVTNFNTSVSQEGSEIIIQAL ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPPLLH TVCHPNTLLTNQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN GLCSSSFPNSGGPSQNFTSNSSRVSVISGPQNTRSSHLNKKGNS ASKRRKKVAPPLIAPNASQNLVTSDLTTMGLIAKSVEIPTTNLH SNVIPTCEPQSLVENLTQKLNNVNNQLFMTDVKENFKTSLESHT VLAPLTLKTENGDSQMMALNSCTTSVNSDLQISEDNVIQNFEKT LEILKTAMMSQILEVKSGSQGAGETSQNAQINYNIQLPSVNTVQ NNKLPDSSP\FSSFISVMPTESNIPQSE\VSHKEDQIQEILEGL QKLKLENDLSTPASQCVLINTSVTLTPTPVKSTADITVIQPVSZ MINIQFNCKUNKPFVCQNQGCNYSAMTKDALFKHYGKHQYTPE EMVKLKIKRPYGRKSQSZNVPASRSTQVKKQLAMTEENKKESQ PALELRAETQNTHSNVAVIPEKQLIEKKSPDKTESSLQVITVTS EQCNTNALTNTQTKGRKIRRHKKEKEEKKRKPVSQSLEFPTRY SPYRPYRCVHQGCFAAFTIQQNLILHYQAVHKSDLPAFSAEVEE ESEAGKESEETETKQTLKEFRCQVSDCSRIFQAITGLIQHYMKL HEMTPZEIESMTASVDVCKPPCDQLECKSSFTTYLNYVVHLEAD HGIGLRASKTEEDGVYKCDCEGCDRIYATRSNLLRHIFNKHNDK HKAHLIRPRRLTPGQENMSSKANQEKSKSKHRGTKHSRCGKEGI KMPKTKRKKKNNLENKNAKIVQIEENKPYSLKRGKHVYSIKARN DALSECTSRFVTQYPCMIKGCTSVVTSESNIIRHYKCHKLSKAF TSQHRNLLIVFKRCCNSQVKETSEQEGAKNDVKDSDTCVSESND NSRTTATVSQKEVBKNE*DEMDELTELFITKLINEDSTSVETQA
			RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA EIAGELLQSNGGPSLLASMILSTNAVNLQQPQQSTFNPEACFKD PSFLQLLAENRSPAFLPNTFPRSGVTNFTNTSVSQEGSEIIIQAL ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPPLLH TVCHPNTLLTNQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN GLCSSSFPNSGGPSQNFTSNSSRVSVISGPQNTRSSHLNKKGNS ASKRRKKVAPPLIAPNASQNLVTSDLTTMGLIAKSVEIPTTNLH SNVIPTCEPQSLVENLTQKLMNVNNQLFMTDVKENFKTSLESHT VLAPLTLKTENGDSQMMALNSCTTSVNSDLQISEDNVIQNFEKT LEILKTAMMSQILEVKSGSQCAGETSQNAQINYNIQLPSVNTVQ NNKLPDSSP\FSSFISVMPTESNIPQSE\VSHKEDQIQEILEGL QKLKLENDLSTPASQCVLINTSVTLTPTPVKSTADITVIQPVSE MINIQFNDKVNKPFVCQNQGCNYSAMTKDALFKHYGKLHQYTPE MILEIKKNQLKFAPFKCVVPTCTKTFTRNSNLRAHCQLVHHFTT EEMVKLKIKRPYGRKSQSENVPASRSTQVKKQLAMTEENKKESQ PALELRAETQNTHSNVAVIPEKQLIEKKSPDKTESSLQVITVTS EQCNTNALTNTQTKGRKIRHKKEKEEKKRKKPVSQSLEFFTRY SPYRPYRCVHQGCFAAFTIQQNLILHYQAVHKSDLPAFSAEVEE ESEAGKESEETETKQTLKEFRCQVSDCSRIFQAITGLIQHYMKL HEMTPEEIESMTASVDVGKPPCDQLECKSSFTTYLNYVVHLEAD HGIGLRASKTEEDGVYKCDCEGCDRIYATRSNLLRHIFNKHNDK HKAHLIRPRLTPGQENMSSKANQEKSKSKHRGTKHSRCGKEGI KMPKTKRKKNNLENKNAKIVQIEENKPYSLKRGKHYYSIKARN DALSECTSRFVTQYPCMIKGCTSVVTSESNIIRHYKCHKLSKAF TSQHRNLLIVFKRCCNSQVKETSEQEGAKNDVKDSDTCVSESND NSRTTATTSQKEVEKNE*DEMDELTELFITKLINEDSTSVETQA NTSSNVSNDFQEDNLCQSERQKASNLKRVNKEKNVSQNKKRKVE
			RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA EIAGELLQSNGGPSLLASMILSTNAVNLQDPQQSTFNPEACFKD PSFLQLLAENRSPAFLPNTFPRSGVTNFTNTSVSQEGSEIIIQAL ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPLLH TVCHPNTLLTNQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN GLCSSSFPNSGGPSQNFTSNSSRVSVISGPQNTRSSHLNKKGNS ASKRRKKVAPPLIAPNASQNLVTSDLTTMGLIAKSVEIPTTNLH SNVIPTCEPQSLVENLTQKLMNVNNQLFMTDVKENFKTSLESHT VLAPLTLKTENGDSQMMALNSCTTSVNSDLQISEDNVIQNFEKT LEIIKTAMMSQILEVKSGSQGAGETSQNAQINYNIQLPSVNTVQ NNKLPDSSP\FSSFISVMPTESNIPQSE\VSHKEDQIGEILEGL QKLKLENDLSTPASQCVLINTSVTLTPTPVKSTADITVIQPVSE MINIQFNDKUNKPFVCQNQGCNYSAMTKDALFKHYGKKHQYTPE MILEIKKNQLKFAPFKCVVPTCTKTFTRNSNLRAHCQLVHHFTT EEMVKLKIKRPYGRKSQSENVPASRSTQVKKQLAMTEENKKESQ PALELRAETQNTHSNVAVIPEKQLIEKKSPDKTESSLQVITVTS EQCNTNALTNTQTKGRKIRRHKKEKEEKKRKPVSQSLEFPTRY SPYRPYRCYHGGCFAAFTIQQNLILHYQAVHKSDLPAFSAEVEE ESEAGKESEETETKQTLKEFRCQVSDCSRIFQAITGLIQHYMKL HEMTPEEIESMTASVDVGKPPCDQLECKSSFTTYLNYVVHLEAD HGIGLRASKTEEDGVYKCDCEGCDRIVATRSNLLRHIFNKHNDK HKAHLIRPRLTPGQENMSSKANQEKSKSKHRGTKHSRCGKEGI KMPKTKRKKKNNLENKNAKIVQIEENKPYSLKRGKHVYSIKARN DALSECTSRFVTQYPCNIKGCTSVVTSESNIIRHYKCHKLSKAF TSQHRNLLIVFKRCCNSQVKETSEQEGAKNDVKDSDTCVSESND NSRTTATVSQKEVBKNE*DEMDELTELFITKLINEDSTSVETQA NTSSNVSNDFQEDNLCQSERQKASNLKRVNKEKNVSQNKKRKVE KAEPASAAELSSVRKEEETAVAIQTIEBHPASFDWSSFKPMGFE
			RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA EIAGELLQSNGGPSLLASMILSTNAVNLQQPQQSTFNPEACFKD PSFLQLLAENRSPAFLPNTFPRSGVTNFTNTSVSQEGSEIIIQAL ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPPLLH TVCHPNTLLTNQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN GLCSSSFPNSGGPSQNFTSNSSRVSVISGPQNTRSSHLNKKGNS ASKRRKKVAPPLIAPNASQNLVTSDLTTMGLIAKSVEIPTTNLH SNVIPTCEPQSLVENLTQKLMNVNNQLFMTDVKENFKTSLESHT VLAPLTLKTENGDSQMMALNSCTTSVNSDLQISEDNVIQNFEKT LEILKTAMMSQILEVKSGSQCAGETSQNAQINYNIQLPSVNTVQ NNKLPDSSP\FSSFISVMPTESNIPQSE\VSHKEDQIQEILEGL QKLKLENDLSTPASQCVLINTSVTLTPTPVKSTADITVIQPVSE MINIQFNDKVNKPFVCQNQGCNYSAMTKDALFKHYGKLHQYTPE MILEIKKNQLKFAPFKCVVPTCTKTFTRNSNLRAHCQLVHHFTT EEMVKLKIKRPYGRKSQSENVPASRSTQVKKQLAMTEENKKESQ PALELRAETQNTHSNVAVIPEKQLIEKKSPDKTESSLQVITVTS EQCNTNALTNTQTKGRKIRHKKEKEEKKRKKPVSQSLEFFTRY SPYRPYRCVHQGCFAAFTIQQNLILHYQAVHKSDLPAFSAEVEE ESEAGKESEETETKQTLKEFRCQVSDCSRIFQAITGLIQHYMKL HEMTPEEIESMTASVDVGKPPCDQLECKSSFTTYLNYVVHLEAD HGIGLRASKTEEDGVYKCDCEGCDRIYATRSNLLRHIFNKHNDK HKAHLIRPRLTPGQENMSSKANQEKSKSKHRGTKHSRCGKEGI KMPKTKRKKNNLENKNAKIVQIEENKPYSLKRGKHYYSIKARN DALSECTSRFVTQYPCMIKGCTSVVTSESNIIRHYKCHKLSKAF TSQHRNLLIVFKRCCNSQVKETSEQEGAKNDVKDSDTCVSESND NSRTTATTSQKEVEKNE*DEMDELTELFITKLINEDSTSVETQA NTSSNVSNDFQEDNLCQSERQKASNLKRVNKEKNVSQNKKRKVE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid .	W=Tryptophan, Y=Tyrcsine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	sequence	\=possible nucleotide insertion)
	sequence		
			VLKQLQEMKPTVSLKKLEVHSNDPDMSVMKDISIGKATGRGQY
5363	8066	703	RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP
1	İ		PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML
}	j		RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS
1.	ł		QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK
i	1		PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS
1	Į		CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT
1	į.		CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR
1	1		ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG
i	ĺ		EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT
1			DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG
1	1		GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQ
j	1		KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR
1			DNMKWCGTTONYDADOKFGFCPMAAHEEICTTNEGVMYRIGDOW
1			• -
1	1		DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN
1	ļ		DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI
i	i		GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI
			TETPSQFNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP
ł	ł		GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST
	Į		PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV
1	l .		SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN
1			VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR
ł			PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN
1			ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTDV
)	i i		KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AEN
			TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN
1	1		ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY
1	i		PLRNLOPASEYTVSLVAIKGNOESPKATGVFTTLOPGSSIPPYN
1		1	TEVTETTIVITWTPAPRIGFKLGVRPSOGGEAPREVTSDSGSIV
į			VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH
1			LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV
ĺ	ĺ		HADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV
<b>,</b>			PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKNE
1			GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEQHESTP
ł			\LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI
ł			TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPGTEYVV
ł			
1			SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD
1			APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD
)			YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNS
j			ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI
1			EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV
1			DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA
1			ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT
			QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS
1			SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR
			ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP
			DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS
			NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP
1			RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP
			QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT
			SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE
1			ALSOTTISWAPFODTSEYIISCHPVGTDEEPLQFRVPGTSTSAT
1			LTGLTRGATYNIIVEALKDOORHKVREEVVTVGNSVNEGLNOPT
1			DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD
1			SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP
		,	HEATCYDDGKTYHVGEOWOKEYLGAICSCTCFGGORGWRCDNCR
1			
			RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ
- 6366	9000	500	ADREDSRE
5364	8066	703	RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP
]			PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML
			RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS
		-	•

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
No:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
-	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
İ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	residue of	residue of	S=Serine, T=Threonine, V=Valine,
l i	amino acid	amino acid sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion,   -possible nucleotide insertion)
			QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK
			PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS
1 1			CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT
			CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR
			ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG
			EWKCERHTSVOTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT
i !			DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG
( (	j		GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQ
	i		KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR
1 1			DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQW
1 1			DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN
	.		DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI
1	ļ		GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP
	•		GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST
1			PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV
1			SGFRVEYELSEEGDBPQYLVLPSTATSV\NIP\DLLPGRKYIVN
			VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR
. j			PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN
1 ]			ITIYAVEENQESTPVVIQQEITGTPRSDTVPSPRDLQFVEVTDV
1 1			KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AEN
. [	-		TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN
1 1			ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN
1 1	}		TEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGSIV
1	1		VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH
1 1			LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV
1			HADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV
	1		PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKNE
1 1			GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEQHESTP
1			\LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI
1 1	i		TGYRIR\HHPEHF\SGRPREDR\VDHSRNSITLTNLTPGTEYVV SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD
1 1			APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD
] ]			YTITVYAVTGRGDSPASSKPISINYRTEIDKPSOMOVTDVODNS
1 1			ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI
1		ŀ	EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV
1			DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA
1 1	ŀ	ļ	ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT
1 1	}		QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS
1			SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR
1	ļ		ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS
1			NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP
1		!	RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP
			QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT
			SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPMVGQE
1	ł	}	ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT
1	ł	1	LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVNEGLNQPT
	1	1	DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD
		İ	SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR
1	1	1	RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ
	1	1	ADREDSRE
5365	8066	703	RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP
1 1			PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML
1 1			RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS
1	Ĭ		QSKPGCYDNGKHYQINQQWBRTYLGNALVCTCYGGSRGFNCESK
1	,		
	İ	ſ	PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS
			PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMWVDCTCLGEGSGR

Description   not leotide   location   corresponding   cofirst   amino acid   amino acid   amino acid   sesidue of   amino acid   sesidue of   amino acid   sesidue of   amino acid   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   seq	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
NO: nucleotide corresponding to first amino acid residue of residue of first amino acid residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of	1		1	(A-Alanine C-Crestoine D-Assault Paris
location corresponding to first amino acid smino acid smino acid smino acid smino acid smino acid smino acid smino acid smino acid smino acid smino acid smino acid smino acid smino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequen	NO:			Glutamic Acid F-Phonylalanina C-Clusica
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### seridue of amino acid sequence   S-Serime, T-Threenime, V-Valime,   Setop amino acid acid sequence   S-Serime, T-Threenime, V-Valime,   Setop acid acid sequence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence   Secuence	1			
maino acid anino acid acquence    M-Tryptophan, Y-Tyrosine, K-Unknown, *-Stop   Codon, /-possible nucleotide deletion,   Codon, /-possible nucleotide deletion,   Codon, /-possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide deletion,   Possible nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nuc	1		l e e e e e e e e e e e e e e e e e e e	
amino acid sequence  Codon, /-possible nucleotide deletion, /-possible nucleotide deletion  ITCTSRNRCONGCTFTTYRIGGTWSKKONRGBLLCCTCTCRRGR  EKKERHTSUCTISSGOFPTUPNANUPODPHOEDPYSHCTT  BEGVVYSUMONIA **CTORKONLA**CTLCRGRGSCGFTAVTOCTG  GENSAGEPCUPPTTWRCTTSCTSGCGGTRUNGOGHLMCSTTSTNRCDG  KYSCCTDHTULVGTRGGSNNALCFFFFYNNHNTTDCTSGGR  DNMCKGCTTONNADACKFSCFMANABCCTFFFYNNHNTDCTSGGR  DNMCKGCTTONNADACKFSCFMANABCCTVDGTTYRSGOG  BKOHDWGHMRRCTCVGNRGGSWTCLAYSGLEBGCTVDGTTYNGY  DTFHRRHEBGHLMLGCTFGGGGGRRWGEPCTAVGTGTG  GUSMERYHGUSYCCCGRGIGEWGCDFLOTTSSSSCFFFYOI  GUSMERYHGUSYCCCGRGIGEWGCDFLOTTSSSCFFFYOI  GUSMERYHGUSYCCCGRGIGEWGCDFLOTTSSSSCFFYOFT  TITPSGCMSBIPCONAPPOSHISTITHASSEVVSWSASDTV  SOFFWEYELSBGDEPCYLLUSTATSTVANIP DLLEGRKTYUK  VYGISEGOGGLILISTGGTTAPDAPPFTYOOUTDTIVAVRSS  FOAPITGTRTVSSSVGGSTEINIPFTANSSVTLSDLQPAQVYN  KYTHMITPESAUTGTWRDVIOGETTGTFRATDTSSSFFYONSAGENTY  FOAPITGTRTVSSSVGGSTEINIPFTANSSVTLSDLQPAQVYN  KYTHMITPESAUTGTWRDVIOGETTGTFRATDTVSSSPLGPFAVITOR  TITVAVERNOESTEVULQGETTGTFRATOVTISGGFGCTAVGTAVGTAVGTAVGTTKALDATTVAVRSS  FOAPITGTRTVSSSVGGSTEINIPFTANSSVTLSDLQPAQVYN  KYTHMITPESAUTGTWRDVIOGETTGTFRATOVTISGGSTIPY  KYTHMITPESAUTGTWRDVIOGETTGTFRATOVTISGGSTIPY  KYTHMITPESAUTGTWRDVIOGETTGTFRATOVTISGGSTIPY  TEVTSTTULVHRYPPAGLITGVRUNGCHTGTSTAVGTVFTLGGGSSIPY  TEVTSTTULVHRYPPAGLITGVRUNGCHTGTTFTGGGGSTIPY  TEVTSTTIVTTYTTARTRARGGRAGVATENTOVTICHTGGGRSSIPY  TEVTSTTIVTTYTTARTRARGGRAGVATENTOVTICHTGGGRSSIPY  TEVTSTTIVTTYTTARTRARGGRAGVATENTOVTICHTGGGRSSIPY  TEVTSTTIVTTYTTARTRARGGRAGVATENTOVTICHTGCGGRSSIPY  TEVTSTTIVTTYTTARTRARGGRAGVATENTOVTICHTGCGGRSGGGAACHACKTAGGGGGGGAACHACKTAGGGGGGAACHACKTAGGGGGAACHACKTAGGGGGGAACHACKTAGGGGGAACHACKTAGGGGGAACHACKTAGGGGGGAACHACKTAGGGGGAACHACKTAGGGGGAACHACKTAGGGGGAACHACKTAGGGGAACHACKTAGGGGAACHACKTAGGGGAACHACKTAGGGGAACHACKTAGGGGAACHACKTAGGGAACHACHACHACHACHACHACHACHACHACHACHACHACH	1	1		
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GBSMERYUNGUNYEGOLISIOQUGMOEUTEPSESGEPUEFI TETESGOMSHIP IQWAN POPSHIS KYILIMHEN PANSYEMMENTIP GHLMSYTIKGLKGGVVYEGOLISIOQUGMOEUTEPSTITISTE PUTSNI'VNGESTTISSININESSYTEITASSTVESWASADTV SGFAVERISEBODEPQLULPSTATSVINI'N NOLLOGKKYIVN VQOISBODEGGILISTSGTTASSVINI'NSFAVESWASADTV VQOISBODEGGILISTSGTTAPBOPUTPOIDTSIVYRMSH POAPITOKRIVYSPSVEGSSTEIMIPETANSVTIJOLOGGVYN ITILYAEENGESTPVIOLOGITOTPESDTVP PEPDLOFVETUDV KYTIMMTPPESANTCKYRDVI'DVILPGEHOGELPLSTNITP\AEN TOLDEPUTVYSTYNAVASHBRESKPLTAQQTTKL\DAPTILOFUN ETDSTULVAMTPPERAQITOTULTVICITRIOGGRYNVGESVSKY PLRNLQPASETYVOLVAI KKNQESPKATGVFTILQGGSSI'PYN VSOLPGGVEYVTI'QUURDOGEROAP\UNK\VVTPLSPPINGH LEAMPDTGVI'NTSWERST:TDITURYRITTPINGQGSNILEEVY VSOLPGGVEYVTI'QUURDOGEROAP\UNK\VVTPLSPPINGH LEAMPDTGVI'NTSWERST:TDITURYRITTPINGQGSNILEEVY HAQGSSCTP\UNKVVTPLSPPINGH GRALGSLEIFFLSON\AVVI'NTLLEGGTZVVSVSSVYEQHBSTF VLANGKRISCLEPSI'NTGKRYTM\APPSI'LDITAPAYPTYTI TGYRIR\HHEEHY\GGGFREDR\VPHARNSITI.TNLTFOTTYV VSILAMRGESSPLILGQGGTVYSUVYROBKSSTATISGLKKGUD YTTITYYAVTGROSPASK'RI SINYRTEIDKRAUTUPUQMS ISVANLABSSOQUVSRYVYTSSEDDGHELPPAPDGEEDTA BELGPTVSVVVAVANDBEGSPLIVTATVI'NTRALAPPATTIL GUGLPTVSVVVAVANDBEGSPLIVTATVI'NTRALAPPATTIL GUGLPTVSVVVAVANDBEGSPLIVTATVI'NTRALAPPATTIL GUGLPTVSVVVAVANDBEGSPLIVTATVI'NTRALAPPATTIL GUGLPTVSVVVAVANDBEGSPLIVTATVI'NTRALAPPATTIL GUGLPTVSVVVANDBEGSPLIVTATVI'NTRALAPPATTILKT OVORSIKIAMESOQGVSRYRVYTSSEDDGHELPPAPDGEEDTA BELGROSSSYTVSVVALIDBURGEQPLI'UTTATVI'NTRALAPPATTILKT OVORSIKIAMESOQGVSRYRVYTSSEDDGHELPPAPDGEEDTA BELGROSSSYTVSVVALIDBURGEQPLI'UTTATVI'NTRALAPPATTILKT OVORSIKIAMESOQGVSRYRVYTSSEDDGHELPPAPDGEEDTA BELGROSSSYTVSVVALIDBURGEQPLI'UTTATVI'NTRALAPPATTILKT OVORSIKIAMESOQGVSRYRVYTSSEDDGHELPPAPDGEEDTA BELGROSSSYTVSVVALIDBURGEQPLI'UTTATVI'NTRALAPPATTILKT OVORSIKIAMESOQGVSRYRVYTSSEDDGHELPPAPDGEEDTA BELGROSSSYTVSVVALIDBURGEQPLI'UTTATVI'NTRAGTSPOTTILRY OVORSIKIAMESOQGVSRYRVYTSSEDGHELPPATTILKTENDYSPER ARVTDATETTITISMRRYKETITOFOUNDAPSANGOTPIOTRI'R DVSSTITIGLGFOTTYTI'UTLINDRARSSSYTVIDATSPATDLAST ONSTTUNDRATTISMSTRYNTYNONCPICERSGFFROD SKORCHDISKNYKIGEKUNTGGROMMOTOTICLGGGGFROD SSRKCHDIGGNYKIGEK				DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN
TETTSQENSHIPIQMNAPQSHISKYTLRWRPKMSVGRWKEATTIP GHLNSTYIKGLKJRQUVVEGOLISIQOQTGUTPOPTTTSTET GHLNSTYIKGLKJRQUVVEGOLISIQOQTGUTPOPTTTSTET PYTSNT\VTGETTEFSPLVATSBSVTETTASSPVWSWASDTV SGFWEYELEREGDEPQUTJUFPATASVITASSPVWSWASDTV SGFWEYELEREGDEPQUTJUFPATASVITASSPVWSWASDTV VYQISBOGGGILISTSQTTAPDAPDPPTVDQUDTSITVRWBS PQARITOXTIVJSBVGWGSTEINLIPPATASVITLDLQDGUQUN ITIVAVERQESTPVVIQGETGTERSDTVSSPRLQFVEVTDV KVTIMMTPPEGAVTGTRVDVTPVALLGEHGGREDISRNTF\ALSN TGLSPGVTYTYKVFWASWASRSKENDATGUTPGGSSIPYN RTTMTTTTVIUWTPRAGITGYKLTVGLTRGGPRQTWYDGSVSKY FLRNLQPAGSTTYGLVAL KONGGSPRARGVTTLQGGSSIPYN VSGLTFGGWYTTJQULRGGERDAP\UNK\VYTFLSPPTNLH LEANPDTGVLTVSWERSTTDJTTGYKITTTFTMGQGRSLEEVV VSGLTFGGWYTTJQULRGGERDAP\UNK\VYTFLSPPTNLH LEANPDTGVLTVSWERSTTDJTTGYKITTTFTMGQGRSLEEVV HADQSSCTF\UNLFVGLEYAVSVYTVQUSSVYKOHESTP QFPTDLRFTN\ILGDTMRVTW\APPPSIDLTMFLWRYSPVKSE GRMLGSLSIFLSDN\AVUTINLIPGTSVSSVYKOHESTP \LSGRKGGLDSP\TGIDFS\DITA\MSFT\VTW\TAPPATCHTYPV HADGSSCTF\SURVALUTNLIPGTSTXTSVSTYKOHESTP \LSGRKGGLDSP\TGIDFS\DITA\MSFT\VTW\TAPPATCHTYPV SIVALMGRESPPLIGQGSTVSDVYRDLEVWAATPTSLI\SSR APAVTVXTYRITTGGTGGRSVDVEFTYGSATTISGLKGGU YTTTVXAVTGGDSPASKPISITNYTTIDKPGQMQVTDUQDMS ISVKLAPSSEPVIGVRVTT\PKRGGP\STATISGLKGGU YTTTVXAVTGGDSPASKPISITNYTTSIDKPGQMQVTDUQDMS ISVKLAPSSEPVIGVRVTT\PKRGGP\GTAPATDLKSTT OVTFTSLLSAMGNESPQLUQTAVTNIDPRKALAFTDV DUSSIKIMBSPQGQUGSFYRVTSSPBEDITEPPADPGEPDA REGGESPTSVVALHDDMSSQPLGTGGTA-PAPATDLKSTT OVTFTSLLSAMGNTSPWQTOTRVTTPKTTDRYGMZINLAPDS SVUSSLAWATKYEVSYVALKDDMSSQPLGTGGTA-PAPATDLKSTT OVTFTSLLSAMGTSTYVALHIDMSSGPLIGRTCHGTTLKTD REGGESPTTSVALHDMSSGPLIGRTCHGTTLTNAPGSFPRR ARTYDATFTITISMTXTTITIGFVDAVPANGGSPRRUVPRR PROUTEATTIGLEEGTSTYTYTYTALKNOKSPPLIGRTTLGTTLKF DVSSYTITGLQFGTDYKTYTYTILKNOKSPPLIGRKTTDLPT ARGUTERATIGLEFGTSTYTYTALKNOKSPPLIGRKTTDLPT SGCQDSVAGGMIFESHGFARTTFPTTTATFTRRPPPPPTNPP DSSKRGDBGSFGCTGGSGGGAFTEDUTGATTYTONAPGSFGLIGPGT DDSCCPPYTTSHYNAGDEWRRMSSGFKLLCCCLGRGGGFKCD REGGESTTGGSTWGGGAFTSPTTTTATTTRRPPPPPPPTTIPP PSSWRGOPPGGGGTRCTGGGGGGAFCDKC REGGESTTGGGSTWGGGATTSLUCTCYGGSGGFNCDK CRIGGESTFGGGSTTGGGGGATTSLUCTCYGGSGGFNCDK CRIGGESTFGGGGGGTTGGGGATTSLUCTCYGGGGGGATS		1		DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI
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GHLMSTIKGLKPOUVTEGOLISLQYGHGEVTREPPTTTSTST PVTSTN'VTGETTFSFPLVAMSESVETTATSVUMTP\DLLGGKYTWS SGFAVEYELSERGDEPOYLVLPSTATSV\NTP\DLLGGKYTWS VYQISBOGGSGLILSTSOTTAPDAPPPTDYDVDDTSTYVWSNE POAPITGYRIVYSBSVEGSSTEINLDSTANSVTLSDLQPGVQYV ITTYAVERNQESTPVUIQOSTTGTPRADTVSSPLQFVETOVT KVTIMITPSSAVTGYRVDVTPVALIGGHEGGLPLSTNTF\ALS TGLSPGVTYYRKVPAVSHGRSKRLIPAQOTTKL\DAPTLQFVN ETDSTULVAMSTPPRAQITGYRLIVGLTRGGPRQYNVOPSVSKY BLRNLQPAGETTVSLVALKGNGSSFRATGVSTLTQGFRQFRVNOPSVSKY PLRNLQPAGETTVSLVALKGNGSSFRATGVSTLTQGFRQFRVNOPSVSKY BLRNLQPAGETTVSLVALKGNGSSFRATGVSTLOGGSIPPRUTLEPTING TGVSTETTVILVTWPPARTIGFDITGYRITTPTMGQGMSLEVY VSGLTGGVYYTTQULRDGGERNAP\LVNK\VVTFLSPTNLH LEANPDTGALTVSWERSTTDJTGYRITTPTMGQGGNSLEVY HADQSSCTP\NNLAVGGLEXVASUVTVKDUKESVPISTIPAV PPPTDLRFTN'ILGPDTNAVTWAAPP BEILTMFLVMYSPVKNE GRMLGSLSIFFLSDN\AVVLTNLLDGTZVVVSUSSVYRQHSTD ARGANTVALTSVILGGGERNAP\LVNK\VTFLMYSPVKNE GRMLGSLSIFFLSDN\AVVLTNLLDGTZVVSUSSVYRQHSTD LYGGRKGGLSSPLLIGGGSTDJVPRDLEVVAATPTSLLI\ND APAVTVRYYRITYGETGGNSSVOEFTVPSGSKSTATISGLKGGUV YTTYVAVTORGORSPLSVLTNAVTTSLKTSILKSGGNQVTUDQDNS ISVALDSSSSPLTGVTNTT'IP\ENGSGYNGKSTATISGLKGGUV YTTYVAVTORGORSPLSVVALHDDMSSGATATISGLKGGUV YTTYVAVTORGAGRASKETSINVTRTRINKSGRQVTUDQDNS ISVANDASSSPTGVTNTT'IP\ENGSGYNGTNETTSLLAVBDDSS SVVSSLMVATKYSVYALKDDMSSGATA-PAPTDLKFT OVTPTSLSAGANTFNVALTDYRVRVTPKEKTGAPDGTEMTI BULQPTVSVVSVSVALHDDMSSGATA-PAPTDLKFT OVTPTSLSAGANTFNVALTDYRVRVTPKEKTGAPGOTFMEINLAPDS SVVVSSLMVATKYSVYALKDTLATSRPAGGVTTLKNSPPRR ARVTDATFTITISKNKTSTTITIGVOUPAGGTPLGTSTA-PAPTDLKFT OVTPTSLSAGANTFNVALTSRPAGGVTTLKNSPPRR ARVTDATFTITISKNKTSTTITIGVOUPAGGTPLGTGSTA-PAPTDLKFT OVTPTSLAGANTFNVALTSRPAGGVTTLKNSPPRR ARVTDATFTITISKNKTSTTITIGVOUPAGGTPLGTSTAT LTGLTRGATYNI VEALKUQQRHKVRESVUTAGGTPLGTSTAT LTGLTRGATYNI VEALKUQQRHKVRESVUTAGGTPLGTSTAT LTGLTRGATYNI VEALKUQQRHKVRESVUTAGGTPLGGGGGGFRECDA SSGNCHDMGVNYLGEENUNGGENGTAGGGFRECDA REGGESTFEGGSTTGGSTANGGFREGDANGSGRECDANTGGGFRECDA REGGESTFEGGSTTGGSTANGGFREGDANGGERGENCESC REGGESTFEGGSTTGGSTANGGFRECDANTGGGFRECDANTGGGFREGGETGANGGGFREGGFREGGERGEGGFREGGETGANGGGFREGGFREGGFREGGFREGGFREGGFREGGFREGGF	1	J		TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP
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POAPITOTRITYSBYEGSSTEINIPETANSVILSDLOPGYQYN ITITAWERQGSTPUTQUQCHTCTPEGPELQGYEVTDY IVTTMWTPESAVTGYRVDVIDWIDGEHGQRLDISRNTP\AEN TGLSGUTTYYFKVRAVSHGRSKRLTAQCTTKI, DAPTNLQFVN ETDSTULVRWTPPRAQITGYGLTUGHGGGRGYNVGPSVSKY FLRNLQPAGETTVSUVAIKSNQSSFKATGYTTLTQGSSIPPXN TEVTETTUTTVTWTPAFFIGKIGWFSGGEAPREVTGBGSIV VSGLTGGVEYYTTQULRGGGERDAP IVMK\VYTPLSPPTNLH LEANPDTGLTVSWERSTTPDITGYSTTPTTGGGGSTPYNN TEVTETTUTTWTTAPFAFGGGEAPREVTGBGSIV VSGLTGGVEYYTTQULRGGGERDAP IVMK\VYTPLSPPTNLH LEANPDTGLTVSWERSTTPDITGYSTTPTTMGGGGANGLEEVV HADGSCTF\NDLEVGGLEYNVSVYTVKDDKSSVSISDTIIPAV PPPTDLRFTN/ILGPTMYTW\APPSILTNIPLGVRYSPVKNE GRMLQSLSIFFLSDN\AVULTNILDGTSYVVSVSVVEGHESTP \LARGKRGGLDSP\TGIDFS\DITA\MSFT\HMW\APPRS\TVXNE GRMLQSLSIFFLSDN\AVULTNILDGTSYVVSVSVVEGHESTP \LARGKRGGANGLOSTVSDVFRDLEVVARTTSILI\SND APAVTVRYTRYTTYGETGRSVOGETPVGSKTATISGLEVV SIVALMGRESSPLLIGQGSTVSDVFRDLEVVARTTSILI\SND APAVTVRYTRYTTYGTGRSVOGETPVGKTKATGDPOG-EMTI GGLQPVGYVVSVVANDDGGSSQLVQTAVTNIDBPGGLAPTDV DVGSIKIMBESPGGVGRVVPYSSPDEDGHLPPAPDGEEDTA EGLQPVGYVVVAANDEGGSSQLVQTAVTNIDBPGGLAPTDV DVGSIKIMBESPGGVGRVVPYSSPDEDGHLPPAPDGEEDTA ELQGLRPGSEYTVSVVALHDDMSQCPLIGTGSTA_PAPTDLKFT QVTPTSLSAGKTFRNQUTTLSWRYPTKSRTGSPWGTBLAPTDS SVVVSSLAWARKYEVSVALKDTLTSRAPQGVVTTLENNSPPRR ARVIDATSTITITSMSTKTETITGFQVDAVPRAGNGTGCTGTTAPP REGULFATTTGLOFGTDYKIYLTHINDARSPNQGTFICRTIKPP PONSTTITGLOFGTDYKIYLTHINDARSPNQGTFICRTIKPP REGULFATTTGLOFGTDYKIYLTHINDARSPNYUDANTGGGCLPGT SCQOPSVGQMIFEBHGFRTTPPTTATPIRRPRPYPPNVQGE ALGCTTISMAPFQDTSETITISLEHVETDEPLGPRYPGTSTSAT LTGLTRGATNNITVEALKDQGRKVREFLIGRKURGEFKCDP HEATCYDDGTTYNSPAVGDERMSSSGFFLLOCCLGFGSGFFRCD SSRWCHDMGVNYKIGEKWDRGGERGMMSCTCLLGNGGFFRCD SSRWCHDMGVNYKIGEKWDRGGERGMMSCTCLGNGGFFRCD SSRWCHDMGVNYKIGEKWDRGGERGMMSCTCLGNGGFFRCD SSRWCHDMGVNYKIGEKWDRGGRGGMMSCTCLGNGGFFRCD PEARCTGDGTTYNSPAVGDTYRRFRGAMILCCCLGNGGGFRC GGGGGLLLAULCGTATVGTTYSGTSGRAFTCESK PEARTCFGDFYNNTYRYGDTYPRFRGAMILCCCLGNGKGFF CKPIARCHGGGGSYKIGDTWRAVCTCTCLGGGGGR CTLANGCHGGGGGFTGTSSGREFRCSPKUPGTYRCHOVCCTCLGNGKGFF CKPIARCHGGGGSYKIGDTWRAVCYCTCLGGGGGR EKCERTSVGTTSSGSGFFTDVRANVQCOPTAVCCTCLGGGGGR EKCERTSVGTTSSGSGFFTDVRANVQCOPTAVCCCT				
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ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG	ļ l		i	
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DSGVVYSVGMQLA+KTQGNKQML\CTCLGNGVSCQETAVTQTYG	[	}	Ì	
	} [			
GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQ			ļ	
	L			GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQ

SEQ Predicted   Predicted end   Amino acid segment containing signa	Acid, E= lycine,
NO: nucleotide location corresponding to first amino acid residue of location corresponding to first amino acid residue of location corresponding to first amino acid residue of location corresponding to first amino acid residue of location Glutamic Acid, F=Phenylalanine, G=Gutamine, K=Lysine L=Leucine, M=Methionine, N=Asparagi P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,	lycine,
location corresponding H=Histidine, I=Isoleucine, K=Lysine corresponding to first L=Leucine, M=Methionine, N=Asparagi to first amino acid residue of S=Serine, T=Threonine, V=Valine,	
corresponding to first Lapleucine, Manufacture, Nanagi Lapleucine, Manufacture, Nanagi Lapleucine, Manufacture, Nanagi Lapleucine, Manufacture, Nanagi Lapleucine, Manufacture, Nanagi Lapleucine, Manufacture, Nanagi Lapleucine, Manufacture, Nanagi Lapleucine, Manufacture, Nanagi Lapleucine, Manufacture, Nanagi Lapleucine, Manufacture, Nanagi Lapleucine, Manufacture, Nanagi Lapleucine, Manufacture, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Lapleucine, Nanagi Laple	
to first amino acid P=Proline, Q=Glutamine, R=Arginine, amino acid residue of S=Serine, T=Threonine, V=Valine,	
amino acid residue of S=Serine, T=Threonine, V=Valine,	ne,
residue of   amino acid   W=Tryptophan, Y=Tyrosine X=thknown	
	. *=Stop
amino acid sequence Codon, /=possible nucleotide deleti	
sequence \=possible nucleotide insertion)	J.,
KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNY	TO COTO DODD
DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEG	
DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCI	
DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQD	
GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPS	SSGPVEVFI
TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSV	GRWKEATIP
GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRF	
PVTSNT\VTGETTPFSPLVATSESVTEITASSFVV	
SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DL	
VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDD	
PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLS	
ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRD	
KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPL	
TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\D;	
ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYI	
PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQ:	
TEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPRE	
VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVT	PLSPPTNLH
LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQ	GNSLEEVV
IIADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVP	ISDTIIPAV
PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLv	/RYSPVKNE
GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSS	VYEOHESTP
\LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\:	
TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNI	TPGTEVVV
SIVALNGREESPLLIGOOSTVSDVPRDLEVVAATP	
APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTAT	
YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMG	
ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAC	
EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRE	
DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPA	
ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIR	
QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKE	
SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTI	
ARVTDATETTITISWRTKTETITGFQVDAVPANGQT	
DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDA	
NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGS:	PREVVPRP
RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIG	RKKTDELP
QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTG	NGIQLPGT
SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRF	YPPNVGQE
ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRV	
LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSV	
DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGF	
SSRWCHDNGVNYKIGEKWDROGENGOMMSCTCLGNG	
HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGOR	
RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIE	
ADREDSRE	
5367 235 3591 KKILNMLCKKNIVIEYLADILYEYLYGFCFSGIKKY	T.TTUV7 DT
ILELWMTRLLLEKSVSLQTQYLLLIVKILSWFPGKE	
EVMMRKQDS/RIVGNGSEQQLQKELADVLMDPPMDD	
KRSQLDGEGDGPLSNQLSASSTINPVPLVGLQKPEM	
GDSEASSPFTPVADEDSVVFSKLTYLGCASVNAPRS	
SILRSQCQISLDVTLSVPNVSEGIVRLLDPQTNTEI	
LFCVRGHDGTPESDCFAFTESHYNAELFRIHVFRCE	
LYSFATAFRRSAKQTPLSATAAPQTPDSDIFTFSVS	
KGYFSAVPKDKDRQCFKLRQGIDKKIVIYVQQTTNK	ELAIERCF
GLLLSPGKDVRNSDMHLLDLBSMGKSSDGKSYVITG	
FQVVNEETPKDKVLFMTTAVDLVITEVQEPVRFLLE	
NERLFWPFSKRSTTENFFLKLKQI KQRERKNNTDTL	
ESERERRKTTASPSVRLPQSGSQSSVIPSPPEDDEE	
SGSGDVSKECAEKILETWGELLSKWHLINLNVRPKQL:	SSLVRNGV
PEALRGEVWQLLAGCHNNDHLVEKYRILITKESPQD:	SAITRDIN

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotice deletion,
Í	sequence		\=possible nucleotide insertion)
<del></del>	<del>                                     </del>	·	RTFPAHDYFKDTGGDGQDSLYKICKAYSVYDEEIGYCOGOSFLA
}			AVLLLHMPEEQAFSVLVKIMFDYGLRELFKQNFEDLHCKFYQLE
}	1	į	RLMQEYIPDLYNHFLDISLEAHMYASQWFLTLFTAKFPLYMVFH
1	j	ļ	IIDLLLCEGISVIFNVALGLLKTSKDDLLJ.TDFEGALKFFRVQL
1			PKRYRSEENAKKLMELACNMKISQKKLKKYEKEYHTMREQQAQQ
			EDPIERFERENRRLQEANMRLEQENDDLAHELVTSKIALRKDLD
1		Ì	NAEEKADALNKELLMTKOKLIDAEEEKRRLEEESAHLKKMCRRE
į	ł	}	LDKAESEIKKNSSIIGDYKQICSQLSERLEKQQTANKVEIEKIR
			QKVDDCERCREFFNKEGRVKGISSTKEVLDEDTDEEKETLKNQL
1			REMELELAQTKL\QLVEASCKIQD\LEHPF*GLPFNE\VQAA\K
1	1		KTWFNRTLSSIKTATGVQGKETC
5368	573	2014	GAAAGAADPRRGSLGGRTMLDFAIFAVTFLLALVGAVLYLYPAS
1			RQAAGIPGITPTEEXDGNLPDIVNSGSLHEFLVNLHERYGPVVS
1	}		FWFGRRLVVSLGTVDVLKQHINPNKTLD/LF*NHAEVIIKVSIW
1			wwqce*kp\qrkklyengvtdslksnfalllklpeelldkwlsy
1			PETQH\VPLSQHMLGFAMKSVTQMVMGSTFEDDQEVIRFQKNHG
ľ	į		TVWSEIGKGFLDGSLDKNMTRKKQYEDALMQLESVLRNIIKERK
1			GRNFSQHIFIDSLVQGNLNDQQILEDSMIFSLASCIITAKLCTW
			AIWFLTTSEEVQKKLYEEINQVFGNGPVTPEKIEQLRYCQHVLC
			ETVRTAKLTPVSAQLQDIEGKIDRFIIPRETLVLYALGVVLQDP
]			NTWPSPHKFDPDRFDDELVMKTFSSLGFSGTQECPELRFAYMVT
			TVLLSVLVKRLHLLSVEGQVIETKYELVTSSREEAWITVSKRY
5369	1	6622	PRSLCFSLWAEAAVLADGGLRRRRRLLRGTMSASFVPNGASLED
			CHCNLFCLADLTGIKWKKYVWQGPTSAPILFPVTEEDPILSSFS
ł			RCLKADVLG/VWRRDQRPERRE\L+IFWGGEDP\VLLTLFTMTY
			QKKKMECGRMDFPMNAVLCFSKAVHNLLERCLMNRNFVRIGKWF
}	}		VKPYEKDEKPINKSEHLSCSFTFFLHGDSNVCTSVEINQHQPVY
			LLSEEHITLAQQSNSPFQVILCPFGLNGTLTGQAFKMSDSATKK
			LIGEWKQFYPISCCLKEMSEEKQEDMDWEDDSLAAVEVLVAGVR
1			MIYPACFVLVPQSDIPTPSPVGSTHCSSSCLGVHQVPASTRDPA
i i			MSSVTLTPPTSPBEVQTVDPQSVQKWVKFSSVSDGFNSDSTSHH GGKIPRKLANHVVDRVWQECNMNRAQNKRKYSASSGGLCEEATA
			AKVASWDFVEATQRTNCSCLRHKNLKSRNAGQQGQAPSLGQQQQ
	1		ILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A
			SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTEMANSPQ
			PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMPTPDPLVPSKPM
			EDRIDSLSQSPPPQYQEAVEPTVYVGTAVNLEEDEANIAWKYYK
			FPKKKDVEFLPPQLPSDKFKDDPVGPFGQESVTSVTELMVQCKK
			PLKVSDELVQQYQIKNQCLSAIASDAEQEPKIDPYAFVEGDEEF
			LFPDKKDRQNSEREAGKKHKVEDGTSSVTVLSHEEDAMSLFSPS
			IKQDAPRPTSHARPPSTSLIYDSDLAVSYTDLDNLFNSDEDELT
] .			PGSKRSANGSDDKASCKESKTGNLDPLSCISTADLHKMYPTPPS
			LEQHIMGFSPMNMNNKEYGSMDTTPGGTVLEGNSSSIGAQFKIE
1			VDEGFCSPKPSBIKDFSYVYKPENCQILVGCSMFAPLKTLPSQY
			LPLIKLPEECIYRQSWTVGKLELLSSGPSMPPIKEGDGSNMDQE
1			YGTAYTPQTHTSCGMPPSSAPPSNSGAGILPSPSTPRFPTPRTP
			RTPRTPRGAGGPASAQGSVKYENSDLYSPASTPSTCRPLNSVEP
] i			ATVPSIPEAHSLYVNLILSESVMNLFKDCNSDSCCICVCNMNIK
1 .			GADVGVYIPDPTQEAQYRCTCGFSAVMNRKFGNNSGLFFEDELD
1 1			IIGRNTDCGKEARKRFEALRATSAEHVNGGLKESEKLSDDLILL
j l		•	LQDQCTNLFSPFGAADQDPFPKSGVISNWVRVEERDCCNDCYLA
1 1		;	LEHGRQFMDNMSGGKVDEALVKSSCLHPWSKRNDVSMQCSQDIL
, !		i	RMLLSLQPVLQDAIQKKRTVRPWGVQGPLTWQQFHKMAGRGSYG
1 1		!	TDESPEPLPIPTFLLGYDYDYLVLSPFALPYWERLMLEPYGSQR
<b>!</b>			DIAYVVLCPENEALINGAKSFFRDLTAIYESCRLGQHRPVSRLL
; i		•	TDGIMRVGSTASKKLSEKLVAEWFSQAADGNNEAFSKLKLYAQV
] l			CRYDLGPYLASLPLDSSLLSQPNLVAPTSQSLITPPQMTNTGNA
] ]		•	NTPSATLASAASSTMTVTSGVAISTSVATANSTLTTASTSSSSS
j. j			SNLNSGVSSNKLPSFPPFGSMNSNAAGSMSTQANTVQSGQLGGQ QTSALQTAGISGESSSLPTQPHPDVSESTMDRDKVGIPTDGDSH
			AVTYPPAIVVYIIDPFTYENTDESTNSSSVWTLGLLRCFLEMVQ
			TITLE I TIME DEDITIONS AND DESCRIPTIONS

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	•	\=possible nucleotide insertion)
			TLPPHIKSTVSVQIIPCQYLLQPVKHEDREIYPOHLKSLAFSAF
			TOCRRPLPTSTNVKTLTGFGPGLAMETALRSPDRPECIRLYAPP
1	1		FILAPVKDKQTELGETFGEAGOKYNVLFVGYCLSHDORWILASC
1			TDLYGELLETCIINIDVPNRARRKKSSARKFGLQKLWEWCLGLV
			QMSSLPWRVVIGRLGRIGHGELKDWSCLLSRRNLQSLSKRLKDM
1			CRMCGISAADSPSILSACLVAMEPQGSFVIMPDSVSTGSVFGRS
1	1		TTLNMQTSQLNTPQDTSCTHILVFPTSASVQVASATYTTENLDL
1			AFNPNNDGADGMGIFDLLDTGDDLDPDIINILPASPTGSPVHSP
Į			GSHYPHGGDAGKGQSTDRLLSTEPHEEVPNILQQPLALGYFVST
	i		AKAGPLPDWFWSACPQAQYQCPLFLKASLHLHVPSVQSDELLHS
1			KHSHPLDSNQTSDVLRFVLEQYNALSWLTCDPATQDRRSCLPIH
Ī			FVVLNQLYNFIMNML
5370	1226	716	RWSRKLELRRAAQATESRPPQSQEMHPPTGKEVHALKRLRDSAN
1		. 20	ANDVETVQQLLEDGADPCAADDKGRTALHFASCNGNDQIVQLLL
1			DHGADPNQRDGLGNTPLHLAACTNHVPVITTLLRGGARVDALDR
1	1		AGRTPLHLAKSKLNILQEGHAQCLKAVR/HGGEADHPYAEGVSG
	]		APRAT*AARCSGVFPSPSRWLGSAPWSRSSCTIWSLPLHEAKCR
}			AVRPLSSAAQGSAPSSSSCCTVSTSLALAESLSLFRACTSLPVG
1			GCISWL
5371	1331	167	IAAMLWKLLLRSQSCRLCSFRKMRSPPKYRPFLACFTYTTDKCS
	1		SKENTRIVEKLYKCSVDIRKIRR\*KDGYF*RMKPMLKKLRI/F
ſ	[		LQELGADETAVASILERCPEAIVCSPTAVNTQRKLWQLVCKNEE
1 :			ELIKLIEQFPESFFTIKDQENQKLNVQFFQELGLKNVVISRLLT
			AAPNVFHNPVEKNKOMVRILQESYLDVGGSEANMKVWLLKLLSO
}	[		NPFILLNSPTAIKETLEFLQEQGFTSFEILQLLSKLKGFLFQLC
			PRSIQNSISFSKNAFKCTDHDLKQLVLKCPALLYYSVPVLEERM
į			QGLLREGISIAQIRETPMVLELTPQIVQYRIRKLNSSGYRIKDG
1			HLANLNGSKKEFEANFGKIQAKKVRPLFNDVAPLNVEE
5372	51	857	SPGAQFLWAAPDMPDPLFSAVQGKDEILHKALCFCPWLGKGGME
1			PLRLLILLFVTELSGAHNTTVFQGVAGQSLQVSCPYDSMKHWGR
			RKAWCRQLGEKGPCQRVVSTHNLWLLSFLRRWNGSTAITDDTLG
<b>\</b>			GTLTITLRNLQPHDAGLYQCQSLHGSEADTLRKVLVEVLADPLD
1 '		,	HRDAGDLWFPG\DLRASRMPMWSTASPGASWKEKSPSHPLPSFS
			SWPASFSSRF*QPAPSGLQPGMDRSQGHIHPVNWTVAMTQGISS
1			KLCQG
5373	2814	346	VKKTKSIFNSAMQEMEVYVENIRRKFGVFNYSPFRTPYTPNSQY
			QMLLDPTNPSAGTAKIDKQEKVKLNFDMTASPKILMSKPVLSGG
1			TGRRISLSDMPRSPMSTNSSVHTGSDVEQDAEKKATSSHFSASE
1	}	ì	ESMDFLDKSTASPASTKTGQAGSLSGSPKPFSPQLSAPITTKTD
1 1			KTSTTGSILNLNLDRSKAEMDLKELSESVQQQSTPVPLISPKRQ
			IRSRFQLNLDKTIESCKAQLGINEISEDVYTAVEHSDSEDSEKS
}		i	DSSDSEYISDDEQKS*GTSQEDTEDKEGCQMDKEPSAVKKKPKP
1 1		[	TNPVEIKEELKSTSPASEKADPGAVKDKASPEPEKDFSGKAKPS
1 1		l	PHPIKDKLKGKDETDSPTVHLGLDSDSE\NELVIDLGEDHSGRE
]			GRKNKKEPKEPSPKQDVVGKTPPSTTVGSHSPPETPVLTRSSAQ
, ,	)	į	TSAAGATATTSTSSTVTVTAPAPAATGSPVKKQRPLLPKE\TAP
, ,	j	j	AVQRSCGTSSTVQQKEITQSPSTSTITLVTSTQSSPLVTSSGSM
) I	1	ł	STLVSSVNGDLPIGTASADVAADIAKYTSKL\MDAIKGTM\TEI
			YNDLSKN\TTWKAQLAEDSQGLRIEIEKLQWLHQQEL\SEMKHN
1 1	1		LELTMAEMRQSWEQERDRLIAEVKKQLELEKQQAVDETKKKQWC
1 (	!	ļ	ANFKKEAIFYCCWNTSYCDYPCQ\QAHWPEH\MKSCTQSATAPQ
	1	j	\QEADAE\VNTETLNKSSQGSSSSTQSAPSETASA\SKEKETSA
] [	Í	İ	EKSKESGSTLDLSGSRETPSSILLGSNQGSDHSR\SNKSSWSSS
11			DEKRGS\TRSDHN/TPSTQHGRSLLPGKESRAGTPFLGTSK
5374	2814	346	VKKTKSIFNSAMQEMEVYVENIRRKFGVFNYSPFRTPYTPNSQY
1 1		j	QMLLDPTNPSAGTAKIDKQEKVKLNFDMTASPKILMSKPVLSGG
<u> </u>	]	ļ	TGRRISLSDMPRSPMSTNSSVHTGSDVEQDAEKKATSSHFSASE
<b>,</b>	ł	ļ	ESMDFLDKSTASPASTKTGQAGSLSGSPKPF9PQLSAPITTKTD
j i			KTSTTGSILNLNLDRSKAEMDLKELSESVQQQSTPVPLISPKRQ
1 1	l	ļ	IRSRFQLNLDKTIESCKAQLGINEISEDVYTAVEHSDSEDSEKS
] ]	ł	j	DSSDSEYISDDEQKS*GTSQEDTEDKEGCQMDKEPSAVKKKPKP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
-	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	sequence	seduence	Codon, /=possible nucleotide deletion,   -possible nucleotide insertion)
<del></del>	- Boguerice	ļ	TNPVEIKEELKSTSPASEKADPGAVKDKASPEPEKDFSGKAKPS
			PHPIKDKLKGKDETDSPTVHLGLDSDSE\NELVIDLGEDHSGRE
			GRKNKKEPKEPSPKQDVVGKTPPSTTVGSHSPPETPVLTRSSAQ
1	ì	}	TSAAGATATTSTSSTVTVTAPAPAATGSPVKKQRPLLPKE\TAP
ļ		1	AVQRSCGTSSTVQQKEITQSPSTSTITLVTSTQSSPLVTSSGSM
			STLVSSVNGDLPIGTASADVAADIAKYTSKL\MDAIKGTM\TEI
İ			YNDLSKN\TTWKAQLAEDSQGLRIEIEKLQWLHQQEL\SEMKHN
ì			LELTMAEMRQSWEQERDRLIAEVKKQLELEKQQAVDETKKKQWC
1			ANFKKEAIFYCCWNTSYCDYPCQ\QAHWPEH\MKSCTQSATAPQ
			\QEADAE\VNTETLNKSSQGSSSSTQSAFSETASA\SKEKETSA
			EKSKESGSTLDLSGSRETPSSILLGSNQGSDHSR\SNKSSWSSS
			DEKRGS\TRSDHN/TPSTQHGRSLLPGKESRAGTPFLGTSK
5375	2907	1116	HIFLAEEEPMLERRCRGPLAMGPAQPRLLSGPSQESPQTLGKES
}			RGLRQQGTSVA\QSGAQAPGRAHRCAHCRRHFPGWVA\LWLHTR
			RCQA/RGLPLPCPECGRRFRHAPFLALHRQVHAAATPDWGFACH
	1		LCGQSFRGWVALVLHLRAHSAAKAGPFACPKMARDAFWRRKAAS
	]		SSILRRCHPSRPRGPRFFICGNCGRSILFTWDQ/LKVAHKRVHV SRRP*ERGPPAKVFWGPRPRGPPTGDTPPGPGGDAVDRPF\OCA
1			CCGKRFRHK\PNLIRSHAACISGERPHQ/CSRECG\KRFTNKPY
1			LTS\HRRITHTARQPYPCKECGRRFRHKPNLLSHSKIHKRSEGS
			AQAAPGPGSPQLPAGPQESAAEPTPAVPLKPAQEPPPGAPPEHP
	ł		QDPIEAPPSLYSCDDCGRSFRLERFLRAHQRQHTGERPFTCAEC
]			GKNFGKKTHLVAHSRVHSGERPFRLARKCGRRFLPRASOSGGRN
			SAEPNAPRFGPFVCPDCGKAFRHKPYLAAHRPIATPAEKPYVCP
1			DCRKAFSQKSNL\VSHRRIHTGERPYACPDCDRSFSQKSNLITH
			RKSHIRDGAFCCAICGQTFDDEERLLAHQKKHDV
5376	4504	591	VSTFSLCLWPAGGGGRGRVSNMAQSKRHVYSRTPSGSRMSAEAS
}			ARPLRVGSRVEV1GKGHRGTVAYVGATLFATGKWVGVILDEAKG
}			KNDGTVQGRKYFTCDEGHGIFVRQSQIQVFEDGADTTSPETPDS
1			SASKVLKREGTDTTAKTSKLRGLKPKKAPTARKTTTRRPKPTRP
1			ASTGVAGASSSLGPSGSASAGELSSSEPSTPAQTPLAAPIIPTP VLTSPGAVPPLPSPSKEEEGLRAQVRDLEEKLETLRLKRAEDKA
1.	·		KLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLKEARKEAKEAL
}			EAKERYMEEMADTADAIEMATLDKEMAEERAESLQQEVEALKER
			VDELTTDLEILKAEIEBKGSDGAASSYQLKQLEEQNARLKDALV
			RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ
			AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEEKVRELRETVG
1			DLEAMNEMNDELQENARETELELREQLDMAGARVREAQKRVEAA
			QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP
			ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD
	ł		SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE
1			RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT
}			KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG
'			RLRAFLQGGQBATDIALLLRDLETSCS\DIRQFCKKIRRRMPGT
[			DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLOEVAAAAAOLI
			APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL
			ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA
	i		EGLGLKLEDRETVIKELKKSLKIKGEELSEANVRLTLLEKKLDS
			AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL
	1	•	eaekaelkorlnsoskrtieglrgpppsgiatlvsgiageeoor
}	j		GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL
1	İ	ļ	KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET
	ĺ	l	LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL
ı l	Į.	ļ	kdevlketvsqrpgatvptdfatfpssaflrakeeqqddtvymg
			KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS
5377	762	1106	DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES*
5377	762	1106	DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK
			DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTX SS*WPGYDGWWGGQYIFIFRGMRWEEQP
5377	762	1106	DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK

Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most   Most	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Docation   Corresponding		1	ì	
Cortesponding to first amin acid residue of serious of amino acid residue of amino acid amino acid sequence   S-Berine, Quellutamine, R-Arginine, S-Berine amino acid amino acid sequence   S-Berine, T-Threonine, V-Publane, S-Berine, Codon, '-possible nucleotide deletion, '-possible nucleotide deletion, '-possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nucleotide deletion,' -possible nu				
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to first amino acid residue of amino acid sequence  sequence  #Tryptophan, Y=Trycosine, K=Duknown, *=Stop codon, y=possible nucleotide deletion,	1	5		
amino acid residue of amino acid sequence whether the sequence with the sequence sequence with the sequence code, /=possible nucleotide deletion, /=possible nucleotide sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequen			to first	
residue of amino acid sequence codon, y-possible nucleotide deletion (	1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
residue of amino acid sequence   w-Tryptophan, x-Tyxosine, x-Unknown, *-stop code, sequence   coden, y-possible nucleotide deletion,   coden, y-possible nucleotide deletion,   coden, y-possible nucleotide deletion,   coden, y-possible nucleotide deletion,   coden, y-possible nucleotide insertion,   coden, y-possible nucleotide insertion,   coden, y-possible nucleotide insertion,   coden, y-possible nucleotide insertion,   coden, y-possible nucleotide insertion,   coden, y-possible nucleotide insertion,   coden, y-possible nucleotide inserticide,   coden, y-possible nucleotide,   coden, y-possible nucleotide,   coden, y-possible nucleotide,   coden, y-possible nucleotide,   coden, y-possible nucleotide,   coden, y-possible nucleotide,   coden, y-possible nucleotide,   coden, y-possible nucleotide,   coden, y-possible nucleotide,   coden, y-possible nucleotide,   coden, y-possible nucleotide,   coden, y-possible nucleotide,   coden, y-possible nucleotide,   coden, y-possible nucleotide,   coden, y-possible nucleotide,   coden, y-possible nucleotide,   coden, y-possible nucleotide,   coden, y-possible nucleotide,   coden, y-possible nucleotide,   coden, y-possible nucleotide,   coden, y-possible nucleotide,   coden, y-possible nucleotide,   coden, y-possible nucleotide,   coden, y-possible nucleotide,   coden, y-possible nucleotide,   coden, y-possible nucleotide,   coden, y-possible nucleotide,   coden, y-possible nucleotide,   coden, y-possible nucleotide,   coden, y-possible nucleotide,   coden, y-possible nucleotide,   coden, y-possible nucleotide,   coden, y-possible nucleotide,   coden, y-possible nucleotide,   coden, y-possible nucleotide,   coden, y-possible,   coden, y-possible,   coden, y-possible,   coden, y-possible,   coden, y-possible,   coden, y-possible,   coden, y-possible,   coden, y-possible,   coden, y-possible,   coden, y-possible,   coden, y-possible,   coden, y-possible,   coden, y-possible,   coden, y-possible,   coden, y-possible,   coden, y-possible,   coden, y-possible,   coden, y-poss	1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
amino acid sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence S	ł	residue of	amino acid	
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SFERRISGQTSGUVFITANMETVGTFRRAKULKSSVOPSGUVFUKHUS VPOMGCVELTYLKEWIGHLISVLEASITUARKSSIPTENDE KHYSLVØNGFAGONPDCLEHLAASSGTGSDFEGLEGILENT (VKYSLVØNGFAGONPDCLEHLAASSGTGSDFEGLEGILENT) (VKYSLDVØNGFAGONPDCLEHLAASSGTGSDFEGLEGILENT) (VKYSLDVØNGFAGONPDCLEHLAASSGTGSDFEGLEGILENT) (VKYSLDVØNGFAGONPDCLEHLAASSGTGSDFEGLEGILENT) (VKYSLDVØNGFAGONPDCLEHLAASSGTGSDFEGLEGILENT) (VKYSLDVØNGFAGONPDCHENTAASADPKNIGAMGHESEGG ELIERDGKKYKLFYGMS'* I VAM KKYAGGGVAFKRASEGKYVDFPFFAGONPOTHTENDEGILENTETTFRYTOQ VMPIFSEAC  5379  5379  664  OASGTTERPLPDLPQLKERREATSRNRALKFRGRIVLMYSCLPAL RFLATPRICAMHIDNOVKLOFKONLEP KRESTLERSESVOLTT SFERRISKONTSGUVFTENDAKULKGRSENOUTH SFERRISKONTSGUVFTENDAKULKGRSENOUTH SFERRISKONTSGUVFTENDAKULKGRSENOUTH KRESTLERSESVOLTH (VKYSLOWGEFAGONPOTCHEHLAASSGTGSSDFEGULEATI OVXYICLDVANGYSEHPVEVKOVKRFPGHTIMAGNVTTGEM EELILISGADII KUGIGGSVCTTRKKTOVYPOLGAULKAINSKONTSGUVFTENDAKULKGAN EELILISGADII KUGIGGSVCTTRKKTOVYPOLGAULKAINSKONTSGUVFTENDAKULKGAN EELILISGADII KUGIGGSVCTTRKKTOVYPOLGAULKAINSKONTSGUVFTENDAKULKGAN EELILISGADII KUGIGGSVCTTRKKTOVAYPOLGAULKAINSKONTSGUVFTENDAKULKGAN EELILISGADII KUGIGGSVCTTRKKTOVAYPOLGAULKAINSKONTSGUVFTENDAKULKAINSKONTSGUVFTENDAKULKAINSKONTSGUVFTENDAKULKAINSKONTSGUVFTENDAKULKAINSKONTSGUVFTENDAKULKAINSKONTSGUVFTENDAKULKAINSKONTSGUVFTENDAKULKAINSKONTSGUVFTENDAKULKAINSKONTSGUVFTENDAKULKAINSKONTSGUVFTENDAKULKAINSKONTSGUVFTENDAKULKAINSKONTSGUVFTENDAKULKAINSKONTSGUVFTENDAKULKAINSKONTSGUVFTENDAKULKAINSKONTSKONTSGUVFTENDAKULKAINSKONTSKONTSGUVFTENDAKULKAINSKONTSKONTSGUVFTENDAKULKAINSKONTSKONTSGUVFTENDAKULKAINSKONTSKONTSKONTSGUVFTENDAKULKAINSKONTSKONTSKONTSGUVFTENDAKULKAINSKONTSKONTSKONTSGUVFTENDAKULKAINSKONTSKONTSGUVFTENDAKULKAINSKONTSKONTSKONTSKONTSGUVFTENDAKULKAINSKONTSKONTSKONTSGUVFTENDAKULKAINSKONTSKONTSKONTSGUVFTENDAKULKAINSKONTSKONTSKONTSGUVFTENDAKULKAINSKONTSKONTSKONTSGUVFTENDAKULKAINSKONTSKONTSKONTSKONTSKONTSKONTSKONTSKON	)		bequence	1.
VPOMOCVPLITKLIFILMENDILISVLIPASILVARKESIPTAVII KHYSUVMQGEPAGONPOLDBIHLANSGOTGSSDEPGULERIT OVKYICLDVANGYSEHFVERVEKDYRKEPFORTINAGENVITEME BELLISGADII KWGIGGSGUCTTRKKTIOVAYORJAMSCADAN HGLKGHIISDGGCSCPGDVAKAFGAGAPFYMLGGMALAGHISBGGG ELIERDGKKYKLIFYGMSS 1 LAM KKYAGGVAFRAGAPAMSCADAN HGLKGHIISDGGCSCPGDVAKAFGAGAPFYMLGGMALAGHISBGGG ELIERDGKKYKLIFYGMSS 1 LAM KKYAGGVAFRAGEKUTEW PFRGDVEHTIRDILGGIRSTCTYVGARALKELSRRTFFIRVTQQ VMPIFSEAC  OASGTTLEPIPDIDEQLKRERBATSENNALKFRGRIVMITSGCLABL FITATFRISAMHIDNOVLOJFROVLLEPRESTLEKKRSEVDLTR SFSFRNSKGYTSGVPIIANNDTVOTFEMAKULCKS 1 VPOSFMD VPOMGCVPLITKLITLMEMILLISVLALPASILVAKERSEVDLTR SFSFRNSKGYTSGVPIIANNDTVOTFEMAKULCKS 1 VPOSFMD VPOMGCVPLITKLITLMEMILLISVLALPASILVAKERSEVDLTR SFSFRNSKGYTSGVPIIANDTVOTFEMAKULCKS 1 VPOSFMD VPOMGCVPLITKLITLMEMILLISVLALPASILVAKERSEVDLTR SFSFRNSKGYTSGVPIIANDTVOTFEMAKULCKS 1 VPOSFMD VPOMGCVPLITKLITLGGIRSTCTTVKKRTGVVYPQLSAVMECADAA HGLKGHIISDGGCSCPODVARAFGAADFWINGGHUREBSGG ELIERDGKKKLFVGMSS 1 LAM (KKYAGGVAFVASSEKTYEW PREDVEHTIRDILGGIRSTCTTVAKARFPOHTMERSENG ELIERDGKKKLFVGMSS 1 LAM (KKYAGGVAFVASSEKTYEW PREDVEHTIRDILGGIRSTCTTVAKARFPOHTMERSENG ELIERDGKKKLFVGMSS 1 LAM (KKYAGGVAFVASSEKTYEW PREDVEHTIRDILGGIRSTCTTVAKARFPOHTMERSENG ELIERDGKKKLFVGMSS 1 LAM (KKYAGGVAFVASSEKTYEW PREDVEHTIRDILGGIRSTCTTVAKARFPOHTMERSENG ELIERDGKKKLFVGMSS 1 LAM (KKYAGGVAFVASSEKTYEW PREDVEHTHRALDGIRSTCTTVANGENGALDENGENG ESPENSHAAR PQDELGGRGSSSSSESQKPCEALBGSSISSISTHLGMS SFJENTTSRGRALDVALLANDRAGENGT CSFPYSPVSSPOSS ROSSNARAR PQDELGGRGSSSSSESQKPCEALBGAGSAPHL SGRKLISJGRSGGGLAGGGSJAM (KINTELL) DONBOHLYMW PREDVETTARREDT INTRODUCCULGRYTHLDSINGSSAPHL SGRKLISJGRSGGGANGENGSVOVKLAS VARBENTYTAMKULSKKLALDGAAF PREPPFRGRRAPAGGCLOP REPREDVENSHAAR PREPPFRGRRAPAGGGASSAPHL CHAPSILSSTRKTSGGALDVARMVTLICTVFOY CPPRODERH CHAPSILSSTRKTSGGALDVARMVTLICTVFOY CPPRODERH CHAPSILSSTRKTSGGALDVARMVTLICTVFOY CPPRODERH CHAPSILSSTRKTSGGALDVARMVTLICTVFOY CPPRODERH CHAPSILSSTRKTSGGALDVARMVTLICTVFOY CPPRODERH CHAPSILSSTRKTSGGALDVARMVTLICTURGCAPPHOPERS PEPPRTDBALLCPPETORTCCAPPLLQVARHVORTE SPENDAR PREPPRTGBGCRAGAPSPTPODLISTGGAPAPGGCOL SPENDAR P		Sequence		
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BELLISGADIIKVOIGFGSVCTTKKKITOVOYPOLSAMMSCADA   HGLKSHIISBGGSCPODVAKAFGADPFVNIGHALGIGESGG   ELIERBGKKYKLFYGMSS 11 AM/KKYAGGGYAFYRASBGKYPKY   PFKGVDVEHTTRUILGGIRSTCTYVGAAKLKEISRRTFTFNTVOO    VNPIFSBAC     OASGTTLRPIPDLPQLKREEATSENRALKFRGKTLVLMTSCLPAL   RFIATPRISAMHIDNDVILDFKOVLLEPRESTLKERSEVDLTK   SPSFRNSKQTYSGVPIIAANDUTOFTENAKULCEN VOGFNO   VPOMSCVFLIYKLFTLKNEMMLLISVLLPASILVAEKFSLFTAVH    KIYSIVVMQEFRGONPOLEBILAASGTGSSDFGULBATI   OVEXTCLUVANGYSEHFVEVKDVKRFPCHTIMAGNVTTGWF   ELILISGADIIKVGGFGSVCTTRKKTOVYPOLSAMMSCADA   HGLKGHIISDGCSCFGDVAKAFGAGADFVMLGGMLAGGISSGG   GLERDGKKYKLFYGMSS 11 AM, KKYAGGVAEFWASHACADA   HGLKGHIISDGCSCFGDVAKAFGAGADFVMLGGMLAGGISSGG   GLERDGKKYKLFYGMSS 11 AM, KKYAGGVAEFWASHACADA   HGLKGHIISDGCSCFGDVAKAFGAGADFVMLGGMLAGGISSGG   GLERDGKKYKLFYGMSS 11 AM, KKYAGGVAEFWASHACADA   HGLKGHIISDGCSCFGDVAKAFGAGADFVMLGGMLAGGISSGG   GLERDGKKYKLFYGMSS 11 AM, KKYAGGVAEFWASHACADA   HGLKGHIISDGCSCFGSSSSSSGKGFCASKJSSISHHGMS   SPSTOVTECTEPCCAVDIGLAARDFLEADGGVPLDTGGSGARPHL   GSGKLSLQERSGGGASSSSSGKPCALSKGSSISHHGMS   SPIVTTECTEPCCAVDIGLAARDFLEADGGVPLDTGGSGARPHL   GSGKLSLQERSGGGASSSSSGKPCALSKGSSISHHGMS   SPIVTTECTEPCCAVDIGLAARDFLEADGGVPLDTGGSGARPHL   KRANDNTYAMKUSKKLIKQAAPFYPODIK KGTEVHYOKTI   HRDIKPSHLVSTITMDGCVQLMQYTLKDSIGKASYGVVKL   AND KRANDNTYAMKUSKKLIKQAAPFYPODIK KGTEVHYOKTI   HRDIKPSHLLVGBOHIKTADFGVSNEFKGSDALLSHTVGKTI   HRDIKPSKLSTKRIFSGKALDVMAMVTLYCFFGC-PMOBERIM   CLHSKIKSGALEFPDQPDIABDLKOLTTRHLDKNPESRIVVPI   KLHPWYTRIGABPLPSENDRTTLYSUTTERVSTOKYTLIPSTGNAAPHI   CLHSKIKSGALEFPDGPDIABDLKOLTTRHLDKNPESRIVVPI   KLHPWYTRIGABPLPSENDRTTLYSUTTERVSTOKYTLIPSTGNAAPHI   CLHSKIKSGALEFPDGPDIABDLKOLTTRHLDKNPESRIVVPI   KLHPWYTRIGABPLGGGGSSSSSSGKOCAGLAGGSLSINGTGG   SPERNAAPODEGGGGGSSSSSSGKOKCAGLAGGSLSINGTGG   SPERNAAPODEGGGGGGSSSSSSGKOKCAGLAGGSLSINGTGG   SPERNAAPODEGGGGGSSSSSSSCKOCAGLAGGSLSINGTGGG   SPERNAAPODEGGGGGGSSSSSSSCKOCAGLAGGSLSINGTGGGG   SPERNAAPODEGGGGGGSSSSSSSCKOCAGGAGGGGGFGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1		ļ	KHYSLVQWQEFAGQNPDCLEHLAASSGTGSSDFEQLEQILEAIP
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HIGHERITISPOGGSCPODVAKAPGAGADPVHLGOMLAGHISSIGG ELLEROGKKYKLEVEMSS*1*1,4M KKTAGGVATSPOKTYSV PFKGDVERTIRDILGGIRSTCTYVGAAKLKELSRRTTFIRVTQQ VNDIPSEAC  5379  664  QASGTTLEPIDDLDGIGKRERATSRIRRALKPEGRIVJMFSCLPAL EPIATPRISAMPHIDNOVALD KOVLLER KERKSESVDLTER SFSRRSKQTYSGVDITAANMDTVGTEBVAKVLCKS*VEGSFUD VPGMGCVELIVKLFTLKNRHLLLSVLLPASIKKRSEVDLTER SFSRRSKQTYSGVDITAANMDTVGTEBVAKVLCKS*VEGSFUD VPGMGCVELIVKLFTLKNRHLLLSVLLPASIKKRSEVDLTER KHISLUGGGRFAGORPDCLEHLLASSGTGSDFFGUEDILEATI QVKYIGLDVANVSSHPVERVEDVREKPPQMTMANVYTCEMV KHISLUGGGSCPGDVAKAFGAGADPVMGMANVTGEMV EELLIGGADIKKYKLEYGMS*1\AM KKKAGGVASYMASGKKYVEV PERGOVERITIRDLIGGIRSTCTYVGAAKLAKGGMASYMASGKKYVEV PERGOVERITIRDLIGGIRSTCTYVGAAKLAKGGKASYMASGKKYVEV PERGOVERITIRDLIGGIRSTCTYVGAAKLAKGLASISLSILHIGMS SFIVYTECEPGCAVDLIGLANDPLEAGGGCPVADISANDPLISAGGGVAV VNDISSEAC  5380  2050  PSERNGGARERGRAAARSGGSAAGMECPSVLDEAGACTNSSCVY KAA KORNATYYAMKULSKKKLERGAAPSPROTRAAPGSGAPSIS RLDERPVTUSHKRUSTTOMOLOVILAVUTLAGEIGKGSYGVVKAA XNSDNDTYYAMKULSKKKLERGAAPSPROTRAAPGSGAPSIS RLDERPVTUSHKRUSTOMOLOVILAVUTLAGEIGKGSYGVVKAA XNSDNDTYYAMKULSKKKLERGAAPSPROTRAAPGSBABH RLDERSPUTSHANDSTAALLSKLERDPSTANDPROTRAAPGSTEAGA XNSDNDTYYAMKULSKKKLERGAAPSPROTRAAPGSTEAGA RGGFI\BQVQGETAA\LLKKLERGAAPSPROTRAAPGSTEAM RGANLSKLERGERGAAARSGGCAARGCLANVACHALADDPHODHOLHAW P\DLVRAARGHFPODTAARDVALUTVALVEPTACPTACHT H\DLKRAMLLAGEBGHILADDRAVVALUTVALVEPTACHT H\DLKRAMLLAGEBGHILADDRAVVALUTVALVETACHT H\DLKRAMLLAGEBGHILADDRAVVALUTVALVETAGLERGSTGVAL XNSDNDTYYAMKULSKKALERGAAPSPROTRAAPGSTAMV KLHPWYTRHGAASPLDSEDGRCCHARGASTALVATTERVANSVENITYATSKLI H\DLKRAMLAGEBGHILADDRAVVALUTVALVETTACHTSTALL KLHPWYTRHGAASPLDSEDGRCCHARGASTALVATTERVANSVENITYATSKLI LLVXYMIRKSSFORPERGSREERSLSAAPGHLAVIHAVGTLERGSTGVAVKLA YEBPRTDERGACRYTTARTSTAND POLVGARGSHFPODTAARDKALTAUTVALTVALVETAGAT TARBOTATAARAVATAGATASTCVA SQPSSRDAAPGDELGGGGSSSSEGKPCEALRGLSSLSTATHLGME STIVVTECEPGCAVDLGLARGRCCHTERGRGSTGVALAN YEBPRTDATAGGATATSCTVA THERBERGALDVARAGVATLYCTVARYCTTRABACTTSSTUT PROBABBARGRARAARARSPGGSAARGERENTAARSTGRACHTSCTVAL SGRKSLAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG		1	lt	EELILSGADIIKVGIGPGSVCTTRKKTGVGYPOLSAVMECADAA
ELIEROKKYKLEYUMSS*1\AM\KKYAGOVAEYRASEKKIVEY PFKGOVERTITEDILGGIRSTCTYVGAAKUKELSRTTPIRVIQO VNPIFSEAC  5379  664  OASGTTLEPIJDLOLGKRERTSRIRELERGEVIMMSGUPLI RFYATTERLSAMPHIDDUVKLDYKOVLLERGESTLKKRESVDUTR SFSRNSKQTYSGVPILANMDTVUTFEMAKVLCKS*VPGSFMD VROMSCYFLIYKLEFILANMDTVUTFEMAKVLCKS*VPGSFMD VROMSCYFLIYKLEFILANMDTVUTFEMAKVLCKS*VPGSFMD VROMSCYFLIYKLEFILANMDTVUTFEMAKVLCKS*VPGSFMD VROMSCYFLIYKLEFILANMDTVUTFEMAKVLCKS*VPGSFMD VROMSCYFLIYKLEFILANMDTVUTFEMAKVLCKS*VPGSFMD VROMSCYFLIKANMUTSKEVERTORGENTYMAKKARESHETENTOR OVRYICLDVANGYSSHVEEVERVAGAKARESHETENTOR REGILIEROKKYKLFYGMSS*I'\AM\KKYAGGVAEYRASEKTVEV PFKGOVERHITANTVOAKUKALSKRRTFIRKTOR VRPISSEAC  2050  PSERGGERGRARAARSPGGSAAGMECPSVLDEAGACTMSSCVS SOPSSNRAAPQDELGGRGSSSSESQKPCERGKISLSHIHIGME SFIVVTECEPGCAVDLGLARDSPLEADGGGPVLDTGGSGAPHL SGRKLSLGERSGGGLAMMGRCICPSLPYSVSSPOSPS RLPRRPTVESHAVSTTMMQDCVJLOVTLKGEIGKGSSGVVKLA VANNINTYTAMKVLSKKLIRQAAFPERPPRRTRAPGGGIQ RGGFLAVORGEVALLANDERGHIKANGLANGVLANGVLIKANSVVKLIR VROMSTYTYAMKVLSKKLIRQAAFPERPPRRTRAPGGGIQ RGGFLAVORGEVALLANDERGHIKANGVLIKGTSVGVVKLA PRAPSISSETRKIFSGRALDWANGVTLVCFVGG*CPFMDERIM CHASKIKGALBEFOODT ALEDDALTVTLVCFVGG*CPFMDERIM CHASKIKGALBEFOODT ALEDDALTVTLVCFVGG*CPFMDERIM CHASKIKGALBEFOODT ALEDDALTVTLVCFVGG*CPFMDERIM CHASKIKGALBEFOODT ALEDDALTVTLVCFVGG*CPFMDERIM CHASKIKGALBEFOODT ALEDDALTVTLVCFVGG*CPFMDERIM CHASKIKGALBEFOODT ALEDDALTVTLVCFVGG*CPFMDERIM CHASKIKGALBEFOODT ALEDDALTVTLVCFVGG*CPFMDERIM CHASKIKGALBEFOODT ALEDDALTVTLVCFVGG*CPFMDERIM CHASKIKGALBEFOODT ALEDDALTVTLVCFVGG*CPFMDERIM CHASKIKGALBEFOODT ALEDDALTVTLVCFVGG*CPFMDERIM CHASKIKGALBARASFGGGSAAGMECPSVLUKERGENGSVGVKLA SELKT*KISPLPACKVT*EFFBFBSGGRESSLSAGONCEPFLHTISGORPHI SGRKLSLGBRSGGGGAAGGSLDMKGRCTCPELPYSEVSSPOSP REPRETALARGSFOODTONOTYLKGEFFETSGAGGGVARA SPENDATYVAMKVLSKKKLIRGAAFPERPPERBERGG SFIVATCEPEGCANDLGLARRIPKTANGCONONOTYLKGEPFLATSGAG SGRUSLIGERGGIAAGGSLDMKGRCTCPELPYSEVSSPOSP REPRETALBRICGERGHIKANDUKLITATVTCPV REMDANTYVAMKVLSKKKLIRGAAFPERSTEND CHASKONGARHFYRTRAFFTSFBFHTGSSL SELKT*KISPLEACKVT*EFFOODT ALEDALTVTCTV REMDANTYVAMKVLSKKKLIRGEGANSFTANTSGAGSLIAFTKSSL SGRKLS	ĺ	1	ĺ	
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RFIATPRISAMPHIUDDUKLDPKOVLLRPKRSTLKSBGSVDLFR SPSPRNSKQTYSGVPIIAANMDTVGTFEMAKVLKS-VPOSFMD VPOMSCVPILYKLFTIKHTMILLSVILJPASILVAEKFSLFTRAYH KHYSLVOWQEFAGQNPDCLERLAASSGTGSDFEQLEGILEAIP OVKYICLDVANGVSEHFVEVKDVKRFPOMTIMAGNVYTGENV EELLISGADIIKVGIGPGSVCTTRKKTGVGYPQLSAVMECDDAA HGUKGHIISDGGSCGFGDVAKATGGAGDFYMLGGMLAGHESSGG ELERGKKYKLFYGMSS-Y-LAM(KKYAGGVABYRASGKTVSV PPKGDVEHITTDLIGGIRSTTTVVGAARLSERTFIRVTQ VNPITSEAC  5380 2 2050 PSRAGGAERGRAAARSPGGSAAGWECPSVLDEAGACTMSSCVS SQPSSNRAAPQDELGGRGSSSSESGKPCEAIRGLSSLSHLIGHE SGRKLSLQERSOGGLAAGGSLDMNGRCICPSLDYSPVSSPOSSP RLPREPTUSHHVSITGMODVOVLNOYTLKGKSSTGVVKLA VNSHDNTYYANKVLSKKLLEQAAFPREPPROTRFASGGCIOP RGPIVGVOVGENA\UKLERDAAFPREPPROTRFASGGCIOP RGPIVGVOVGENA\UKLERDAAFPREPPROTRFASGGCIOP RGPIVGVOVGENA\UKLERDAAFPREPPROTRFASGGCIOP RGPIVGVOVGENA\UKLERDAAFPREPPROTRFASGGCIOP RGPIVGVOVGENA\UKLERDAAFPREPPROTRFASGGCIOP RGPIVGVOVGENA\UKLERDAAFPREPPROTRFASGGCIOP RGPIVGVOVGENA\UKLERDAAFPREPPROTRFASGGCIOP RGPIVGVOVGENA\UKLERDAAFPREPPROTRFASGGCIOP RGPIVGVOVGENA\UKLERDAAFPREPPROTRFASGGCIOP RGPIVGVOVGENA\UKLERDAAFPREPPROTRFASGGCIOP RGPIVGVOVGENA\UKLERDAAFPREPPROTRFASGGCIOP RGPIVGVOVGENA\UKLERDAAFPREPPROTRFASGGCIOP RGPIVGVOVGENA\UKLERDAAFPREPPROTRFASGGCIOP RGPIVGVOVGENA\UKLERDAAFPREPPROTRFASGGCIOP RGPIVGVOVGENA\UKLERDAAFPREPPROTRFASGGCIOP RGPIVGVOVGENA\UKLERDAAFPREPPROTRFASGGACTMSCVS SELKT*KISFLAPACKVI*BPPHBGGGREPUTPGGGARPHL SERVENTUSEBROGGLAAGGSLANDRGCICPHSPHSTGGRE *EPPRTDEALCPYBTGTCAAPLLQVUMWOTPLPPPLSTSWL PULVARGSFWRSVPILKPLSEQGALAGGSCTMSCVS SPENRARDOPDLAGGGGSSESGKOCPEALRGLSSISTHIGME SPIVYTECEPGCAVDLALADRPLBADGGSVDUDESGGARPH RGPREPTUSEHHVSTTGMODCVQLIOVTLADELGRGSSGVVKLA VNENDTYYAMKVLSKKLLIRQAAFPRRPPPPROTRFAGGCIOP RGPIVGVYQETA\TIKKTLIRAPGVVSREFEGGDALLSNTVGTPA FRAPBSLSETRKIFSGKALDVAAMVTLYCPVFG-CPPDERIM CHASKISGALDVAAMVTLYCPVFG-PSPUSSGSCS SCREENSLASFGGRADAARFSFGGRADAARTHTKRFTBLBLIVGSSLI HRDIKFSHLIVADBAGGGERSGRADAARTHTKRFTBLBLIVGSSLI HRDIKFSHLIVADBAGGARTHTKATSRGDALLTRITCHPSPSTVVPI KHAPVTRHGABPLSBEBCCTIVEVTEBEVENSWALITSSRV  1536 203 GRAGGGGDABAAGGERRAAARRSFGGRANGATKARLPELBEURGS 1DFNSELSHLIVADBAGGARTFTRAASLL				
SFSFRNSKOTYSGVPILANNDITVGTENALVCKS-VPGGFRD VPOMGGVSLIYKLFTLKKNEMLLSVLIPALVARKFSLFTAVH KHYSLOVIGGFRAGONPDCLERLAASSTOSDFOLEGILEAIP OVKYICLDVANGYSEHFVEFVKDVRKRFPGHTIMAGNVVTGENV ERLILSGADI KVGIGPGSVCTTRKKTCVGY PQLSAVMECADAA HGLKGHIISDGCSCFGDVRKAFGAGADFVMLGGMLAGHESGGG ELLERDGRKYKLFYGMS-Y. LAN(KKXGAVAFRASGKTVSV PFKGDVEHTIRDLIGGIRSTCTTVGAAKLKELSRRTTIRVTQ VNPISBAC  5380 2 2050 PSRAGGARGRAAARSPGGSAAGMECPSVLDEAGACTMSSCVS SOPSSNRAPODELGGRGSSSSESGKPCEALRGLSSLSIHLGME SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTIGGGAAPHL SGRKISLORER OGGALAAGGLMORGCI OP DESPOYSSPOSS PLERRPTVESHINGSTITGMQDCVQLIAOYTLKDEIGKGSVGVKLA VNENDNTYYAMKVLSKKLIRQAAFPRPPPERTPAPGGCI OP RGPI LEQVYQEIA\LIKKLDHRWV\KLVEVL\DDPNEDHLHW FELDWIGSPWIEVPTIKFLESDQARFYFQDLIKGIETHYGKII H\PDIKPSHLVSTERGKALDVMAMGVTLYCFVFG-CFFMDERIM CHSSIKSGLALEPPDQPDIADELDKLITTRHLDKNPESRIVVPEI KLHPWTHHGAEPLDSBEDKTLVSVTEERVENSVKHIPSLATV ILVKTMIKRKSFONPFEGSRERSISAPELDIKKKPTRCGSL SELKT-KISPLPACCKVT-SPPHPSGCRPSGWACHTSCPS VEPPRTTDEALLCYSTGRTGAFALLQULWATHICKPPRECSEL SELKT-KISPLPACCKVT-SPPHPSGCRPSGWACHTSCPS VEPPRTTBALLCYSTGRTGAFALLQULWATHICKPPRECSEL SELKT-KISPLPACCKVT-SPPHPSGCRPSGWACHTSCPSV VEPPRTTBALLCYSTGRTGAFALLQULWATHICKPPRECSEL SELKT-KISPLPACCKVT-SPPHPSGCRPSGWACHTSCPSV VEPPRTTBALLCYSTGRTGAFALLQULWATHICKPPRECSEL SELKT-KKISPLPACCKVT-SPPHPSGCRPSGWACHTSCPSV VEPPRTTBALLCYSTGRTGAFALLQULWATHICKPPRECSEL SCHENSLAGERGGAAAGRSFGGSAAGWECPSVLDEAGACTHSSCVS SOPSSNRAAPQDELGGRGSSSSESKOKPCEALRSLSSISHILGME SFIVVTECEPGCAVDLGLARDRPLEADGQSVPLDTSGGARPH SGRKLSLQBERSGGAAGMECPSVLDEAGACTHUSCCVS VEPPRTTBALLCYSTGRTCARALLQULWATHICKPPRECSEL SCHENSLYBRANGVANKYLSKKLURGAPPREPPRSTPAPGGCIQP FRAPSISSETERKFSKALDVANMOVTLYCHGCPVSPVSPQSSP REPRRTPVESHHVSITGMQDCVQLMQVTLKDEIGKSSGARPHE SGRKLSLQBERSGGAAGMECPSVLDEAGACTHUSCCVS VEPPRTTBALLLVARDSGHIKTARDAFTRAPPGGCIQP FRAPSISSETERKFSKALDVANMOVTLYCHGCPMSCPWINDERIM CLHSKIKGQALEFDQDP LADLKDLITRHDKNPSSRIVVPDI KKHWVTRHABPPLSSEDENCTI-VEVTSEEVENNSKHIPSLATV ILVKTMIKRSFSGNFFGSSARRERSLSASPANLTTKRFTENDIATV ILVKTMIKRSFSGNFFGSSARRERSLSASPANLTTKRFTENDIATV ILVKTMIKRSFSGNFFGSSARRERSLSASPANLTTKRFTENDIATV PPPRTTBALLCYS	5379	2009	664	***
VPOMSCVELLYKLETIKMEMLLSVLEPASILVAEKFELTTAVH KHYSLOVQHOEPAGONPOLCHILAASSGTOSPOLGOILEAIP OVEYICLDVANGVSEHFVEFVKDVRKPPGOHTIMAGNUVTGEMV EELLIGGAD I KVGIOPGOVOTTREKTOVDOLGAVMECADAA HOLKGHIISDGGCSCPODVAKAFGAGADFVMLGGMLAGHESGG ELIERGKKYKLEYGMSS*I VAN (KKYAGGVASYRASGKYVEV PPKGDVEHITDLIGGIRSTTTVVGAALKHSJERKTTFIRVTQ VARIFSEAC  2050 PERAGGAERGRAAARSPGGSAAGMECPSVLDEAGACTMSCVS SQPSSNRAAPQDELGGRGSSSSESGKPCEALRGLSSILHILGME STIVVTECEPGCAVDLILAADRPILEADGGVPLDTGSGARPHL SGRKLSLQERSQGGLAAGGSLDMNGRCICESLEYSPVSSPQSSP RLPREPTVESSHVSTTGMQDVOVQLNQYTLAGIGKSSTGVVKLA VNENDNTYYANKVLSKKLLIRQAAPPRPPPROTRPARGGCIOP RGPILGGVYGLA\ILKKLDHPMVYKLVSGRGSSISSDALSHTVGTAA FRAPESLSETRKIFSGKALDVMRMQTILYCFVSG*CPPMDERIM CLHSKIKSQALEPPDQPDIAEDLKDLITRRLDKNPESRIVVPEI KHPWYTRHGAEPLBSRDSREERSLSAPGNLITKRPREGEL SELKT*KISPLPACCKYT*SPPFBGGSREGWPFPHTRSGQR *EEPPRTDEALCPYSTGRTCMAPLLQVMWOTPLPFPLSTSWL PULVGARGSHFOFLINLLLKINSHTM  5381 2 2050 PSRAGGAERGRAAARSFGGSAAGMECPSVLDEAGACTMSCVS SQPSSNRAAPODELGGRGSSSESSKOKPEARRISSLSIFIHIGME STIVVTECEFGGAUDGLAAGASCHMORCICEPSPPOSGAPHL GGKRISLQERSGGGAGAGARSFGGSAAGWECPSVLDEAGACTMSCVS SQPSSNRAAPODELGGRGSSSESSKOKPEARRISSLSIFIHIGME STIVVTECEFGGAUDGLAARDFLEADGGVPPLTGRGGARPWCAA VMENDNTYVAMKVLSKKLLURQAPPRPPDFPAFSPAGGCIOP RGPILGDVYGEIALIKARDAPVKRYDFPFOSGARPHAGACTMSCVS SQPSSNRAAPODELGGRGSSSESSKOKPEARSDAGACTMSCVS SQPSSNRAAPODELGGRGSSSESSKOKPEARSDAGACTMSCVS SQPSSNRAAPODELGGRGSSSESSKOKPEARSDAGACTMSCVS SQPSSNRAAPODELGGRGSSSESSKOKPEARSDAGACTMSCVS SQPSSNRAAPODELGGRGSSSESSKOKPEARSDAGACTMSCVS SQPSSNRAAPODELGGRGSSSESSKOKPEARSDAGACTMSCVS STIVTTECEFGGAUDGLAARDFLEADGGVPLTCHDELGGGSVGVVLLA VMENDNTYVAMKVLKKKLURADAPPREPSTRPAPGGCIOP REPRPTVESHHYSTOMODOVOLONVAVVAVOTPLAPFSGSDAF FARPESLSETRKIFSGKALDVAMMVTLYCPFVG*CFPDEREIM CLHSKIKSQALEPTAVGFTAARTUKAPCTANFTWATHTAAPTSTARFT KKISPLADGCKVT*SFFFFFFTARFTSRCHILDKBPSSRIVVPEI KHPRVTRHGAPPLSBEDERCTLVEVTEEVENSVRHIPSLATV ILVKTMTRKRSFGNPFGGSRERGERSAGARNLTTKRFPTERSSL SSLKT*KISPLPACKCKT*SFFFFFFTARFTSRCHILDKPSFFTARFTSML PPRPTTEBALLTYMBHAARTUKAPTSRCHETUKSPT-PPLSTSWL PPLVGAPGSHFFTARFTGRAGALTHNTKFRWIVTGSSLAH CLHSKIKSGALDVABAGATTARFTBAG		(		RFIATPRLSAMPHIDNDVKLDFKDVLLRPKRSTLKSRSEVDLTR
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KHYSLVOMOEPAGONPOCLEHLAASSTGSSDPEDLEGILEAIP OVEYICLOWANCYSEHPEVEWUNDKEPPOHTMAGNUVYGENW EELLILGGADIIKVGIGGGSUCTTRKKTGVGYPOLGAVMECADAA HGLKGHIISDGGCSCPGDVAKAFGAGADFVMLGGMLAGHSESGG ELLERORKYKLEYGGSS'IAMKKYAGGVAEWASGGKTUEV PPKGOVEHTIADILGGIRSTCTYVGAAKLKELSRRTFTIRVTQQ VMPIPSEAC  \$ 2050 PSEAGGAERGAAAARSPGGSAAGWECPSVLDEAGACTMSSCVS SQPSSNRAAPODELGGRGSSSSESKPCEALRGLSSLSIHLGME SFIVVTECEPGCAVDLGLARDBPLEADGGEVPLDTGGGARPHL SGRKLSLGGERSGGSLAGGSLDMAGGTCSPLTYGGSQAPPHL SGRKLSLGGERSGGSLAGGSLDMAGGTCSPLYBVSSPSSPSSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPS	1			
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HGLKGHIISDGGCCPGDVARAFGADFYMIGGALGAHASESGG ELERRGKYKLFYGNS *I\AM\KXVAGVABYBASEKTVEV PFKGDVEHTIRDILGGIRSTCTYVGAAKLKELSRRTTFIRVTQQ VWPISEAC  \$ 2050 \$ PERAGGABERGRARAARSPGGSAAGWECPSVLDEAGACTMSSCVS \$ \$ SQPSSNRAAPQDELGGRGSSSSESQKPCEALKGLSSLS HLGME \$ \$ FIVTTECEPPCAVDILGARDR PLEAGOVENDTOSGGARPHL \$ \$ SGRKLSLQERSGGGLAAGGSLDAMGRCICPSLPYSPVSSPOSSP REPRPTVESHWSITAMDCVCULOVIKLBISGGKGYGVKLA VMENDNTYYAKKULSKKKLIROAAFPRRPPPPBGTRPAPGGCIQP RGPI\QVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV F\ELWQCPPVMEVPTLKSLBEQARFYFQDLIKGIELHYQKTI H\RDLKPSNLLVGBOHIKIADFGVSNGFKGGBALLSNTVGTPA FMAPESLSETTKIFSGKALDWAMGVUTVFGG*CPFMDERIM CHSKIKSQALBEPDQPDIAEDLKDLITRMLDKNPESTIVVPET KLHPWYTHGABPLPSEDENCTLEVTEVFGG*CPFMDERIM CHSKIKSQALBEPDQPDIAEDLKDLITRMLDKNPESTIVVPET KLHPWYTHGASPLPSEDENCTLEVTEVFGG*CPFMDERIM CHSKIKSQALBEPDQPDIAEDLKDLITRMLDKNPESTIVVPET KLHPWTHGASPLPSEDNCTLEVTEVFGG*CPFMDERIM CHSKIKSQALBEPDQDPDIAEDLKDLITRMLDKNPESTIVVPET KLHPWTHGASPLPSEDNCTLEVTEVFGG*CPFMDERIM CHSKIKSQALBEPDQDPDIAEDLKDLITRMLDKNPESTIVVPET SPEPRTDEALCPYETGRTCMAPLLQVLNWVGTPLPFPLSTSWL PDLVGARGSHFCHINALLRINSHIM  \$ \$ PEPPRTDEALCPYETGRTCMAPLLQVLNWVGTPLPFPLSTSWL PDLVGARGSHFCHINALLRINSHIM \$ \$ \$ SQRKSILGERSGGGAAGGSLDAMGCCPGFVLDFGSGGARPHL \$ \$ SGRKLSLQERSGGGAAAGGSLDAMGCCPGFVLDFGSGARPHL \$ \$ SGRKLSLQERSGGGAAAGGSLDAMGCCPGFVLDFGSGARPHL \$ \$ SGRKLSLQERSGGGAAAGGSLDAMGCCPGFVLDFGSGARPHL \$ \$ SGRKLSLQERSGGGAAAGGSLDAMGCCPGFVLDFGSGARPHL \$ \$ SGRKLSLQERSGGGAAAGGSLDAMGCCPGFVLDFGSGARPHL \$ \$ SGRKLSLQERSGGGAAAGGSLDAMGCCPGFVLDFGSGARPHL \$ \$ SGRKLSLQERSGGGAAAGGSLDAMGCCPGFVLDFGSGARPHL \$ \$ SGRKLSLQERSGGGAAAGGSLDAMGCCPGFVLDFGSGARPHL \$ \$ SGRKLSLQERSGGGAAAGGSLDAMGCCPGFVLDFGSGARPHL \$ \$ SGRKLSLQERSGGGAAAGGSLDAMGCCPGFVLDFGSGARPHL \$ \$ SGRKLSLQERSGGAAAGGSLDAMGCCPGFVLDFGSGARPHL \$ \$ SGRKLSLQERSGGAAAGGSLDAMGCCPGFVLDFGGGARPHL \$ \$ SGRKLSLQERSGGAAAGGSLDAMGCCPGFVLDFGGGGARPHL \$ \$ SGRCSGGAAAGGSLDAMGCCPGFTPFGDFGGCAPP \$ \$ SGRGGGAAGGSLDAMGCCPGFTPFGFTGFCAPP \$ \$ SGRGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1			
BLIERDGKRYKLFYGMSS*I_AM\KRYAGGVAEVRASEGKTVEV PPRODUEHTIRDIJGGTSTCTYVGAAKKBLSRRTTFIRVTQQ VNPIPSEAC  5380  2 2050  PSRAGGAERGRAAARSPGGSAAGWECPSVLDEAGACTMSSCUS SQPSSMRAPQDELGGRGSSSSESQKPCEALRGLSSLSILICME SPIVVTECEPGCAVDLGLAABGPLEADGGEVPLDTSGSQARPHL SGRKLSLGBRSGGGLAAGGSLDMRGCTGPSLYPSBYSSPOSP RLPRRPTVESH+VSITTMQDCVQLMQYTIKDEIGKGSYGVVKLA YNENDNTYYAHKVLSKKLIRQAAFPRPPPRGTRPAPGGCIQP RGPI\EQVYQEIA\ILKKLDHRWV\KLVEUL)DDDNEDHLMW F\ELVNQGFVWEVFTLKPLSEDQARFYFQDLIKGIEVLHYOKII H\RDIKFSNLLVGSBGHIKTADPGSNRFKGSDALLSNTVGFTA FMAPESLSETRKIFSGRALDWMAGVTLYCFVG*CPFMDERIM CLHSKKSQALFFPDQPDIAEDLKDLITMMLXMPSERIVVPEI KLHPWTHRGABPLPSBCDRCTLVEVTEEWSWKHIPSLATV ILVKTMIRKRSFGNPFGGSREERSLSAAGMLCFSVLDERGACTMSSCUS SELKT*KISPLPACCKVT*EPPHFSGCRPSCWDPFFLHTHSQFR *EEPPRTDEALCFYETGRTCWAPLLQVLWWGTPLFFPLSTSWL PDLVGAPGSSHCFLNILLZRINSHILL SGRKLSLQERGGGGGSSSSESGKPCGALRGLSSLSIHLGME SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL SGRKLSLQERGGGGSSSESGKPCGALRGLSSLSIHLGME SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL SGRKLSLQERGGGGSSSESGKPCGALRGLSSLSIHLGME SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL SGRKLSLQERGGGLAAGGSLDMNGCCICPELFYSFVSSPQSSP RLPRRPTVESHHVSITIMODCVCULMQYTLKDEIGKGSYGVVKLA YNENDNTYYAMKVLSKKKLIRQAAFPRRPPFRGTRAPGGCIQP RGFI\EQVYQGIA\ILKKLDHRUVY\KLVEUL\UDDHTSKKVII H\RDIKTGPNLYGGGLARGHIKIADPGVAYKLVEUL\UDDHTSKRIVGTPA FMAPESLSETRKIFSGKALDWMMQVTLYCFYFG*CPFMDERIM CLHSKIKSQALEFFDQPDIAEDLKDLITRHDURFBSRIVVPEI KLHPWYTHGABELLPSEDBDRCTLUFEDVENSVHITHSLATV ILVKTMIRKRSFGMFFEGSRRERSLSAPGMLITKRPTBECSSL SELKT*KISPLPACKUT*EFFBFSBENCHSPAPGRSGVYVCLA VEMDLTYTHGAGSCPLPSEDBDRCTLYEEPEVENSVHITHSLATV ILVKTMIRKRSFGMFFEGSRRERSLSAPGNLITKRPTBECSSL SELKT*KISPLPACKUT*EFFBFSBENCHSPAPGRSGVPOPPEITHTHSDPR *PEPPRTDEALCPYETGRTCWAPLLQVLWWGTPLPFPLSTSWL PDLVGAPGSHFCFNILLLRYNSHTM.  5382  1536 203 GRAGSQQDDFALGGABVGPGRAGRRYKRARLPFRIWLVLGS UPMILLIIVWBAGAAHFYLLTSFSRPHTGPPLPTTCEPRDRGR YWBSPDARRSPDQGRQARRSVLRGFCANSSLAPFYKERFPD DIPMSELSHILVDORGALYCCVYCATTMRXYMITUJGSLLH RGAPYRDPLRI PREHVHNASAHLTFNKFWRYGKLSRHEMKVKL KKYTKFLFVEDPFVRLISAFRSKPELENEEF*OPQOVERHEADAR				
PPRODUETTIRDIGGIRSTCTYVGAAKLKELSRRTTFIRVTQQ VNIPSEAC  5380  2 2050  PSRAGGAERGRAAAARSPGGSAAGWECPSVLDEAGACTMSSCVS SQPSSNRAAPQDELGGRGSSSSESQKPCBALRGLSSLSIHLGME SGIVVTECEPGCAUDLGLARDPLEAGGEVPLDTSGQARPHL SGRKLSLQBRSGGSLAAGGSLDMNGRCICBLYSPVSSPOSSP RLPRPTVESH-WSITUMODCVQLAOQYTLKDEIGKGSYGVVLLA VNENDNTYYAMKVLSKKLIRQAAFPRRPPPRGTRPAPGGCIQP RGPI\EQVYQEIA\LKKLLDHENVV\KLVEVL\DDNNEDHLKMV F\BLNVQGPVWEVPILKPLSEDQAAFYRQDLIKSIEPLHYQKII H\RDIKPSNLLVGBDGHIKIADFGVSNEFKGSDALLSNTVGTPA FYADRSLSETRKIPSGKALDUWAMGPFYRQDLIKSIEPLHYQKII H\RDIKPSNLLVGBDGHIKIADFGVSNEFKGSDALLSNTVGTPA FYADRSLSETRKIPSGKALDUWAMGTLIVEVTG-CPHDERIM CHSKIKSQALEPPDQPDIAEDLKDLITTMSVKHIPSLATV ILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECSSL SELKT*KISPLPACCKVT*5PPHPSGCRPSCWOPPFLHTHSQPR *DEPPRTBEALCPYETGRTCWAPLLQVLWWGTPLPFPFLSTSWL PDLUVGAPGSHFCFLNIALLRYNSHTM  STIVVTECEPGCAVDLGLARDPLEADQGEVPLDTEGSQARPHL SGRKLSLGERSGGSLAAGGSLDMNGCTCPSLYFDSVSPQSSP RLPRRPTVESHHVSITGMQDCVQLMQYTLKDEIGKGSVGVVKLA YNENDNTYYAMKVLSKKKLIRQAAFPRPPPRGRTPAPGGCIQP RGPI\EQVYQEIA\ILKKLDHENVV\KLVEVL\DDPNEDHLYMV P\BLVNQGPVWBVFTLKPLSEQQARFYFQDLIKGISKJNTVGTPA FRAPESLSETRKIFSGKALDWAMGVTLVGFVG*CPPMDERIM CHSKIKSQALEPPDGPIAEDLKGTFSSDALRFVTPEI H\RDIKSPALLVERDGHIKIADFGCRSCWGVPFLITHSQFR FRAPESLSETRKIFSGKALDWAMGVTLVGFVG*CPPMDERIM CHSKIKSQALEPPDGPIAEDLKDITKHPTTMLDKNPPESRIVVPII ILVKTMIRKRSFGNPFEGSRRERSLSAPGNLLTKKPTRECSSL SSLKT*KISPLPACCKVT*EFFHPSERSTWVPLTTSUL PDLVGAPGSHFCTLNTALLLRYNSHTM  STRUTTECEPGCAUDLIALARDSHENTUNGTPLFFFDFDTTSTSWL PROFTSTALTARDAAFFTCHALLTRYSHTML TILVKTMIRKRSFGNPFEGSRRERSLSAPGNLTKKPTRECSSL SSLKT*KISPLPACCKVT*EFFHPSERSTWVPTPA **EPPRTDEALCPTTTRTCAMPLLQVLWWGTPLPFPLSTSWL DPLVGAPGSHFCTLNTALLLRYNSHTML STRUTTECEPGCROPS **PEPRTDEALCPTTTRTCAMPLLQVLWSTPLFFFPDFDRDRR TYMSFRDARRSPDQGRQABRSVLRGFCANSSLAPFYRERFPFD DIPNSELSHLIVDDRRGARYCYVEATARDWWINLYGGSLLAPFNERFPFD DIPNSELSHLIVDDRRGARYCYVEATARDWWINLYGGSLLAPFNERFPFD DIPNSELSHLIVDDRRGARYCYVEATARDWWINLYGGSLLAPFNERFPFD DIPNSELSHLIVDDRRGARYCYVEATARDWYNLYGGSLAPFNERFPFD DIPNSELSHLIVDDRRGARYCYVEATARDWYNUTGSGLLAPFNERFPFD DIPNSELSHLIVDDRRGARYCYVEATARDWYNLYGGSLAPFNERFPFD	1			
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S980 2 2050 PSRAGGAERGRAAARS PGGSAAGWECPSVLDEAGACTMSSCVS SOPSSNRAAPQDELGGROSSSSESQKPCEALRGLSSLSILLGME SFIVVTECEPGCAVDLGLARIPELEAGGQEVPLDITGGSQARPHL SGRKLSLQBRSGGGLAAGGSLDMMGRCICPSLPYSPVSSPQSSP RLPRRPTVESHAVSITGMQDCUNDTILDEIGKGSYGVVKLA YMENDNTYYAMKULSKKKLIRQAAFPRRPPPRGTRAPAGGCIQP RGPI\EQVYQEIA\ILKKLDHPNVVKLVEVL\DDPNEDHLYMV F\ELVNQGPVMEVPTLKPLSBDQARFYFQDLIKGIEYLHYQKII H\RDIKPSNLLVGBDGHIKTADFGVSMEFKGSDALLSNTVGTFA FMAPESLSETRKIFSGKALDWMGVTLVCFVFG*CPFMDERIM CLHSKIKSQALSFPDQPDIABDLKDLITRHIDKNHPSRIVVGFI KLHPWVTRIGAZPLPSEDENCTLVEVTEEPVENSVKHIPSLATV ILVKTMIRKRSFGNPFEGSRREERSJBAPGNLLTKKPTRECSSL SSLKT*KISPLPACCKVT*EPFHSGGRAGGWECPSVLDEAGACTMSSCVS SQPSSNRAAPQDELGGRGSSSSESQKPCEALRGLSSLSIHLGME SFIVVTECEPGCAVDLGLARDRPLEADGGVFLDTSGSQARPHL GGRKLSLQBRSGGGAAGGSLDMMGRCICPSLPSFUSSPQSSP RLPRRPTVESHVSITGMODCVDLNOYTLKDEIGKGSYGVVKLA YMENDNTYAMKUSKKKLIRQAAFPRPPPRGTRPAPGGCIQP RGPI\EQVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV F\ELDNOGSPVMEVPTLKPLSEDGARFYFCDLIKGIEKGSYGVVKLA YMENDNTYAMKUSKKKLIRQAAFPRPPPRGTRPAPGGCIQP RGPI\EQVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV F\ELDNOGSPVMEVPTLKPLSEDGARFYFCDLIKGIEKGSTGVVVKLA H\RDIKPSNLLVGEGGIKKADGSLDLITRHIDKNPSRIVVPEI KLHPWVTRHGAEPLPSPDQPDIABLLISTTVGTPA FMAPESLSETKKISGKALDVWAMGVTLVCFVFG*CPFMDERIM CLHSKIKSQALEFPDQPDPIABLLITTHNDMFSRIVVPEI KLHPWVTRHGAEPLPSEDGENCTLVEVTEEEVENSVKHIPSLATV ILVKTMIRKRSFGMFFGGSRAEGRSKLSRFGLINFERSCNSCLPPFLKTHSQPR **PEPPRTDEALCPVETTGRTCWAPLLQVLMWVGTPLPFPLSTSWL DDLVGAPGSHFCFINIALLEYNTATM** SSLKT*KISPLAFCKCKVT**EPFHSCCRSCKQPPFLKTHSQPR **PEPPRTDEALCPVETTGRTCWAPLLQVLMWVGTPLPFPLSTSWL DDLVGAPGSHFCFINIALLEYNTGFPPPTFGFPDFTFCPPDRDRE ILTADSDVDEFLJKKFTSARSLAFFTKERPFD DTMSELSHLIVONDRAAGATHTTM** GARGGQQDAPALQEAEVRGPERAQPARGMTKARLFRIMLVLGS VYMILLIIVYMDSAGAAHFYLHTTSFSPPTFGPPDTFTCPPDRDRE ILTADSDVDEFLJKHERGERSLAGAPGSNLESKFTCFPPPTFGPDRDRE ILTADSDVDEFLJKHCTGARAFTKARLFRIMLVLGS VYMSPRDARRSPDQGRQGARRSVLKGFCANSSLAFPTKERPFD DINSELSHLIVONDRHAAITCHSPRSKYGKLSRILMKVKL KKYTKFIFURDPFVRLISAFRSKFELLENEEF,**PQVCRARAAANV RQPHQPARLGARGUFRNPQVVCSFAMFIQVLLDDHTJSKLAFPNEH				
SQPSSNRAAPQDELGGRGSSSSESQKPCEALRGLSSLSIHLGME SFIVVTECEPGCAVDLGLARDRPLEADGGVPLDTGGSGARPHL SGRKLSLQERSGGGLAAGGSLDMMGRCI CPSLPYSPVSSPQSSP RLPRRPTVESHAVSITGMQCCVQLNQYTLKDEIGKGSYGVVKLA YMENDNTYYAMKUL KKKLIRQAAFPRRPPPRGTRPAPGGCIQP RGPI\EQVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV F\SLVNQGPVMEVPTLKPLSSDQARFYFQDLIKGIEYLHYQKII H\RDIKTPSNLLVGBGGHIKIADFGVSMEFKGSDALLSNTVGTPA FMAPBSLSETRXIFSGKALDWAMGVTLYCFVFG*CPFMDERIM CHISKIKSQALEPPDQPDIABDLITTMLDKNPSRIVVPEI KLHPWVTRHGAEPLPSEDDENCTLVEVTEEEVENSVKHIPSLATV ILVKTMIRKRSFGMPFEGSRREERSLSAPGNLLTKKPTRECGSL SELKT*K1SPLPACCKVT*EPBTGGCRSCMSPCFLNGHSGYRR *PEPPRTDBALCPYBTGRTCWAPLLQVLWWVGTPLPFPLSTSWL PDLVGAPGSHPFCFLNIALLRYNSHTM SGRKLSLQERSGGRAGAGGREGRAGGEPSVLDEAGACTMSSCVS SGPSSNRAAPQDELGGRGSSSSESGKPCEABRGLSSLSIHLGME SFIVVTECEPGCAVDLGLARDRPLEADGGSVPLDTGSGARPHL SGRKLSLQERSGGGLAAGGSLDMMGRCICPSLPYSPVSSPQSSP RLPRRPTVESHNVSITGMQCVQLNGYTLXDEIGGGSYGVVKLA YMENDNTYYAMKVLSKKKLLRQAAFPRRPPRGTRFAPGGCIQP RGPI\EQVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNSDHLYMV FBLUNGGPVMEVPLLKPLESGDAFFFODLIKGIPLSHYKKI H\RDIKPSNLLVGEDGHIKTADPGVSDAFHYDDLIKGIPLSHYKKI LTVKTMIRKRSFGRPFEGSREESLSAPGNLLTKLPTREGSL SCHKT*KISPLAPGCVBPLFLFLEBGCRPFCODLIKGIPLSHYKKI ILVKTMIRKRSFGRPFFGGSTRESLAPGNLLTKRPTECSSL SCLKT*KISPLAPGCFTINALLEXNISAACHLTKLPTRECSSL SCLKT*KISPLAPGCCVT*EFFPPSGCRPSCWQPPFLTHTHOOPR *PEPPRTDBALCPYETGRTCWAPLLQULWWVTPPLFFFLSTSWL DPLVGAPGSHFCTINALLEXNISAAPHTLKRPTRECSSL SELKT*KISPLAPGCKVT*EFFPPSGCRPSCWQPPFLTHTHOOPR *PEPPRTDBALCPYETGRTCWAPLLQULWWVTPPLFFELSTSWL DPLVGAPGSHFCTINALLEXNISAAPHTLKRPTREMLVLGS SELKT*KISPLAPGCKVT*EFFPPSGRRESSVRG YDWSPRDARRSPDQGRQQARRSVLRGFCANSSLAFPTKREPFD DIVNSELSHLIVUNDRAGAAHFYLHTSFSP PHTGPPLPTPGPDRDRE YEBPSTBALCPYETGRTCWAPLLGVACTNIKRWIVLVGGSLLH RGAPYRDDLRIPRESHLVTHORAGALLFVACTNIKRWIVLVLGSLLH RGAPYRDDLRIPRESHLVTHSSAHVTVLSGSLLH RGAPYRDDLRIPRESHLVTHSFRFYGKLKSRHLMKVKL KKYTKFLFUNDFHALLARDARSAHLTFRKFRRYGKLSRHLMKVKL KKYTKFLFUNDFHALGAGRAFFRYPQVLLDBHTSKLAFPTNEH				1 - 11 - 1 - 1 - 1
SFIVVTECEPGCAVDLGIARDEPLEADGQEVPLDTGGSQARPHL SGRKLSLQERSQGIAAGGSLDMMGCICPSLPYSPVSSPQSSP RIPRRPTVESHAVSITGMQDCVQLNQYTLKDEIGKGSYGVVKIA YMENDNTYYAMKUJSKKKLIRQAFPRRPPRGTRPAFGGCIQP RGPI\DQVQGEIA, LIKKLDHPNVV\KLVEVL\DDPNEDHLMWV F\ELVNQGPVMEVPTLKPLSGDQARFYFQDLIKGIEYLHYQKII H\RDIKFSGLLUGBDGHLKIADFGVSMEFKGSDALLSHTVGFFA FMAPESLSETRKIFSGKALDWMGVTLYCFVPG*CPFMDERIM CLHSKIKSQALEFPDQPDIABDLKDLITRHJDKNPESRIVVEFI KLHPWVTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV ILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECSSL SSLK**KISPLPACCKVT*EPPHPSGCRPSCWQPPFLHTHSQPR *PEPPRTDEALCPYETGRCTGAPLUQVMWUGTPLPFPLSTSWL PDLVGAPGSHPCFLNIALLRYNSHTM  5381 2 2050 PSRAGGAERGRAAAARSPGGSAAGWECPSVLDEAGACTMSSCVS SQPSSMRAPQDELGGGSSSSSESGVPCEALRGLSSLSIHLGME SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTGGSQARPHL SGRKLSLGERGSGLAGGSLDMMGRCICEPLYFEPSSPSSPS RIPRRPTVESHHVSITGMQDCVQLNQYTLKDEIGKGSYGVVKLA YMENDNTYYAMKVLSKKKLIRQAAFPRRPPRGTRRAPGGCIQP RGPI\CQVYQEIA\LIKKLDHPNVV\KLVEVL\DDPNEDHLYMV F\ELVNQGPVMEVPTLKPLEEDGARFYFGDLIKGIEVLHYQKII H\RDIKPSNLLVGEDGHIKTADRGVSMEFKGDALLSSTVUTPA FAPAESLSETKKIFSGKALDWAMGVTLVCFVFG*CPPMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITRHLDKNPESRIVVPEI KLHWVTRHGAEPLPSSEDENCTLVEVTEBEVENSVKHIPSLATV ILVKTMIRKRSFGGRFEGSARERSLSAPGNLIKKPTRECESSL SSLKT*KISPLPACCKVT*EFFFPSGCRPSCWQPPFLHTHSQPR *PEPPTTDEALCPYETGRTCWAPLLQVLMWVGTPLPFPLSTSWL UNITNIKRRSFGGRFEGSGARERSLSAPGNLIKKPTRECESSL SSLKT*KISPLPACCKVT*EFFFPSGCRPSCWQPPFLHTHSQPR *PEPPTTDEALCPYETGRTCWAPLLQVLMWVGTPLPFPLSTSWL PDLVGAPGSHPCFLINALLERNSHTM  5382 1536 203 GRRGSQQDAPALQEAEVRGPERAQPARGRMTARLFRIWLVLGS UNINLITYMORAGAHFYLHTSFSRPHTGPPLDFDCPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMESVRG YDWSPRDARRSPDQGRQARRSVLRGFCANSSLAFPTKREPFD DINNSELSHLVYDDRGAAHFYLHTSFSRPHTGPPLDFTDCPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMESVRG YDWSPRDARRSPDQGRQARRSVLRGFCANSSLAFPTKREPFD DINNSELSHLVDDRHGAITCYVYACCTNMRVMVLVLSGSLLH RGAPYRDPLRIPRESHLHVDRGAPRSKFELENEEF/*PQVRRAHAARV KQPHQDPARLGARGLPRWPQVVSFAWFIQULDDRTSKLAFPNEH	5380	2	2050	PSRAGGAERGRAAAARSPGGSAAGWECPSVLDEAGACTMSSCVS
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CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI  KLHPWVTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV  ILVKTMIRKRSFGNFFEGSRREERSLSAPGNLLTKKPTRECESL  SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR  *PEPPRTDEALCPYETGRTCWAPLLQVLWWVGTPLPFPLSTSWL  PDLVGAPGSHFCFLNIALLRYNSHTM.  5382 1536 203 GARGSQQDAPALQEAEVRGPERAQPARGRMTKARLFRLWLVLGS  VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRE  LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMESVRG  YDWSPRDARRSPDGGRQQAERRSVLRGFCANSSLAFPTKERPFD  DIPNSELSHLIVYDDRHGAIYCYVPKVACTNWKRVMIVLSGSLLH  RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL  KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV  RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTEKLAPFNEH	1	į		· ·
KLHPWVTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV  ILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESL  SELKT*KISPLPACCKVT*EFFHPSGCRPSCWQPPFLHTHSQPR  *PEPPRTDEALCPYETGRTCWAPLLQVLWWVGTPLPFPLSTSWL  PDLVGAPGSHFCFLNIALLRYNSHTM.  5382  1536  203  GARGSQQDAPALQEABVRGPERAQPARGRMTKARLFRLWLVLGS  VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRE  LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG  YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD  DIPNSELSHLIVVDDRHGAIYCYVPKVACTNWKRVMIVLSGSLIH  RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL  KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV  RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTEKLAPFNEH	1 1	}		
ILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESL SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR *PEPPRTDEALCPYETGRTCWAPILQVLWWVGTPLPFPLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM.  5382 1536 203 GARGSQQDAPALQEAEVRGPERAQPARGRMTKARLFRLWLVLGS VFMILLILVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD DIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLSGSLLH RGAPYRDPLRIPREPHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTEKLAPFNEH			İ	
SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR  *PEPPRTDEALCPYETGRTCWAPILQVLWWVGTPLPFPLSTSWL  PDLVGAPGSHFCFLNIALLRYNSHTM.  5382 1536 203 GARGSQQDAPALQEAEVRGPERAQPARGRMTKARLFRLWLVLGS  VFMILLILVYWDSAGAAHFYLHTSPSRPHTGPPLPTPGFDRDRE  LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG  YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD  DIPNSELSHLIVDDRHGAIYCTVPKVACTNWKRVMIVLSGSLLH  RGAPYRDPLR I PREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL  KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV  RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTEKLAPFNEH	1	j		=
*PEPPRTDEALCPYETGRTCWAPLLQVLWWVGTPLPFPLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM.  5382 1536 203 GARGSQQDAPALQEAEVRGPERAQPARGRMTKARLFRLWLVLGS VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGFDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMESSVRG YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD DIPNSELSHLIVVDDRHGAIYCYVPKVACTNWKRVMIVLSGSLLH RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTEKLAPFNEH	] ]	,		
PDLVGAPGSHFCFLNIALLRYNSHTM  5382 1536 203 GARGSQQDAPALQEAEVRGPERAQPARGRMTKARLFRLWLVLGS VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMESVRG YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERFFD DIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLSGSLLH RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTEKLAPFNEH	! 1	1		· · · · · · · · · · · · · · · · · · ·
GARGSQQDAPALQEABVRGPERAQPARGRMTKARLFRLWLVLGS VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMESVRG YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD DIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLSGSLIH RGAPYRDPLRIPRFBHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFBLENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTEKLAPFNEH	1 1	l		1
VFMILLIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD DIPNSELSHLIVVDDRHGAIYCYVPKVACTNWKRVMIVLSGSLLH RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHT3KLAPFNEH				
LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG YDWSPRDARRSPDQGRQQAERRSVLRGFCAMSSLAFPTKERPFD DIPNSELSHLIVDDRHGAIYCTVPKVACTMWKRVMIVLSGSLLH RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHT3KLAPFNEH	5382	1536	203	GARGSQQDAPALQEABVRGPERAQPARGRMTKARLFRLWLVLGS
YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD DIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLSGSLLH RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFBLENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTEKLAPFNEH	[ ]	4		VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRE
YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD DIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLSGSLLH RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFBLENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTEKLAPFNEH	]	J		3
DIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLSGSLLH RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFBLENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTEKLAPFNEH	[	[		
RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFBLENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTEKLAPFNEH		į	ļ	
KKYTKFLFVRDPFVRLISAFRSKFBLENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTEKLAPFNEH		ľ	1	
RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTEKLAPFNEH	ļ j	ł		
	i	1	İ	• = •
WRQVYRLCHPCQIDYDFVGKLETLDEDAAQLLQULQADLAPLP			ļ	
	L			WKQVYKLCHPCQIDYDFVGKLETLDEDAAQLLQLLQVDLAAPLP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalarine, G=Glycine
i	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
<b>!</b>	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion.
ļ	sequence	<u> </u>	\=possible nucleotide insertion)
1			PELPGTGPPSSWEEDWFAKIPLAWRQQLYKLYEADFVLFGYPKP
			ENLLRD
5383	45	5250	VERLLGCRNSKRTWRMLISKNMPWRRLQGISFGMYSAEELKKLS
			VKSITNPRYLDSLGNPSANGLYDLALGPADSKEVCSTCVQDFSN
			CSGHLGHIELPLTVYNPLLFDKLYLLLRGSCLNCHMLTCPRAVI
			HLLLCQLRVLEVGALQAVYELERILSRFLEENADPSASEIREEL
1	i i		EQYTTEIVQNNLLGSQGAHVKNVCESKSKLIALFWKAHMNAKRC
1	]		PHCKTGRSVVRKEHNSKLTITFPAMVHRTAGQKDSEPLGIEEAQ
i			IGKRGYLTPTSAREHLSALWKNEGFFLNYLFSGMDDDGMESRFN
			PSVFFLDFLVVPPSRSRPVSRLGDQMFTNGQTVNLQAVMKDVVL
1	1		IRKLLALMAQEQKLPEEVATPTTDEEKDSLIAIDRSPLSTLPGQ SLIDKLYNIWIRLQSHVNIVFDSEMDKLMMDKYPGIRQILEKKE
i	1		GLFRKHMMGKRVDYAARSVICPDMYINTNBIGIPMVFATKLTYP
1	1		QPVTPWNVQELRQAVINGPNVHPGASMVINEDGSRTALSAVDMT
			QREAVAKQLLTPATGAPKPQGTKIVCRHVKNGDILLLNRQPTLH
			RPSIQAHRARILPEEKVLRLHYANCKAYNADFDGDEMNAHFPQS
[			ELGRAEAYVLACTDQQYLVPKDGQPLAGLIQDHMVSGASMTTRG
(	i i		CFFTREHYMELVYRGLTDKVGRVKLLSPSILKPFPLWTGKQVVS
			TLLINIIPEDHIPLNLSGKAKITGKAWVKETPRSVPGFNPDSMC
1 .			ESQVIIREGELLCGVLDKAHYGSSAYGLVHCCYEIYGGETSGKV
			LTCLARLFTAYLQLYRGFTLGVEDILVKPKADVKRORIIEESTH
1	[		CGPQAVRAALNLPEAASYDEVRGKWQDAHLGKDORDFNMIDLKF
			KEEVNHYSNEINKACMPFGLHROFPENTLOLMVOSGAKGSTVNT
1			MQISCLLGQIELEGRSTPLMASGKSLPCFEPYEFTPRAGGFVTG
			RFLTGIKPPEFFFHCMAGREGLVDTAVKTSRSGYLQRCIIKHLE
] ]		j	GLVVQYDLTVRDSDGSVVQFLYGEDGLDIPKTQFLQPKQFPFLA
1 1	1		SNYEVIMKSOHLHEVLSRADPKKALHHFRAIKKWOSKHPNTLLR
1			RCAPLSYSQKIQEAVKALKLESENRNGR/RPWDS/G/RMLRMWY
1 1	i i		ELDEESRRKYQKKAAACPDPSLSVWRPDIYFASVSETFETKVDD
1 1			YSQEWAAQTEKSYEKSELSLDRLRTLLQL\KWQRSLCEPGEAVG
			LLAAQSIGEPSTQMTLNTFHFAGRGEMNVTLGIPRLREILMVAS ANIKTPMMSVPVLNTKKALKRVKSLKKQLTRVCLGEVLQKIDVQ
1			ESFCMEEKQNKFQVYQLRFQFLPHAYYQQEKCLRPEDILRFMET
] [	` [	Ī	RFFKLLMESIKKKNNKASAFRNVNTRRATQRDLDNAGELGRSRG
1 1	Í		EQEGDEEEGHIVDAEAEEGDADASDAKRKEKQEEEVDYESEEE
1 1			EEREGEENDDEDMQEERNPHREGARKTOEODEEVGL/GH*GGPV
1		i	PSRPPDAAPETHPQPGAPGA\EAMERRVQAVREIHPFIDDYQYD
j ,	1.	ļ	TEESLWCQVTVKLPLMKINFDMSSLVVSLAHGAVIYATKGITRC
J	1	j	LLNETTNNKNEKELVLNTEGINLPELFKYAEVLDLRRLYSNDIH
	1		AIANTYGIEAALRVIEKEIKDVFAVYGIAVDPRHLSLVADYMCF
1 1			EGVYKPLNRFGIRSNSSPLQQMTFETSFQFLKQATMLGSHDBLR
5384	196		SPSACLVVGKVVRGGTGLFELKQPLR
	173	886	QSCGQRLPTVL*L*GPPGSCPCILSLF\PGRPHALPEIRPYINI
	l		TILKGDKGDPGPMGLPGYMGREGPQGEPGPQGSKGDKGEMGSPG
]			APCQKRFFAFSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMAT GQFAAPLRGIYFFSLNVHSWNYKETYVHIMHNQKEAVILYAQPS
1 1			ERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITF
1		1	SGHLIKAEDD
5385	326		LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM
			SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A
1 1		1	VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ
		1	SDGERKAYVRLAPDYDALVVATKIGIT
5386	326	799	LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM
		İ	SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A
! !			VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ
		Į,	SDGERKAYVRLAPDYDALVVATKIGIT
5387	2		FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWATA
	}	<b>]</b> ;	SDDLVFPGFFELVVRVLWWIGILTLYLMHRGKLDCAGGALLSSY
' 1		. [ ]	LIVLMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL
ł	ļ	1.2	ALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVVVSWIIIAA
			TVVSIIIVFDPLGGKMAPYSSAGPSHLDSHDSSQLLNGLKTAAT

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ΙĎ	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
}	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	1	\=possible nucleotide insertion)
	<del> </del>		SVWETRIKLLCCCIGKDDHTRVAFSSTAELFSTYFSDTDLVPSD
ı			IAAGLALLHQQQDNIRNNQEPAQVVCHAPGSSQEADLDAELKNC
1		l	HHYMQFAAAAYGWPLYIYRNPLTGLCRIGGDCCRSKNPQTMT/M
i			VGGDQLQL/CTSAPILHTHRAAVQGLHPRQLPWTRFTELPFLVA
J		)	LDHRKESVVVAVRGTMSLQDVLTDLSAESEVLDVECEVQDRLAH
1			KGISQAARYVYQRLINDGILSQAFSIAPEYRLVIVGHSLGGGAA
ſ			ALLATMVRAAYPQVRCYAFSPPRGLWSKALQEYSQSFIVSLVLG
Į.	ì	i	KDVIPRLSVTNLEDLKRRILRVVAHCNKPKYKILLHGLWYELFG
i			GNPNNLPTELDGGDQEVLTQPLLGEQSLLTRWSPAYSFSSDSPL
1			DSSPKYPPLYPPGRIIHLQEEGASGRFGCCSAAHYSAKWSHEAE
1			FSKILIGPKMLTDHMPDILMRALDSVVSDRAACVSCPAGGVSSV
1	<b>{</b>		DVA
5388	1569	753	TADGGAGGGGRQAGVRRHYLYPFTGGYRRRAACOAERPAARS
1		, 55	KDTDLAAYQKGNLGVQLRNMAQETNHSQVPMLCSTGCGFYGNPR
			TNGNCSVCYKEHLQRQNSSNGRISPPVQCTDGSVPEAQSALDST
1	1		SSSMQPSPVSNQSLLSESVASSQLDSTSVDKAVPETEDVQASVS
	l		DTAQQPSEEQSKSLE\NRNKKRIAVSCAGRKWDLLGLNAGVEMF
ŀ		•	TVVYTVTQMYTIALTITKQMLKNFVFQQEFKSFGSFHQQLLEYK
			ILEHLOTKN
5389	1569	753	TADGGAGGGGRRQAGVRHYLYPFTGGYRRRAACQAERPAARS
1			KDTDLAAYQKGNLGVQLRNMAQETNHSQVPMLCSTGCGFYGNPR
			TNGMCSVCYKBHLQRQNSSNGRISPPVQCTDGSVPEAQSALDST
			SSSMQPSPVSNQSLLSESVASSQLDSTSVDKAVPETEDVQASVS
			DTAQQPSEEQSKSLE\NRNKKRIAVSCAGRKWDLLGLNAGVEMF
			TVVYTVTQMYTIALTITKQMLKNFVFQQEFKSFGSFHQOLLEYK
1			ILEHLQTKN
5390	217	1332	EDPRKLMEDKMWSECEGPEMSLVCLTDFOAHAREOLSKSTRDFI
			EGGADDSITRDDNIAAFKRIRLRPRYLRDVSEVDTRTTIOGEEI
			SAPICIAPTGFHCLVWPDGEMSTARAAQAA\GICYITSTFASCS
i i			LEDIVIAAPEGLRWFQLYVHPDLQLNKQLIQRVESLGFKALVIT
1			LDTPVCGNRRHDIRNQLRRNLTLTDLQSPKKGNAIPYFQMTPIS
			TSLCWNDLSWFQSITRLPIILKGILTKEDAELAVKHNVQGIIVS
1			NHGGRQLDEVLASIDALTEVVAAVKGKIEVYLDGGVRTGNDVLK
1			ALALGAKCIFLGDAILWALASKGEHGVKEVLNILTNEFHTSMA\
			LTGCRSVAEINRNLVQFSRL
5391	1	1292	VKKAAGRSRGPPTAGGQRCEEAPGTVMERRLGVRAWVKENRGSF
			QPPVCNKLMHQEQLKVMFVGGPNTRKDYHIEEGEEVFYQLEGDM
			VLRVLEQGKHRDVVIRQGEIFLLPARVPHSPQRFANTVGLVVER
{			RRLETELDGLRYYVGDTMDVLFEKWFYCKDLGTQLAPIIQEFFS
]	i		SEQYRTGKPIPDQLLKEPPFPLSTRSIMEPMSLDAWLDSHHREI.
1 1		•	QAGTPLSLFGDTYETQVIAYGQGSSEGLRQNVDVWLWQLEGSSV
			VTMGGRRLSLGPWMDSLLVLSWGPSY\AW\ERTQGSVALSVT\Q
]			DPACKKSPWGEPSCHGLKAATGVPSTLEVPSLPNNSPSPHYLSV
1 1			YCRCVPHRPAHCCHPPSCPSQPRCHAPGRAAAPHLLWQTQPTAL
			PVLPGGLPPAPLLPIPLSLQTQCSTSTPRRPSIKAS
5392	l l	1623	IRGSNAQKVVGASGSGGAGPQPDPAGPGGVPALAAAVLGACEPR
1 1		•	CAAPCPLPALSRCRGAGSRGSRGGRGAAGSGDAAAAAEWIRKGS
			FIHKPAHGWLHPDARVLGPGVSYVVRYMGCIEVLRSMRSLDFNT
1			RTQVTREAINRLHEAVPGVRGSWKKKAPNKALASVLGKSNLRFA
j	}		GMSISIHISTDGLSLSVPATRQVIANHHMPSISFASGGDTDMTD
	1		YVAYVAKDPINQRACHILECCEGL\AQSIISTVGQAFELRFKQY
) [	1		LHSPPKVALPPERLAGPEESAWGDEEDSLEHNYYNSIPGKEPPL
	ŀ		GGLVDSRLALTQPCALTALDQGPSPSLRDACSLPWDVGSTGTAP
] ]	ļ		PGDGYVQADARGPPDHEEHLYVNTQGLDAPEPEDSPKKDLFDMR
] [	I	. [	PFEDALKLHECSVAAGVTAAPLPLEDQWPSPPTRRAPVAPTEEQ
[ [	1	ĺ	LRQEPWYHGRMSRRAAERMLRADGDFLVRDSVTNPGQYVLTGMH
j [	į		AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE
			SELHLRGVVSREP
5393	2	982	GGDSAGMTMETQMSQNVCPRNLWLLQPLTVLLLLASADSQAAAP
<u> </u>			PKAVLKLEPPWINVLQ\EDSVTLTCQGAPQP/ERSDSIQWFHNG

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
Į.	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ì	amino acid	sequence	Codon, /=possible nucleotide deletion,
Į	sequence		\=possible nucleotide insertion)
			\NLIPTHTQPS\YRFKANNN\DSGEYTCQTGQTSL\SDPVHLTV
(	1		LSEWLVLQTPHLEFQEGETIMLRCHS\WRDKP\LVKVTFFONGK
1	ì		SQKFSHLDPTFSIPQANHSHSGDYHCTGNIGYTLFSSKPVTITV
1		ļ	QVPSMGSSSPMGIIVAVVIATAVAAIVAAVVALIYCRKKRISAN
1	İ		STDPVKAAQFEPPGRQMIAIRKRQLEETNNDYETADGGYMTLNP
1	!		RAPTDDDKNIYLTLPPNDHVNSNN
5394	2	982	GGDSAGMTMETQMSQNVCPRNLWLLQPLTVLLLLASADSQAAAP
"""	-	""	PKAVLKLEPPWINVLQ\EDSVTLTCQGAPQP/ERSDSIQWFHNG
1	ĺ		\NLIPTHTQPS\YRFKANNN\DSGEYTCOTGOTSL\SDPVHLTV
	ł		LSEWLVLQTPHLEFQEGETIMLRCHS\WRDKP\LVKVTFFQNGK
1			SQKFSHLDPTFSIPQANHSHSGDYHCTGNIGYTLFSSKPVTITV
	İ		
ł	}		QVPSMGSSSPMGIIVAVVIATAVAAIVAAVVALIYCRKKRISAN
1			STDPVKAAQFEPPGRQMIAIRKRQLEETNNDYETADGGYMTLNP RAPTDDDKNIYLTLPPNDHVNSNN
5395	3135		
3333	3235	531	RASDAKNQEGLLNTRRKSTDSVPISKSTLSRSLSLQASDFDGAS
1			SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKQTTK
Ì			KPTETPPVKETQQEPDEESLVPSGENLASETKTESAKTEGPSPA
			LLEETPLEPAAGPKAACPLDSESVEGVVPPASGGGRVQNSPPVG
1			RKTLPLTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS
İ	]		SWDNQQENPPPTKKIGKKPVAKMPLRRPKMKKTPEKLDNTPASP
i			PRSPAEPNDIPIAKGTYTFDIDKWDDPNFNPFSSTSKMQESPKL
ł i			PQQSYNFDPDTCDESVDPFKTSSKTPSSPSKSPASFEIPASAME
Į '			ANGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP
1			TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD
1			YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD
ļ			DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFEETE
			ALVNTAAKNQHPVPRGLAPNQESHLQVPEKSSQKELEAMGLGTP
(			SEATEITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN
}			PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ
			POLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAE
1			YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLNSVEK
	·		\SLADLFRRYEKMKEVLEGFRKNEEVLKRCAQEYLSRVKKEEQR
]			YQALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHQASLAERSS
			CRV\DALERTLEQKNKEIBELTKICDELIAKMGKS
5396	3135	531	RASDAKNQEGLLNTRRKSTDSVPISKSTLSRSLSLQASDFDGAS
1			SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKQTTK
]			KPTETPPVKETQQEPDEESLVPSGENLASETKTESAKTEGPSPA
			LLEETPLEPAAGPKAACPLDSESVEGVVPPASGGGRVQNSPPVG
1.	' I		RKTLPLTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS
1 1			SWDNQQENPPPTKKIGKKPVAKMPLRRPKMKKTPEKLDNTPASP
			PRSPAEPNDIPIAKGTYTFDIDKWDDPNFNPFSSTSKMQESPKL
			PQQSYNFDPDTCDESVDPFKTSSKTPSSPSKSPASFEIPASAME
]. [			ANGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP
			TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD
(	Ì		YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEXMEKIGSSLPQD
1 1			DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFEETE
, ,			ALVNTAAKNQHPVPRGLAFNQESHLQVPEKSSQKELEAMGLGTP
}			SEAIBITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN
! !			PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ
]	ļ		PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAE
			YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLNSVEK
[ [	1		\SLADLFRRYEKMKEVLEGFRKNEEVLKRCAQEYLSRVKKEEQR
			YQALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHQASLAERSS
			CRV\DALERTLEQKNKEIEELTKICDELIAKMGKS
5397	3135	531	RASDAKNQEGLLNTRRKSTDSVPISKSTLSRSLSLQASDFDGAS
J	,		SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKQTTK
{	1		KPTETPPVKETQQEPDEESLVPSGENLASETKTESAKTEGPSPA
	ŀ	İ	LLEETPLEPAAGPKAACPLDSESVEGVVPPASGGGRVQNSPPVG
	ļ		RKTLPLTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS
ļ J	ŀ	Ì	SWDNQQENPPPTKKIGKKPVAKMPLRRPKMKKTPEKLDNTPASP
		ſ	PRSPAEPNDIPIAKGTYTFDIDKWDDPNFNPFSSTSKMQESPKL
		<del></del>	

SEQ	Predicted	Predicted end	Amino acid goment containing
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
10.	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Scrine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
j	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
			PQQSYNFDPDTCDESVDPFKTSSKTPSSPSKSPASFEIPASAME
1	1		ANGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSODP
ľ	!	1	TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKOD
}	}		YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD
1			DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFEETE
1			
1		ľ	ALVNTAAKNOHPVPRGLAPNQESHLQVPEKSSQKELEAMGLGTP
1	1	ĺ	SEAIEITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN
j	J		PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ
	ł		PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAE
			YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLNSVEK
	1		\SLADLFRRYEKMKEVLEGFRKNEEVLKRCAQEYLSRVKKEEQR
1	1	[	YQALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHQASLAERSS
	L		CRV\DALERTLEQKNKEIBELTKICDELIAKMGKS
5398	56	5426	SGEVCRMESNFNQEGVPRPSYVFSADPIARPSEINFDGIKLDLS
1	1		HEFSLVAPNTEANSFESKDYLQVCLRIRPFTQSEKELESEGCVH
	}		ILDSQTVVLKEPQCILGRLSEKSSG\QM\AQKFSFPPGFLGPAT
			TQKEFFQGCIMHP\VKDLLKGQSRLIFTYGLTNSGKTYTFQGTE
	1		ENIRILPRTLNVLFDSLQERLYTKMNLKPHRSRBYLRLSSEOEK
]	1		EEIASKSALLRQIKEVTVHNDSDDTLYGSLTNSLNISEFEESIK
	ţ		DYEQANLNMANSIKFSVWVSFFEIYNEYIYDLFVPVSSKFQKKK
ļ	ł		MLRLSQDVKGYSFIKDLQWIQVSDSKEAYRLLKLGIKHQSVAFT
1	1		KLNNASSRSHSIFTVKILQIEDSEMSRVIRVSELSLCDLAGSER
1			TMKTQNEGERLRETGNINTSLLTLGKCINVLKNSEKSKFQQHVP
}	1		
1	<b>\</b>		FRESKLTHYF/QSFFNGKGKICMIVNISQCYLAYDETLNVLKFS
İ	1		AIAQKVCVPDTLNSSQEKLFGPVKSSQDVSLDSNSNSKILNVKR
1	]		ATISWENSLEDLMEDEDLVEELENAEETED/VGETKLLDEDLDK
1			TLEENKAFISHEEKRKLLDLIEDLKKKLINEKKEKLTLEFKIRE
Í	ľ		EVTQEFTQYWAQREADFKETLLQEREILEENAERRLAIFKDLVG
	1		KCDTREEAAKDICATKVETEEATACLELKFNQIKAELAKTKGEL
	1		IKTKEELKKRENESDSLIQELETSNKKIITQNQRIKELINIIDQ
1	J		KEDTINEFONLKSHMENTFKCNDKADTSSLIINNKLICNETVEV
1			PKDSKSKICSERKRVNENELQQDEPPAKKGSIHVSSAITEDQKK
1			SEEVRPNIAEIEDIRVLQENNEGLRAFLLTIENELKNEKEEKAE
Į j	j		LNKQIVHFQQELSLSEKKNLTLSKEVQQIQSNYDIAIAELHVQK
			SKNQEQEEKIMKLSNEIETATRSITNNVSQIKLMHTKIDELRTL
1	!		DSVSQISNIDLLNLRDLSNGSBEDNLPNTQLDLLGNDYLVSKQV
			KEYRIQBPNRENSFHSSIEAIWEECKEIVKASSKKSHQIEELEO
	ſ		QIEKLQAEVKGYKDENNRLKEKEHKNQDDLLKEKETLIQQLKEE
}			LQEKNVTLDVQIQHVVEGKRALSELTQGVTCYKAKIKELETILE
1 !			TQKVERSHSAKLEQDILEKESIILKLERNLKEFQEHLQDSVKNT
[ [			KDLNVKELKLKEEITQLTNNLQDMKHLLQLKEEEEETNRQETEK
1 1			LKEELSASSARTON\LNADLQRKEEDYADLKEKLTDAKKOIKOV
<b>j</b>			QKEVSVMRDEDKLLRIKINELEKKKNQCSQELDMKQR\TIQQLK
1 1			EQLINQKVEEAIQQYBRACKDLNVKEKIIEDMRMTLEEQEQTQV
, l			EQDQVL\EAKLEEVERLATELDRWRVKCNDLETKNNQRSNKEHE
	•		NNTDVLGKLTNLQDELQESEQKYNADRKKWLEEKMMLITQAKEA
( l			ENIRNKEMKKYAEDRERFFKQQNEMEILTAQLTEKDSDLQKWRE
			ERDQLVAALEIQLKALISSNVQKDNEIEQLKRIISETSKIETOI
	}		MDIKPKRISSADPDKLQTEPLSTSFEISRNKIEDGSVVLDSCEV
1 1	I		
	<b>\</b>		STENDOSTRFPKPELEIQFTPLQPNKMAVKHPGCTTPVTVKIPK
į i	ĺ		ARKRKSNEMEEDLVKCENKKNATPRTNLKFPISDDRNSSVKKEQ
1 }	}	i	KVAIRPSSKKTYSLRSQASIIGVNLATKKKEGTLQKFGDFLQHS
į l	Í		PSILQSKAKKIIETMSSSKLSNVEASKENVSQPKRAKRKLYTSE
1-6365-1		·	ISSPIDISGQVILMDQKMKESDHQIIKRRLRTKTAK
5399	705	230	GPRMAKFLSQDQINEYKECFSLYDKQQRGKIKATDLMVAMRCLG
j (	1		ASPTPGEVQRHLQTHGIDGNGELDFSTFLTIMHMQIKQEDPKKE
1 !	ł		ILLAMLMVDKEKKGYVMASDLRSKLTSLGEKLTHKEV\DDLFRE
<u> </u>			\ADIEPNGKVKYDEFIHKITSYLDGTY
5400	931	248	SHCSSGMEIPPTNYPASRAALVAONYINYQQGTPHRVFEVQKVK
į į	ļ		QASMEDIPGRGHKYRLKFAVEEIIQKQVKVNCTAEVLYPSTGQE
	1	1	TAPEVNFTFEGETGKNPDEEDNTFYQRLKSMKEPLEAQNI\PDN

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	b=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T-Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
İ	sequence		\=possible nucleotide insertion)
	<del></del>		FGNVSPEMTLVLHLAWVACGYIIWQNSTEDTWYKMVKIOTVKOV
l	ļ	}	QRNDDFIELDYTILLHNIASQEIIPWQMQVLWHPQYGTKVKHNS
j	}		RLPKEVQLE
5401	3	1360	TGWSYGPTTSLAFLAPRDFPFPPKLLIHPQAVVRLSCGAGSMGS
1 2.02	1	1500	QAAAEWRNWASWEGSSSLSGCSMGCFKDDRIVFWTWMFSTYFME
ł	1		KWAPRODDMLFYVRRKLAYSGSESGADGRKAAEPEVEVEVYRRD
1	ł		SKKLPGLGDPDIDWEESVCLNLILOKLDYMVTCAVCTRADGGDI
1	į,		HIHKKKSQQVFASPSKHPMDSKGEESKISYPNIFFMIDSF\BE\
	}		VFSDMTVGKGEMVCVELVASDKTNTFQGVIFQGSIRYEALKKVY
	i		DNRVSVAARMAQK\MSFGFSKYSNMEF\VR\MKGPQGKGHAEMA
ļ			VSRVSTGDTSPCGTEEDSSPASPMHERVTSFSTPPTPERNNRPA
ł	ł		FFSPSLKRKVPRNRIAEMKKSHSANDSEEFFREDDGGADLHNAT
ł		}	NLRSRSLSGTGRSLVGSWLKLNRADGNFLLYAHLTYVTLPLHRI
			LTDILEVROKPILMT
5402	3445	1563	<u> </u>
3402	3443	1303	GECFIMAAVVQQNDLVFEFASNVMEDERQLGDPAIFPAVIVEHV PGADILNSYAGLACVEEPNDMITESSLDVAEEEIIDDDDDDITL
1			TVEASCHDGDETIETIEAAEALLNMDSPGPMLDEKRINNNIFSS
	i		
			PEDDMVVAPVTHVSVTLDGIPEVMETQQVQEKYADSPGASSPBQ
		,	PKRKKGRKTKPPRPDSPATTPNISVKKKNKDGKGNTIYLWEFLL
			ALLQDKATCPKYIKWTQREKGIFKLVDSKPVSRLWRKHKNKP\D
			MNYEPMGRALRYYYQRGILAKVEGQRLVYQFKEMPKDLIYINDE
1			DPSSSIESSDPSLSSSATSNRNQTSRSRVSSSPGVKGGATTVLK PGNSKAAKPKDPVEVAQPSEVLRTVQPTQSPYPTQLFRTVHVVQ
1	· .		
i			PVQAVPEGEAARTSTMQDETLNSSVQSIR\TIQAPTQVPVVVSP RNQQ\LHTVTLQTVPLTTVIASTDPSAGTGSQKFILQAIPSSQP
1	[		MTVLKENVMLQSQKAGSPPSIVLGPARV\QQVLTSNVOTICNGT
1			VSV\ASSPSFS\ATAPVVTLFLLGSSQLVAHPPGTVITSVIKTQ
1			
1			ETKTLTQEVEKKESEDHLKENTEKTEQQPQPYVMVVSSSNGFTS QVAMKQNELLEPNSF
5403	3445	1563	GECFIMAAVVQQNDLVFEFASNVMEDERQLGDPAIFPAVIVEHV
3203	2442	1303	PGADILNSYAGLACVEEPNDMITESSLDVAEBEIIDDDDDDITL
			TVEASCHDGDETIETIEAAEALLNMDSPGPMLDEKRINNNIFSS
	1		PEDDMVVAPVTHVSVTLDGIPEVMETQQVQEKYADSPGASSPEO
			PKRKKGRKTKPPRPDSPATTPNISVKKKNKDGKGNTIYLWEFLL
	ł		ALLQDKATCPKYIKWTQREKGIFKLVDSKPVSRLWRKHKNKP\D
1			MNYEPMGRALRYYYORGILAKVEGORLVYOFKEMPKDLIYINDE
			DPSSSIESSDPSLSSSATSNRNOTSRSRVSSSPGVKGGATTVLK
			PGNSKAAKPKDPVEVAQPSEVLRTVQPTQSPYPTQLFRTVHVVQ
	i i		PVQAVPEGEAARTSTMQDETLNSSVQSIR\TIQAPTQVPVVVSP
	' I	•	RNQQ\LHTVTLQTVPLTTVIASTDPSAGTGSQKFILQAIPSSQP
			MTVLKENVMLQSQKAGSPPSIVLGPARV\QQVLTSNVQTICNGT
1 .			VSV\ASSPSFS\ATAPVVTLFLLGSSQLVAHPPGTVITSVIKTQ
			ETKTLTQEVEKKESEDHLKENTEKTEQQPQPYVMVVSSSNGFTS
1			QVAMKQNELLEPNSF
5404	187	1111	LPVTLIFAKMKTLQSTLLLLLLVPLIKPAPPTQQDSRIIYDYGT
1 1	1		DNFEESIFSQDYEDKYLDGKNIKEKETVIIPNEKSLQLOKDEAI
1	i		TPLPPKKENDEMPTCLLCVCLSGSVYCEEVDIDAVPPLPKESAY
1	J		LYARPNKIKKLT\AKDFADIPNLRRLDFTGNLIEDIEDGTFSKL
j i	<b>]</b>		SLVEELSLAENOLLKLPVLPPKLTLFNAKYNKIKSRGIKANAFK
1			KLNNLTFLYLDHNALESVPLNLPESLRVIHLQFNNIASITDDTF
1	ļ		CKANDTSYIRDRIEEIRLEGNPIVLGKHPNSFICLKRLPIGSYF
5405	2199	1220	QNSRSLHMDPONOHGSGSSLVVIQOPSLDSRPRLDYEREIOPTA
			ILSLDQIKAIRGSNEYTEGPSVVKRPAPRTAPRQEKHERTHEII
			PINVNNYEHRHTSHLGHAVLPSNARGPILSRSTSTGSAASSGS
1 1	1		
{	}		NSSASSEQGLLGRSPPTRPVPGHRSERAIRTQPKQLIVDDLKGS
1	1		LKEDLTQHKFICEQCGKCKCGECTAPRTLPSCLACNRQCLCSAE
j j	j		SMVEYGTCMCL\VKGIFYHCSNDDEGDSYSDNPCSCSQSHCCSR
] [			YLCMGAMSLFLPCLLCYPPAKGCLKLCRRCYDWIHRPGCRCKNS
5406			NTVYCKLESCPSRGQGKPS
_ 5±06	279	2732	RWRTYNVEGPLTFMDVAIEFCLEEWQCLDTAQQNLYRNVMLENY

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
<u>}</u>	amino acid	residue of	
[	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł		sequence	Codon, /=possible nucleotide deletion,
<b></b>	sequence		\=possible nucleotide insertion)
	1		RNLVFLG/IIAVSKPDLITCLEQEKEPWEPMRRHEMVAKPPVMC
1		!	SHFTQDFWPEQHIKDPFQKATLRRYKNCEHKNVHLKKDHKSVDE
1	1	i	CKVHRGGYNGFNQCLPATQSKIFLFDKCVKAFHKFSNSNRHKIS
ł	1		HTEKKLFKCKECGKSFCMLSHLAQHKIIHTRVNFCKCEKCGKAF
1	1	Į.	NCPSIITKHKRINTGEKPYTCERCGKVFNWSSRLTTHKKNYTRY
ł	ł		KLYKCEECGKAFNKSSILTTHKIIRTGEKFYKCKECAKAFNQSS
1	t	1	NITEHKKIHPGEKPYKCEECGKAFNNPSTLTKHKRIHTGEKPYT
1	ł	ĺ	CEECGKAFNQFSNLTTHKRIHTA\EKFYKCTECGEAFSRS\SNL
1			TKHKEIHTEKKPYKCEECGKAFKWSSKLTEHKLTHTGEKPYKCE
	l .	ŀ	KCGKAFNCPSIITKHNRINTGEKPYTCEECGKVFNWSSRLTTHK
1			KNYTRYKLYKCEECGKAFNKSSILTTHKKIHIEKKFYKCEECGK
(	1		AFKWSSKLTEHKITHTGEKPYKCEECGKAFNHFSILTKHKRIHT
	1		GEKPYKCEECGKAFTQSSNLTTHKKIHTGEKFYKCEECGKAFTQ
1	]	J	SSNLTTHKKIHTGGKPYKCEECGKAFNQFSTLTKHKIIHTEEKP
			YKCEECGKAFKWSSTLTKHKIIHTGEKPYKCEECG\KAFKLSST
Į.			LSTHKIIHTGEKPYKCEKCGKAFNRPSNLIEHKKIHTGEQPYKC
1			EECGKAFNYSSHLNTHKRIHTKEQPYKCKECGKAFNQYSNLTTH
1			NKIHTGEKLYKPEDVTVILTTPQTFSNIK
5407	3	659	RPRRRQSSCCTGWLAGWLLRAAPRFCRRTETDMEOGKGLAVLIL
1			Alillogtlagsikgnhlvkvydygedgsvlltcdaeaknitwf
1			KDGKMIGFLTEDKKKWNLGSNAKDPRGMYQCKGSQNKSKPLQVY
1			YRMCQNCIELNAATISGFLFAEIVSIFDLAVGVYFIAGTGMEFR
ļ			QS\RASDKQTLLP\NDPAPTQPLKDPRKMTQYSHLQGN\QLRRN
5408	2745	6128	QGSKGTCHPQAQQPWDEGVWQEAPSQSEPWGQSQEPPTMPORLP
		0220	HARQHTPLPLGSADYRRVVSVRPQGPHRDPXDSRDAAKREQGSL
			APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF
1			STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP
			RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE
J			VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM
ł			NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD
			LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAFL
			LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS
1			IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL
			BITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL
			LAEVHGSNIKNFPQDNOKVRLSVSGFLCAFEIPVPVSPISASSP
ł			
}	1		TQTDFSSSPSTNEMFTLTTNGDLPRPIFIPNGMPNTVVPCGTEX
			NFTNGMVNGHMPSLPDSPFTGYIIAVHRKMMRTELYFLSSQKNR
			PSLFGMPLIVPCTVHTRKKDLYDAVWIQVSRLASPLPPQEASNH
			AQDCDDSMGYQYPFTLRVVQKDGNSCAWCPWYRFCRGCKIDCGE
( )			DRAFIGNAYIAVDWHPTALHLRYQTSQERVVDEHESVEQSRRAQ
			VEPINLDSCLRAFTSEEELGENEMYYCSKCKTHCLATKKLDLWR
			LPPILIIHLKRPQFVNGRWIKSQKIVKFPRESFDPSAFLVPRDP
1			ALCOHKPLTPQGDELSEPRILAREVKKVDAQSSAGEEDVLLSKS
1 1	ĺ		PSSLSANIISSPKGSPSSSRKSGTSCPSSKNSSPNSSPRTLGRS
			KGRLRLPQIGSKNKLSSSKENLDASKENGAGQICELADALSRGH
1	ļ		VLGGSQPELVTPQDHEVALANGFLYEHEACGNGCGNGYSNGQLG
<b>j</b> 1			NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN
1 1			PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK
<u></u>			TDGKKMADTSSMDEDFESDY\EKYCVLQ
5409	2745	6128	QGSKGTCHPQAQQPWDEGVWQEAPSQSBPWGQSQEPPTMPQRLP
1 1			HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL
<b>]</b>			APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF
			STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP
[ [			RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE
j i	ļ		VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGN'I'CFM
, ,	1		NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD
j		Ì	LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAFL
[	-	[	LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS
1		İ	IVVDLFHGQLRSQVKCKTCGHISVRFDFFNFLSLPLPMDSYMHL
, ,	ļ		EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL
L			LAEVHGSNIKNFPQDNQKVRLSVSGFLCAFEIPVPVSPISASSP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
j	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
ļ	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
-	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	boquonoc	\=possible nucleotide insertion)
		<del> </del>	TOTOFSSSPSTNEMFTLTTNGDLPRPIFIPNGMPNTVVPCGTEK
}	•		NFTNGMVNGHNPSLPDSPFTGYIIAVHRKMMRTELYFLSSOKNR
1		<b>\</b> ·	PSLFGMPLIVPCTVHTRKKDLYDAVWIQVSRLASPLPPQEASNH
1		[	AQDCDDSMGYQYPFTLRVVQKDGNSCAWCPWYRFCRGCKIDCGE
1		1	DRAFIGNAYIAVDWHPTALHLRYQTSQERVVDEHESVEQSRRAQ
		ì	VEPINLDSCLRAFTSEEELGENEMYYCSKCKTHCLATKKLDLWR
1	1	·	LPPILIIHLKRFQFVNGRWIKSQKIVKFPRESFDPSAFLVPRDP
i			ALCOHKPLTPOGDELSEPRILAREVKKVDAQSSAGEEDVLLSKS
			PSSLSANIISSPKGSPSSSRKSGTSCPSSKNSSPNSSPRTLGRS KGRLRLPQIGSKNKLSSSKENLDASKENGAGQICELADALSRGH
1			VLGGSQPELVTPQDHEVALANGFLYEHEACGNGCGNGYSNGQLG
1	!		NHSBEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN
	1		PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK
[,	1		TDGKKMADTSSMDEDFESDY\EKYCVLQ
5410	2	710	LRFPGQARHVWLAARMQAPHKEHLYKLLVIGDLGVGKTSIIKRY
			VHQNFSSHYRATIGVDFALKVLHWDPETVVRLQLWDIAGQERFG
			NMTRVYYREAMGAFIVFDVTRPATFEAVAKWKNDLDSKLSLPNG
ł			KPVSVVLLANKCDQGKDVLMNNGLKMDQFCKEHGFVGWFETSAK
			ENINIDEASRCLVKHILANECDLMESIEPDVVKPHLTSTKVASC
5411	1302	289	SG\CAKILVGTFAGVW
3411	1302	209	TGPAAAGRRKALGSFGKPSPVTGLRAARRRTRPSAPAAPSVGC GKRRESDAGAGGERASVRTGSGRRGGRTMAGDSEQTLONHOOPN
			GGEFFLIGVSGGTASGKSSVCAKIVQLLGQNEVDYRQKOVVILS
1			QDSFYRVLTSEQKAKALKGQFNFDHPDAFDNELILKTLKEITEG
ļ	)		KTVQIPVYDFVSHSRKEETVTVYPADVVLFEGILAFYSQER/IR
	J		DLFQMKLFVDTDADTRLSRRVLKDISERGRDLEQILSSSTLRFV
	ļ		KPA\FEEFCLPPK\KYADVIIPR\GADN\RVPINLIVQHIQ\DI
			LNGGPS\NRQTNGCLNGYTPSRKRQASESSSRPH
5412	3180	313	QGISNFFHKEANFWFEVSGYLISPLRSPFVDPALENSLMASPNN
	Ì		KMEGESSRFEIHTPVSDKKKKKCSIHKERPQKHSHEIFRDSSLV
1			NEQSQITRRKKRKKDFQHLISSPLKKSRICDETANATSTLKKRK KRRYSALEVDEBAGVTVVLVDKENINNTPKHFRKDVDVVCVDMS
1			IEQKLPRK\PKTDKFQVLAKSH\AHKSEALHSKVREKKNKKHQR
1			KAASWESQRA\RDTLPQSEFPTQEESWLSVGPGGEITELF\ASA
1			HKNKSKKKKKKSSNREYET\LAMPEGSQAGREAGTDMQESQPTV
			GLDDETPQLLGPTHKKKSKKKKKKKKNHQEFESLAMPEGSQVGS
1			EVGADMQES\RPAVGLHGETAGIPAPAYKNKSKKKKKKSNHQEF
			EAVAMPESLESAYPEGSQVGSEVGTVEGSTALKGFKESNSTKKK SKKRKLTSVKRARVSGDDFSVPSKNSBSTLFDSVEGDGAMMEEG
	İ	•	VKSRPRQKKTQACLASKHVOEAPRLEPANEEHNVETAEDSEIRY
			LSADSGDADDSDADLGSAVKQLQEFIPNIKDRATSTIKRMYRDD
1		ı	LERFKEFKAQGVAIKFGKFSVKENKQLEKNVEDFLALTGIESAD
1	}		KLLYTDRYPEEKSVITNLKRRYSFRLHIG\RNIARPWKLIYYRA
			KKMFDVNNYKGRYSEGDTEKLKMYHSLLGNDWKTIGEMVARRSL
•			SVALKFSQISSQRNRGAWSKSETRKLIKAVEEVILKKMSPQELK
			EVDSKLQENPESCLSIVREKLYKGISWVEVEAKVQTRNWMQCKS
			KWTEILTKRMTNGRRIYYGMNALRAKVSLIERLYEINVEDINEI
			DWEDLASAIGDVPPSYVQTKFSRLKAVYVPFWQKKTFPEIIDYL YETTLPLLKEKLEKMMEKKGTKIQTPAAPKQVFPFRDIFYYEDD
			SEGGGHRKRKRPRRHAWFTPVIPVLWEAKAGWII
5413	3753	1304	RFPAGVAPRRAMANVSKKVSWSGRDRDDEEAAPLLRRTARPGGG
			TPLLNGAGPGAARQSPRSALFRVGHMSSVKLDDELLEP\DMDPP
, 1	1		HPFPKEIPHNEKLLSLKYESLDYDNSENQLFLEEERRINHTAFR
	1		TVEIKRWVICALIGILTGLVACFIDIVVENLAGLKYRVIKGNID
[	1		KFTEKGGLSFSLLLWATLNAAFVLVGSVIVAFIEPVAAGSGIPQ
]	1		IKCFLNGVKIPHVVRLKTLVIKVSGVILSVVGGLAVGKEGPMIH
}	,	j	SGSVIAAGISQGRSTSLKRDFKIFEYLRRDTEKRDFVSAGAAAG
	Į		VSAAFGAPVGGVLFSLEEGASFWNQPLTWRIFFASMISTFTLNF
] ]	1		VLSIYHGNMWDLSSPGLINFGRFDSEKMAYTIHEIPVFIAMGVV
			GGVLGAVFNALNYWLTMFRIRYIHRPCLQVIEAVLVAAVTATVA FVLIYSSRDCQPLQGGSMSYPLQLFCADGEYNSMAAAFFNTPEK
<b></b>		1	F VIII TO THE TANGET I LANGE IN SMARAF FRITPER

SEQ	Predicted	Predicted end	Imino nedd committee
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	2	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Į.	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
[	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
		·	SVVSLFHDPPGSYNPLTLGLFTLVYFFLACWTYGLTVSAGVFIP
1	ł	ł	SLLIGAAWGRLFGISLSYLTGAAIWADPGKYALMGAAAQLGGIV
1	1	j .	RMTLSLTVIMMEATSNVTYGFPIMLVLMTAKIVGDVFIEGLYDM
		!	
1		t	HIQLQSVPFLHWEAPVTSHSLTAREVMSTPVTCLRRREKVGVIV
1			DVLSDTASNHNGFPVVEHADDTQPARLQGLILRSQLIVLLKHKV
	ì	ì	FVERSNLGLVQRRLRLKDFRDAYPRFPFIQSIHVSQDERECTMD
Í	ĺ	ľ	LSEFMNPSPYTVPQEASLPRVPKLFRALGLRHLVVVDNRNQVVG
		<b>L</b>	LVTRKDLARYRLGKRGLEELSLAQT
5414	2130	390	GVASAWDRALFSPLLSPTSRVFRTSPPRCVSTETGRRDRARVPS
1			QWCSVLQGKLPVSGRTSLACVRSILLSPASSPRKVGIVGGTGAR
1	l	]	AGAAPRDHGRVRHRRPSSARRMTRTTGQCLAPRGCQGPRGTRSP
1	ł	1	RSPRSRTRRGCSASPACLP/CRSALIVAVLCYINILNYMDRFTV
1	1	1	AGVLPDIEQFFNIGDSSSGLIQTVFISSYMVLAPVFGYLGDRYN
į	i	1	
ł	l	1	RKYLMCGGIAFWSLVTLGSSFIPGEHFWLLLLTRGLVGVGEASY
	1	}	STIAPTLIADLFVADQRSRMLSIFYFAIPVGSGLGYIAGSKVKD
ſ		1	MAGDWHWALRVTPGLGVVAVLLLFLVVREPPRGAVERHSDLPPL
		Į.	NPTSWWADLRALARNPSFVLSSLGFTAVAFVTGSLALWAPAFLL
l l	į.	1	RSRVVLGETPPCLPGDSCSSSDSLIFGLITCLTGVLGVGLGVEI
1		ĺ	SRRLRHSNPRADPLVCATGLLGSAPFLFLSLACARGSIVATYIF
1	l	ľ	IFIGETLLSMNWAIVADILLYVVIPTRRSTAEAFQIVLSHLLGD
	ļ	}	AGSPYLIGLISDRLRRNWPPSFLSEFRALQFSLMLCAFVGALGG
			AAFLGTAHLH
5415	693	2986	IPPKTKLELQKH/LTTLT/NQEQATIFEEVQKLRPRNEQRENEL
	}		IISFLRCLFEEKQKEHIHIGEMKQTSQMAAENIGSELPPSATRF
			RLDMLKNKAKRSLTESLESILSRGNKARGLOBHSISVDLDSSLS
1			STLSNTSKEPSVCEKBALPISESSFKLLGSSEDLSSDSESHLPE
1	Ì		EPAPLSPQQAFRRRANTLSHFPIECQEPPQPARGSPGVSQRKLM
1			RYHSVSTETPHERKDFESKANHLGDSGTPVKTRRHSWRQQIFL
1			
1		}	RVATPQKACDSSSRYEDYSELGELPPRSPLEPVCEDGPFGPPPE
1	<b>l</b> ;		EKKRTSRELRELWQKAILQQILLLRMEKENQKLQASENDLLNKR
			LKLDYEEITPCLKEVTTVWEKMLSTPGRSKIKFDMEKMHSAVGQ
f			GVP\RHHRGEIWKFLAEQFHLKHQFPSKQQPKDVPYKELLKQLT
ì			SQQHAILIDLGRTFPTHPYFSAQLGAGQLSLYNILKAYSLLDQE
ì	i i		VGYCQGLSFVAGILLLHMSEEEAFKMLKFLMFDMGLRKQYRPDM
	·		IILQIQMYQLSRLLHDYHRDLYNHLEEHEIGPSLYAAPWFLTMF
			ASQFPLGFVARVFDMIFLQGTEVIFKVALSLLGSHKPLILQHEN
			LETIVDFIKSTLPNLGLVQMEKTINQVFEMDIAKQLQAYEVEYH
			VLQEELIDSSPLSDNQRMDKLEKTNSSLRKQNLDLLEQLQVANG
			RIQSLEATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRRS
1 1	}		AKPSDREPECTOPEPTGD
5416	27	4074	KSQLFCFWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLK
]			YVDDIQKGNTIKRLNIQKRRKPSVPCPEPRTTSGQQGIWTSTES
1	ľ		LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTIP
] !			
] 1			ENRQLPPPSPQLPKHNLHVTKTLMETRRLEQERATMQMTPGEF
(		1	RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYG
) 1			SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIREQM
]			AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAA
1 [	ſ		SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEME
! i			TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEC
, ,	j		RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE
i I			AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMT
			KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH
1	1		MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWWIVKER
	1		VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT
1 1	i	į	NINLKEVRS IGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV
<b>i</b>	ì		
1 1		ļ	MAVPRIADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ
	[	(	TSTQTVETRTVAVGRGRVKDINSSTKTRSIGVGTLLSGHSGFDR
: 1		1	PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR
; I	}		RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ
1 !	ĺ		TLLAENYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSAST
L			EELRNPDFQKTSLGKITGSYLGYTCKCGGLQSGSPLSSQTSQPE

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ĺ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
Ī	corresponding	to first	L=Laucine, M=Methionine, N=Asparagine,
J	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
i		İ	QEVGTSEGKPISSLDAFPTQEGTLSPVNLTDDQIAAGLYACTNN
1	}	ļ	ESTLKSIMKKKDGNKDSNGAKKNLQFVGINGGYETTSSDDSSSD
1			ESSSESDDECDVIEYPLEBEEEEEDBDTRGMAEGHHAVNIEGL
ĺ			KSARVEDEMQVQECEPEKVBIRERYELSEKMLSACNLLKNTIND PKALTSKDMRFCLNTLQHEWFRVSSQKSAIPAMVGDYIAAFEAI
(		-	SPDVLRYVINLADGNGNTALHYSVSHSNFEIVKLLIDADVCNVD
1	1	1	HONKAGYTPIMLAALAAVEAEKDMRIVEELFGCGDVNAKASOAG
1	}		QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG
ĺ			HVEIVKLLLAQPGCNGHLEDNDGSTALSIALEAGHKDIAVLLYA
1			HVNFAKAQSPGTPRLGRKTSPGPTHRGSFD
5417	27	4074	KSQLFCFWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLK
1			YVDDIQKGNTIKRLNIQKRRKPSVPCPEPRTTSGQQGIWTSTES
		1	LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTIP
}	Ì		ENRQLPPPSPQLPKHNLHVTKTLMETRRRLEQERATMQMTPGEF
	1		RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYG
			SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIREQM
1	İ		AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAA
1			SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEME
			TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEC
			RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE
1			AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMT KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH
			MDLVDTCVGTSVETNSVGISCOPECKNKVVGPELPMNWWIVKER
			VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT
			NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV
1			MAVPRIADODISTDLEQVHQFINTETATLIESCINTCLSTLDKQ
Ì	,	'	TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR
			PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQI.TVGLTASR
			RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ
			TLLAENYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSAST
1			EELRNPDFQKTSLGKITGSYLGYTCKCGGLQSGSPLSSQTSQPE
i			QEVGTSEGKPISSLDAFPTQEGTLSPVNLTDDQIAAGLYACTNN
1			ESTLKSIMKKKDGNKDSNGAKKNLQFVGINGGYETTSSDDSSSD
ł			ESSSSESDDECDVIEYPLEEEEEEEDBDTRGMAEGHHAVNIEGL
1	•	•	KSARVEDEMQVQECEPEKVEIRERYELSEKMLSACNLLKNTIND PKALTSKDMRFCLNTLQHEWFRVSSQKSAIPAMVGDYIAAFEAI
1			SPDVLRYVINLADGNGNTALHYSVSHSNFEIVKLLLDADVCNVD
1		-	HONKAGYTPIMLAALAAVEABKDMRIVEELFGCGDVNAKASQAG
1			QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG
1	İ	1	HVBIVKLLLAQPGCNGHLEDNDGSTALSIALEAGHKDIAVLLYA
L	· .		hvnfakaqspgtprlgrktspgpthrgsfd
5418	24	1133	SVPRAGGDMETGAAELYDQALLGILQHVGNVQDFLRVLFGFLYR
			KTDFYRLLRHPSDRMGFFPGAAQALVLQVFKTFDHMARQDDEKR
1			RQELEEKIRRKEEEEAKTVSAAAAEKEPVPVPVQEIEIDSTTEL
	1		DGHQEVEKVQPPGPVKEMAHGSQEAEAPGAVAGAAEVPR\EPPI
Į į	ļ .		LPRIQEQFQKNPDSYNGAVRENYTWSQDYTDLEVRVPVPKHVVK
		ı	GKQVSVALSSSSIRVAMLEENGERVLMEGKLTHKINTESSLWSL
		i	EPGKCVLVNLSKVGEYWWNAILEGEEPIDIDKINKERSMATVDE
'			EEQAVLDRLTFDYHQKLQGKPQSHELKVHEMLKKGWDAEGSPFR
5419	1395	350	GQRFDPAMFNISPGAVQF GTHPLDPDLVSRTSVOGPLMTMACPGMSDTEESPFLGPRAAEEG
7479	כבנו	259	
] ]			SESEACEAFGRRKSEEEGRRSDTSGFGRSRKHKVNWKHPERADA KDFASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL
(			PORIOOWOOSPCIAEEHGKKLLERIRREOOSARTRLOEMERRFH
į i			ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPINPR
, ,		1	VALRHMERCYAKYESOTSFGSMYPTRIEGATRLFCDVYNPOSKT
	i		YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK
[ [			RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVRTAMTN
]			RAGLLALMLHQTIQHDPLTTDLRSSADR
5420	117	1733	NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG
[ [			GGFLPARPPRAQRHLGFSHAEQSMEAPDYEVLSVREQLFHERIR
			<u> </u>

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
{	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
-	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ĺ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ľ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Į	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	}	\=possible nucleotide insertion)
			ECIISTLLFATLYILCHIFLTRFKKPAEFTT\GMMKMPPSTRL/
		{	LLELCTFTLAIALGAVLLLPFSIISNEVLLSLPRNYYIQWLNGS
	1	1	LIHGLWNLVFLFSNLSLIFLMPFAYFFTESEGFAGSRKGVLGRV
}	1		YETVVMLMLLTLLVLGMVWVASAIVDKNKANRESLYDFWEYYLP
1			YLYSCISFLGVLLLLVCTPLGLARMFSVTGKLLVKPRLLEDLEE
			QLYCSAFEEAALTRRICNPTSCWLPLDMELLHRQVLALQTQRVL
			LEKRRKASAWQRNLGYPLAMLCLLVLTGLSVLIVAIHILELLID
7			EAAMPRGMQGTSLGQVSFSXLGSFGAVIQVVLIFYLMVSSVVGF
}			YSSPLFRSLRPRWHDTAMTQIIGNCVCLLVLSSALPVFSRTLGL
1	]		TRFDLLGDFGRFNWLGNFYIVFLYNAAFAGLTTLCLVKTFTAAV
5421	117	1733	RAELIRAFGERE
		2,23	NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG GGFLPARPPRAQRHLGFSHAEQSMEAPDYEVLSVREQLFHERIR
1			ECIISTLLFATLYILCHIFLTRFXKPAEFTT\GMMKMPPSTRL/
1			LLELCTFTLAIALGAVLLLPFSIISNEVLLSLPRNYYIOWLNGS
			LIHGLWNLVFLFSNLSLIFLMPFAYFFTESEGFAGSRKGVLGRV
1 .			YETVVMLMLLTLLVLGMVWVASAIVDKNKANRESLYDFWEYYLP
			YLYSCISFLGVLLLLVCTPLGLARMFSVTGKLLVKPRLLEDLEE
ĺ			QLYCSAFEEAALTRRICNPTSCWLPLDMELLHRQVLALQTQRVL
1			LEKRRKASAWQRNLGYPLAMLCLLVLTGLSVLIVAIHILELLID
			EAAMPRGMQGTSLGQVSFSKLGSFGAVIQVVLIFYLMVSSVVGF
			YSSPLFRSLRPRWHDTAMTQIIGNCVCLLVLSSALPVFSRTLGL
			TRFDLLGDFGRFNWLGNFYIVFLYNAAFAGLTTLCLVKTFTAAV
5422	3	1263	RAELIRAFGERE SCGESLPTWLAGASRPGIGRKGGAWGGRGGSSPAQVLLSPGPVF
	_	2203	KAGCNWWHLSRDQAGVQRCDLGSSQPPPLGFKRFSCLSLPSSWD
1			YRSTVLCVSKMEADLSGFNIDAPRWDQRTFLGRVKHFLNITDPR
			TVFVSERELDWAKVMVEKSRMGVVPPGTQVEQLIYAKKLYDSAF
j			HPDTGEKMNVIGRMSFQLPGGMIITGFMLQFYRTMPAVIFWQWV
1			NQSFNALVNYTNRNAASPTSVRQMALSYFTATTTAVATAVGMNM
j i			LTKKAPPLVGRWVPFAAVAAANCVNIPMMRQQELIKGICVKDRN
			ENEIGHSRRAAAIGITQVVISRITMSAPGMILLPVIMERLEKLH
			FMQKVKVL/SAPLQVMLSGCFLIFMVPVACGLFPQKCELPVSYL
5423	3186	905	EPKLQDTIKAKYGELEPYVYFNKGL GVSMALGEEKAEAEASEDTKAQSYGRGSCRERELDIPGPMSGEQ
		505	PPRLBAEGGLISPVWGAEGIPAPTCWIGTDPGGPSRAHOPQASD
			ANREPVAERSEPALSGLPPATMGSGDLLLSGESQVEKTKLSSSB
1	Í		EFPQTLSLPRTTICSGHDADTEDDPSLADLPQALDLSQOPHSSG
			LSCLSQWKSVLSPGSAAQPSSCSISASSTGSSLQGHQBRAEPRG
1 1			GSLAKVSSSLEPVVPQEPSSVVGLGPRPQWSPQPVFSGGDASGL
	ļ		GRRRLSPQAEYWACVLPDSLPPSPDRHSPLWNPNKEYEDLLDYT
	}		YPLRPGPQLPKHLDSRVPADPVLQDSGVDLDSFSVSPASTLKSP
			TNVSPNCPPAEATALPFSGPREPSLKQWPSRVPQKQGGMGLASW
	1		SQLASTPRAPGSRDARWERREPALRGAKDRLTIGKHLDMGSPQL
	ł		RTRDRGWPSPRPEREKRTSQSARRPTCTESRWKSEEEVESDDEY
1 1	1	ļ	LALPARLTQVSSLVSYLGSISTLVTLPTGDIKGQSPLEVSDSDG PASFPSSSSQSQLPPGAALQGSGDPEGONPCFLRSFVRAHDSAG
1	ļ		EGSLGSSQALGVSSGLLKTRPSLPARLDRWPFSDPDVEGQLPRK
j l	ļ	j	GGEQGKESLVQC\VKTFC\CQLEELICWLYNV\ADVTDHGTPAR
			SNLTSLK\SSLQLYRQFKKDIDEHQSLTESVLOKGEILLOCLLE
			NTPVLEDVLGRIAKQSGELESHADRLYDSILASLDMLAGCTLIP
		ĺ	DKKPMAAMEHPCEGV
5424	3186	905	GVSMALGEEKAEAEASEDTKAQSYGRGSCRERELDIPGPMSGEQ
	ļ		PPRLEAEGGLISFVWGAEGIPAPTCWIGTDPGGPSRAHQPQASD
			ANREPVAERSEPALSGLPPATMGSGDLLLSGESQVEKTKLSSSE
			EFPQTLSLPRTTICSGHDADTEDDPSLADLPQALDLSQQPHSSG
		Ì	LSCLSQWKSVLSPGSAAQPSSCSISASSTGSSLQGHQERAEPRG
		ł	GSLAKVSSSLEPVVPQEPSSVVGLGPRPQWSPQPVFSGGDASGL
}	1	Į.	GRRRLSFQAEYWACVLPDSLPPSPDRHSPLWNPNKEYEDLLDYT
		į	YPLRPGPQLPKHLDSRVPADPVLQDSGVDLDSFSVSPASTLKSP TNVSPNCPPAEATALPFSGPREPSLKQWPSRVPQKQGGMGLASW
			NSWITCHER SOLVE STRUKTURE SALVE STRUKTURE SALVE STRUKTURE SALVE STRUKTURE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALVE SALV

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
			(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G-Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
Į.	1	sequence	\=possible nucleotide insertion)
<u> </u>	sequence		
1		i	SQLASTPRAPGSRDARWERREPALRGAKDRLTIGKHLDMGSPQL
	i	1	RTRDRGWPSPRPEREKRTSQSARRPTCTESRWKSEEEVESDDEY
	Į	İ	LALPARLTQVSSLVSYLGSISTLVTLPTGDIKGQSPLEVSDSDG
1	[	i	PASPPSSSSQSQLPPGAALQGSGDPEGQNPCFLRSFVRAHDSAG
1	Į.	ł	EGSLGSSQALGVSSGLLKTRPSLPARLDRWPFSDPDVEGQLPRK
		]	GGEOGKESLVQC\VKTFC\CQLEELICWLYNV\ADVTDHGTPAR
		i	SNLTSLK\SSLQLYRQFKKDIDEHQSLTESVLQKGEILLQCLLE
ŀ	}	1	NTPVLEDVLGRIAKQSGELESHADRLYDSILASLDMLAGCTLIP
1		Į.	
			DKKPMAAMEHPCEGV
5425	1086	115	GFCPSPSLGHQPPRVLHPTMSMAVETFGFFMATVGLLMLGVTLP
1	1	1	NSYWRVSTVHGNVITTNTIFENLWFSCATDSLGVYNCWEFPSML
1	1	[	ALSGYIQACRALMITAILLGFLGLLLGIAGLRCTNIGGLELSRK
}	1	i	AKLAATAGAPH\ILPGICGMVAI\SWYAFNITR\DFSDPLYPGT
1	j		KYELGPALYLGWSASLISILGGLCLCSACCCGSDEDPAASARRP
1	1	1	YOAPVSVMPVATSDOEGDSSFGKYGRNALRVAALCRGPRCLPTA
1		}	1 3
1	,	1	PKKRGPGRGPFPYSNLRGRPRPVPVAPPRPRPRVLHSHGPSQAK
	<del> </del>		NCSWEVAYLPSEAGSLIF
5426	42	3435	ATSSQSLGRADPPRGGTMERSPGEGPSPSPMDQPSAPSDPTDQP
			PAAHAKPDPGSGGQPAGPGAAGBALAVLTSFGRRLLVLIPVYLA
1	1	ĺ	GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLLDDEEQL
1	1	ļ	TAKTLYMSHRELPAWVSFPDVEKAEWLNKIVAQVWPFLGQYMEK
-	ł	l .	LLAETVAPAVRGSNPHLQTFTFTRVELGEKPLRIIGVKVHPGQR
	i	ł .	KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL
		J	EPLIGDLPFVGAVSMFFIRRPTLDINNTGMTNLLDIPGLSSLSD
1		ł	TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL
1	1	ĺ	LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN
1	,	Į.	
	<b>!</b>	1	POWGETYEVMVHEVPGQEIEVEVFDKDPDKDDFLGRMKLDVGKV
1	ł	ì	LQASVLDDWFPLQGGQGQVHLRLEWISLLSDAEKLEQVLQWNWG
1		1	VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP
ļ	1	l .	MVQLSIQDVTQESKAVYSTNCPVWBEAFRFFLQDPQSQBLDVQV
ł	1	ł .	KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM
1			KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR
İ	1		PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY
1	ł	l	VKLKLAGRSFRSHVVREDLNPRWNEVFEVIVTSVPGQELEVEVF
1	Í		The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
	}	[	DKDLDKDDFIGRCKVRLTTVLNSGFLDEWLTLEDVPSGRLHLRL
1		1	ERLTPRPTAABLEEVLQVNSLIQTQKSAELAAALLSIYMERAED
1	}		LPLRKGTKHLSPYATLTVGDSSHKTKTISQTSAPVWDESASFLI
ľ	1	ļ	RKPHTESLELQVRGEGTGVLGSLSLPLSELLVADQLCLDRWFTL
1	l	}	SSGQGQVLLRAQLGILVSQHSGVEAHSHSYSHSSSSLSEEPELS
j '	<b>[</b>		GGPPHITSSAPEV\RQRLTHVDSPLEAPAGPLGQVKLTLWYYSE
			ERKLVSIVHGCRSLRQNGRDPPDPYVSLLLLPDKNRGTKRRTSQ
1			KKRTLSPEFNERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL
		}	LGKVQLDLAETDLSQGVARWYDLMDNKDKGSS
5427	42	3435	ATSSQSLGRADPPRGGTMERSPGEGPSPSPMDQPSAPSDPTDQP
1 -42.		3433	PANHAKPDPGSGGOPAGPGAAGEALAVLTSFGRRLLVLIPVYLA
1	l		· · · · · · · · · · · · · · · · · · ·
		· ·	GAVGLSVGFVLFGLALYLGURRVRDBKERSLRAARQLLDDEEQL
1			TAKTLYMSHRELPAWVSFPDVEKAEWLNKIVAQVWPFLGQYMEK
	)		LLAETVAPAVRGSNPHLQTFTFTRVELGEKPLRIIGVKVHPGQR
1			KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL
1			EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD
1			TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL
1	1	İ	LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN
1	}		POWGETYEVMVHEVPGOEIEVEVFDKDPDKDDFLGRMKLDVGKV
			LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG
1			VSSRPDPPSAA1LVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP
			MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV
1			KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM
1			KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR
1			PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY
1			VKLKLAGRSFRSHVVREDLNPRWNEVFEVIVTSVPGQELEVEVF
1			DKDLDKDDFLGRCKVRLTTVLNSGFLDEWLTLEDVPSGRLHLRL
1	L		STORY OF STREET AND STREET OF STREET

Designating   Cocation   Cortesponding   Cocation   Cortesponding   Coffee   Cocation   Cortesponding   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffe	SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
No:   nucleotide				
Cocresponding to first smin acid amino acid residue of amino acid amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent of amino acid sequence   Percent o				
L-Loucine, M-Mechicmine, N-Asparagine, brists maino acid residue of amino acid residue of amino acid sequence   S-Serine, T-Threonine, V-Valine, and the sequence   S-Serine, T-Threonine, V-Valine, sequence   S-Serine, T-Threonine, V-Valine, maino acid sequence   S-Serine, T-Threonine, V-Valine, which main acid sequence   S-Serine, T-Threonine, V-Valine, which main acid sequence   S-Serine, T-Threonine, V-Valine, which main acid sequence   S-Serine, T-Threonine, V-Valine, which main acid sequence   S-Serine, T-Threonine, V-Valine, which main acid sequence   S-Serine, T-Threonine, V-Valine, which main acid sequence   S-Serine, T-Threonine, V-Valine, which main acid sequence   S-Serine, T-Threonine, V-Valine, which main acid sequence   S-Serine, T-Threonine, V-Valine, which main acid sequence   S-Serine, T-Threonine, V-Valine, which main acid sequence   S-Serine, T-Threonine, V-Valine, W-Threat Main acid sequence   S-Serine, T-Threonine, V-Valine, W-Threat Main acid sequence   S-Serine, T-Threonine, V-Valine, W-Threat Main acid sequence   S-Serine, T-Threonine, V-Valine, W-Threat Main acid sequence   S-Serine, T-Threonine, V-Valine, W-Threat Main acid sequence   S-Serine, T-Threonine, V-Valine, W-Threat Main acid sequence   S-Serine, T-Threonine, V-Valine, W-Threat Main acid sequence   S-Serine, T-Threonine, V-Valine, W-Threat Main acid sequence   S-Serine, T-Threonine, V-Valine, W-Threat Main acid sequence   S-Serine, T-Threonine, V-Valine, W-Threat Main acid sequence   S-Serine, T-Threonine, V-Valine, W-Threat Main acid sequence   S-Serine, T-Threonine, V-Valine, W-Threat Main acid sequence   S-Serine, T-Threonine, V-Valine, W-Threat Main acid sequence   S-Serine, T-Threonine, V-Valine, W-Threat Main acid sequence   S-Serine, T-Threonine, V-Valine, W-Threat M-Threat Main acid sequence   S-Serine, T-Threat M-Threat M-Threat M-Threat M-Threat M-Threat M-Threat M-Threat M-Threat M-Threat M-Threat M-Threat M-Threat M-Threat M-Threat M-Threat M-Threat M-Threat M-Threat M-Threat M-Threat M-Threat M-Threat M-Threat M	NO:			
to first amino acid residue of amino acid amino acid sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  seq	ı			
amino acid residue of amino acid sequence    Sescrime, T-Threcomine, V-Vallme, amino acid sequence    Sequence    RETTRETABLE RETURNS A CONTROL OF SETTING AND AND AND AND AND AND AND AND AND AND	1		to first	L=Leucine, M=Methionine, N=Asparagine,
##TYPYDODHAR. Y=TYPOSIAE, X=DKROMON, *=Stop coden, *=possible nucleotide daletion,	]	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
main acid sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequen	1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
amino acid sequence   Codon, /=possible nucleotide deletion.   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Seq	1	residue of	amino acid	
Sequence	l		1	
RETPREPTALELEVIQUNS.LTGGOGASELAMLISTYMERAED  LRLKKSTHILSPYPALLVIGSSITKTTISGTSAPWIRSSISSISTERPIS  SQGQVLIARQUIGSTGVLGSLGFLSELLVADQLCLDRWFI  SQGQVLIARQUIGVGSTGVLGSLGFLSELLVADQLCLDRWFI  SQGQVLIARQUITVGNGGTGVASHISTSYSHSSSSSISSERPIS  GGPPHTTSSAPEVIGOLITVGNGGGTGVASHISTSYSHSSSSSISSERPIS  GGPPHTTSSAPEVIGOLITVGNGGGTGVASHISTSYSHSSSSISSERPIS  RKHYSIVHGGRIGOGGAPPUVSLLIAPDKNGTKRRTSQ  KKRTLSPEPERFEREIDLDEAGRRILDVSVASNASSMGREREL  LGKVQLOLARTIDSGGVARPTUDMKKKGSS  \$ 1839 SSRSEELSACATAPPHLVSSPPARAPAQLORPGGWATGGARELIV  LAASIPYHAMFTINDMECKODE VVQCMDPSALERLINFACIGU  LAASIPYHAMFTINDMECKODE VVQCMDPSALERLINFACIGU  RQFAETMKCAVLYDAANSFINGHSVESWSBEPLALDLEDVLIA  RQFAETMKCAVLYDAANSFINGHSVESWSBEPLALDLEDVLIA  PCRPQSLSDRVQQDDLVRCCHKCRDLVDEARDYLLMPERRPHLE  PCRPQSLSDRVQQDDLVRCCHKCRDLVDEARDYLLMPERRPHLE  AFRER PROCTS LAGILYTANGGLANGADGLAVVESTOLMPERRPHLE  AFRER PROCTS LAGILYTANGGLANGADGLAVVESTOLMPERRPHLE  PCRPQTASSRVGVAVVNGLLYALGOTOGOLGLIFSTVQAYHTSTOL  MTRVGSMNSKRSAMTVVLDGGI VYGGGYDGNSSISSVSTYSPP  TDKWTVVTSMSSNRSAA\GVTVFEGRIVVSGGHDGLGIFSSVMTYSPP  TDKWTVVTSMSSNRSAA\GVTVFEGRIVVSGGHDGLGIFSSVMTYSPP  TDKWTVVTSMSSNRSAA\GVTVFEGRIVVSGGHDGLGIFSSVMTYSPP  TOGSBL\SSWGDVLTPPTDCTGTFMA\PAPACKERGGYDGSGFLSI  ABMYSSV\ADQWCLLVPM\HTRR\SRVSLGGAVGRLYAVWGUT  TGGSBL\SSWGDVLTPPTDCTGTFMA\PAPACKERGGYDGSGFLSI  ABMYSSV\ADQWCLLVPM\HTRR\SRVSLGGAVGRLYAVWGUT  TGGSBL\SSWGDVLTPPTDCTGTFMDDDMSSARGGGPPSSNS  GISATCTSGGGMRGGPP TYTSSVTGHTMGSSFGBOQSSGPPSL  LESTITLHHTHIALPYTAGGSLATACUTORTVTAVALINRSTILVA  GRANGGAPHTSPALMAVTYTYPYTLGHEIDLPFTISLSGGEPPPSGGPCTSVNS  GISATCTSGGGMRGGPP TYTSSVTGHTMGSSFGBOQSSGPPSL  FORWADDRAFTARGATATARGATARGYCHAPPTSTARGGCPPSSNS  GISATCTSGGGMRGGPP TYTSSVTGHTMGSSFGBOQSSGPPSL  SAGOR GARREREREDARGATARGYCHAPPTSTARGATARGYCHAPPT  GRANGGAPTARGATARGATARGATARGATARGATARGATARGAT	1		Dequence	
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LAMSIPYEHAMPTNOMMECKQDEIVMQGMDPSALEALINFAYNO MAIDQQWQOSLMGASFLQQGSIKDACTTHERERHENCLGV RQFARTMCAVILUDANNSFINQHFVEVSMSERIALINFAYNO MAIDQQWQOSLMGASFLQQGSIKDACTTHERERHENCLGV RQFARTMCAVILUDANNSFINQHFVEVSMSERIALIPEOVLEIL VSDBLINVKSEOVFRALAUVEYDREGGFFIL\RNLQSNIRLL FCRPQSLSDRVQQDDLVRCCHKCRDLVDEARDYLLMPERRHLDF AFACTRRCCTS IAGLIYAVGGLNSAGDSLNVSVPPPJANNCHER CRPMTTARSRVGVAVVNGLLLYAIGGDQQLELSTUQANTETDT WTRVSSMMSKSAMGTVUNGQILVAGGTDGASLSSVETTSPE TDKWTVVTSMSSNSAA\QVTVFEGRIYVSGGDGLQLFSSVBNTSPE TDKWTVVTSMSSNSAA\QVTVFEGRIYVSGGDGLQLFSSVBNTSPE TDKWTVVTSMSSNSAA\QVTVFEGRIYVSGGDGLQFSSSSVETTSPE TDKWTVVTSMSSNSAA\QVTVFEGRIYVSGGDGLQFSSSSVETTSPE TDKWTVTVTSMSSNSAA\QVTVFEGRIYVSGGDGLQFSSSVBTSPE TDKWTVTSMSSNSAA\QVTVFEGRIYVSGGDAVGHLYSSVBN YNHHATAMPHAAGMLNKRCKGMGASLGSMBWVCGQVDGSGFLSI ABMYSSV\ADDWCLLVPM\HTRR\SRVSLGGPAVGGTLSSVB TGQSBL\SSVQDVLTPETOTCTFM\APPACHAGEGQVGVGCIPLLT I  5429 628 202 RREDALSEGCLMPSSSTVSGNGIPEPQVYAPPEPTDRLAVPPP AQRERFHRRQDFTYPTJQHEIDLPPTTSLSDGESPPPYQGPCTTJQ LRDPEQQLEIRRSVNAPHNTTTPGDLDMSARLGGPCPPSSNS GLSTCYGSGCRMEGPPP\TYSBVICHYPGGSSPQHQQSSGPPSL LEGTRLHHTHIAPLSSAAIBSKRKNCQKGHPL SGNKMCLDFRKRINKTTQFFNRNTTTPGDLAMGAPQPPPSSNS GLSTCYGSGCRMEGPPP\TYSBVICHYPGGSSPQHQQSSGPPSL LEGTRLHHTHIAPLSSAAIBSKRKNCQKGHPL FXTSRVHLIVQVSPKTVATSSDISINBGNNISLITATGRPEP TVTWRRIISPKANDVTVXQGSSATLRCTIDMRVTRVAHLHSSTILVA GNOKMCLDBRAVLJSSNIGHTSSTRAGGTVTRVQVTDN HPKTSRVHLIVQVSPKTVATSSDISINBGNNISLITATGRPEP TVTWRRIISPKANDVPYTAGGSSATLLCTIDMRVTRVAHLHSSTILVA APV\VBRVKVTVNYPPYISSEAKGTCVPYGGKGTLQCEASAVPSA EFCWYKDDKKLI/JCKKCVVENRPPLSKIPTYSGMYCNNT CVASNKLCHTNASINLJEKGPQAVSEVSNGTSRRAGCVWLLPLLVL HLLLKP  5431 2 1312 AAAAPGSRRRPPLPDPPRHMAGYEAPPPPABRSPRAMRSFKPV TORNSYNAPSBRLQCHTHYSVQSDISMGLSLVELAVGRYPIPPP DAKELEAIFGRPVVDGEGGBPHSISBRRPPPGRPVSCHGMDSRP AMAIPELLDTVINSPPPLNAGYTPGDGSTVTKCUHRBS GLIMARKLIHLEKPAIRNQIIRELQCHTRENGVTYTVQHRPS GLIMARKLIHLBIKPAIRNQIIRELQCHTRENGVTYTVQHRPS GLIMARKLIHLBIKPAIRNQIIRELQCHTRENGVTYTVQHRPS GLIMARKLIHLBIKPAIRNQIIRELQCHTRENGVTYTVQHRPS GLIMARKLIHLBIKPAIRNQIIRELQCTPRGVSGLIDBMAN FVGTRSYNAPSRLQCTTTYSVQSDIIRMGCLIVELAVGRYPIPPP DAKELBAIFGRPVVDGEGGBPHSISPRPPPGRP		<u> </u>		LGKVQLDLAETDLSQGVARWYDLMDNKDKGSS
LAS1 PYPHAMFINDMECKQDEIVMOCMDPSALERALINFAYNO NIATDQMOVOS_LIMGASFIQIGS IKMOCTIPERCHIPPKICLGV RQFAETWMCAV_YDAANSTIQHPVEVENSEEP_AD_PLEDVLEI VSRDELNVKSEGVOFFAALAAVRYDREQROTPL_NRILQSNIRLI PCRPQFISDRVQQDDLVRCGKKCRLVLVPERADVILMPERRHID AFRTRRCCTSIAGLIYAVGGLNSAGDELNVVEVPPIPLANCWER CRPNTTANSRNSAAQVVTVFGEIVYJGGHDGLEISTVQANTHTOTD WTRVGSMNSKSAMGTVVLDQIIVVGGYDGNSSLSSVETYSPE TDKWTVVTSMSNSKSAAQVTVFGEIVYJGGHDGGLIFSSVEN YNHHTATWHPAAGMLAKKCRIGAASLGSKMPVCGGVDGSGFLSI ABMYSSV_ADQWCLLVPPM HTMR Q RSVELGGPAVGRLYAVWGVT TGQSBLASSUGDLIPPTOCWTFM\APMACKEGGVGGCIPLLT I  5429 828 202 REBDALSSEGCLAPBESTYSGNGIPPPQVYAPPRPPDRLAVPPP AQREFYHRFQPTYPYLQHEIDLPPTISLSDGEBPPPYQGPCTLQ LRIPPRQQLELMRSSVRAPPNRTIFDSJAMDSARLGGPCPPSSNS GISATCYGSGGRNEGPPP\TYSSVIGHTPGSSPGNGSGPPSL LGGTRUHHTHALLESAALBSKEKKQKGHBD  5430 441 1507 GKRRKRRKKIMKTIDPKNINSISMAIPTGLAALC-FÇGVPVKS GISATCYGSGGRNEGPPP\TYSSVIGHTPGSSPGNGSGPPSL GONDATPYKAMDNIVTVRQGSSATLACTIDMXVALINNSSTILVA GNDKWCLDPRVVLLSNTGTQYSIELGNVDVYDEGPYTCSQVTNN HPKTGSVALITVQVPSKIVETSSISISINGNISLTCTIATGPRP TVTWRHISPKAVGPVSEBEVLEIQGITREGGGDVEGSSNDVA APV\VBRVVLTVVPPPYSEBAKTGVPVPGKGTLGCGASAVPGA EFOWYNDKALIJFGGAVSESNGTSRRAGCVWLLPLLVL LLLKP  AARAPGSRRRPLPDPRPMAHGYEAPPPPARRSPAWRARSKEVV CVASNKLGHTNASIMLFGGAVSEVSGTSRRAGCVWLLPLLVL LLLKP  AARAPGSRRRPLPDPRPMAHGYEAPPPPPARRSPAWRARSKEVV CVASNKLGHTHASINLFGGAVSEVSGTSRRAGCVWLLPLLVL LLLKP  AARAPGSRRRPLPDPRPMAHGYEAPPPPPARRSPAWRARSKEVV LPGITTINP\TTAGGSPP\TSEGASSANLVVLOKKLEELELDEGO KKRLBAFLTOKAKVGELKDDDFRRISELGAGNGGVVTKVQHRPS GLIMARKLIHLBIKPAIRNQIIRELQULHSKGVILVGHRSB TVTRSYMAPPELQGTHYSVQSDINSMGLSLVELAVGRYPIPPP DAKELAFLTOKAKVGELKDDDFRRISELGAGNGGVVTKVQHRPS GLIMARKLIHLBIKPAIRNQIIRELQULHSCHVSCHVIPPS GLIMARKLIHLBIKPAIRNQIIRELQULHSCHVSCHVIPPS GLIMARKLIHLBIKPAIRNQIIRELQULHSCNSPTVYCHPRS GLIMARKLIHLBIKPAIRNQIIRELQULHSCNSPTVYCHPRS GLIMARKLIHLBIKPAIRNQIIRELQULHSCNSPTVYCHPRS GLIMARKLIHLBIKPAIRNQIIRELGVARSPVNKCLIKNPAERA DLAMLINHTTIRASSVESUPPAGMLCKTLERLOQDITHRTAV YLERHQIMIRDVKSSIILVUNSGBIKLCDFGAVVTKCLIKNPAERA DLAMLINHTPIRRSSVLSVYDSDINGNGLGATGADACVEKQDISMAS FVOTRSYMAPERLQCTHTWYNSDINGHLGWATGATGADACVEKGHDSRP AMAIF	5428	] 3	1839	SSRSERLSACAIAPPWLVSSRPARPAQLQRPGKMVEDGAEELED
LAS1 PYPHAMFINDMECKQDEIVMOCMDPSALERALINFAYNO NIATDQMOVOS_LIMGASFIQIGS IKMOCTIPERCHIPPKICLGV RQFAETWMCAV_YDAANSTIQHPVEVENSEEP_AD_PLEDVLEI VSRDELNVKSEGVOFFAALAAVRYDREQROTPL_NRILQSNIRLI PCRPQFISDRVQQDDLVRCGKKCRLVLVPERADVILMPERRHID AFRTRRCCTSIAGLIYAVGGLNSAGDELNVVEVPPIPLANCWER CRPNTTANSRNSAAQVVTVFGEIVYJGGHDGLEISTVQANTHTOTD WTRVGSMNSKSAMGTVVLDQIIVVGGYDGNSSLSSVETYSPE TDKWTVVTSMSNSKSAAQVTVFGEIVYJGGHDGGLIFSSVEN YNHHTATWHPAAGMLAKKCRIGAASLGSKMPVCGGVDGSGFLSI ABMYSSV_ADQWCLLVPPM HTMR Q RSVELGGPAVGRLYAVWGVT TGQSBLASSUGDLIPPTOCWTFM\APMACKEGGVGGCIPLLT I  5429 828 202 REBDALSSEGCLAPBESTYSGNGIPPPQVYAPPRPPDRLAVPPP AQREFYHRFQPTYPYLQHEIDLPPTISLSDGEBPPPYQGPCTLQ LRIPPRQQLELMRSSVRAPPNRTIFDSJAMDSARLGGPCPPSSNS GISATCYGSGGRNEGPPP\TYSSVIGHTPGSSPGNGSGPPSL LGGTRUHHTHALLESAALBSKEKKQKGHBD  5430 441 1507 GKRRKRRKKIMKTIDPKNINSISMAIPTGLAALC-FÇGVPVKS GISATCYGSGGRNEGPPP\TYSSVIGHTPGSSPGNGSGPPSL GONDATPYKAMDNIVTVRQGSSATLACTIDMXVALINNSSTILVA GNDKWCLDPRVVLLSNTGTQYSIELGNVDVYDEGPYTCSQVTNN HPKTGSVALITVQVPSKIVETSSISISINGNISLTCTIATGPRP TVTWRHISPKAVGPVSEBEVLEIQGITREGGGDVEGSSNDVA APV\VBRVVLTVVPPPYSEBAKTGVPVPGKGTLGCGASAVPGA EFOWYNDKALIJFGGAVSESNGTSRRAGCVWLLPLLVL LLLKP  AARAPGSRRRPLPDPRPMAHGYEAPPPPARRSPAWRARSKEVV CVASNKLGHTNASIMLFGGAVSEVSGTSRRAGCVWLLPLLVL LLLKP  AARAPGSRRRPLPDPRPMAHGYEAPPPPPARRSPAWRARSKEVV CVASNKLGHTHASINLFGGAVSEVSGTSRRAGCVWLLPLLVL LLLKP  AARAPGSRRRPLPDPRPMAHGYEAPPPPPARRSPAWRARSKEVV LPGITTINP\TTAGGSPP\TSEGASSANLVVLOKKLEELELDEGO KKRLBAFLTOKAKVGELKDDDFRRISELGAGNGGVVTKVQHRPS GLIMARKLIHLBIKPAIRNQIIRELQULHSKGVILVGHRSB TVTRSYMAPPELQGTHYSVQSDINSMGLSLVELAVGRYPIPPP DAKELAFLTOKAKVGELKDDDFRRISELGAGNGGVVTKVQHRPS GLIMARKLIHLBIKPAIRNQIIRELQULHSCHVSCHVIPPS GLIMARKLIHLBIKPAIRNQIIRELQULHSCHVSCHVIPPS GLIMARKLIHLBIKPAIRNQIIRELQULHSCNSPTVYCHPRS GLIMARKLIHLBIKPAIRNQIIRELQULHSCNSPTVYCHPRS GLIMARKLIHLBIKPAIRNQIIRELQULHSCNSPTVYCHPRS GLIMARKLIHLBIKPAIRNQIIRELGVARSPVNKCLIKNPAERA DLAMLINHTTIRASSVESUPPAGMLCKTLERLOQDITHRTAV YLERHQIMIRDVKSSIILVUNSGBIKLCDFGAVVTKCLIKNPAERA DLAMLINHTPIRRSSVLSVYDSDINGNGLGATGADACVEKQDISMAS FVOTRSYMAPERLQCTHTWYNSDINGHLGWATGATGADACVEKGHDSRP AMAIF		1		LVHFSVSELPSRGYGVMEEIRRQGKLCDVTLKIGDHKFSAHRIV
NLATDOONVOSLIMGAS FLOUGS INDACKSTRANDERSHAPLEDULSI. ROPAETIMKOAT VIDANAS PINGHPEVENSEFLAIPLEDULSI. VSRDELNVESEGOVERALAMUR VDRORGGTFL\RILGGNIRLI. FCRRQFLSROWQDDLVRCKIKCRULVDENDUTALIMPERRPHILE AFRIR PROCTS I AGLI YAVGGLNSAGDSLRVVEVFDP LANGER CRPHITARSRYGVAVNGLLIZAGGOTDGLELSTVQANTRETDI WTROSMINS KRSAMGTVVLOGQI YVGGEYGONSSISSVETYSER TDLKYTVITSMSNRSAN GVIVVEGRIYVSGGHOGLIFSSVEN YNHHITATHPRAGMAINKEGRGASLGSHAWVCGGYDGSGFLSI ABMYSSV\ADDWCLTVPM\HTRR\SRVSIGGPAVGGLISTSVEN YNHHITATHPRAGMAINKEGRGASLGSHAWVCGGYDGSGFLSI ABMYSSV\ADDWCLTVPM\HTRR\SRVSIGGPAVGGLISTSVEN YNHHITATHPRAGMAINKEGRGASLGSHAWVCGGYDGSGFLSI ABMYSSV\ADDWCLTVPM\HTRR\SRVSIGGPAVGGLISTSVEN YNHHITATHPRAGMAINKEGRGASLGSHAWVCGGYDGSGFLSI ABMYSSV\ADDWCLTVPM\HTRR\SRVSIGGPAVGGLISTSVEN YNHHITATHPRAGMAINKEGRGASLGSHAWVCGGGVGCGLISTSVEN ARBABLSBEGCLWPGBSTVSGNGIPEPQVVAPPPTDRLAVPPF AQRERPHRFQFTYPYLOHELDLPPTISLSDGEBPPPYGGFCTLO LEGTRIHHTHIH ALLERSAL HISKEKKDKOKGHDL LEGTRIHHTHIH ALLERSAL HISKEKKDKOKGHDL LEGTRIHHTHIH ALLERSAL HISKEKKDKOKGHDL GRANDENDEN TENGHOSSGFPBL LEGTRIHHTHIH ALLERSAL HISKEKKDKOKGHDL GRANDEN TENGHOSSGFPBLIVAN GDATPPKAMGENVTVRGBSATLACTIDINGTVALINGSINGTILVX GNDKWCLDPRVVILGNTQYSISIQNVVYDEGPETTCSVQTINN HPKTSRVILLVQVSRCIVALISSDISIMSGNISLITLATGRPRP TVTWHHIIS SPRAVOFVSBEDELBLGQITRESGGYPSCSANSDV\A APV\VERKVATVHYPPYISEAKGTGVPVGGKGTLQCESAVPSA EFGWYEDDKAL JECKGVVERNPFISK HIPVSSGHDVSNTT CVASNKLCHTINAS JILLFGPGAVSEVSNOTSGRRGCVMLVELVLU LLLLKY  SHADIL JECKGVVERNPFISK HIPVSSGHDVSNTT CVASNKLCHTINAS JILLFGPGAVSEVSNOTSGRRGCVMLVELULU LLLLKY LLLLLE SHADIS JECKGVVERNPFISK HIPVSSGHDVSNTT CVASNKLCHTINAS JILLFGPGAVSEVSNOTSGRRGCVMLVELHLU LLLKY SDGEIS I GMEHDDOGSLDQULKEAKRI PEBILLGKVS LAVLRGLA YLEKKQIMHRUVRSDILLVNSRGBIKLCDFSVGQLI DSMANS FVOTRSYNADSERLQCHTHYSVQGDLYBANGLICLDEGO KKELEAFTCVKAVGELEDDOFFRISELGAGNGGVVTKVQHRPS GLIMARKLIHLEIKPARNOLI SERLUGHTENDYTVOFYGAPY SDGEIS I GMEHDDOGSLDQULKEARRI PEBILGKVS LAVLRGLA YLEKHQIMIRDVKSSRILLVNSRGBIKLCDFGYGGLIDBMANS FVOTRSYNADSERLQCHTHYSVQGDLYBANGCVTRVGHRPS GLIMARKLIHLEIKPARNOLIKRARGEPFOTFRTAV AAAAGNGERREPLPDPROHMAGVSEAPDFOTHERAVOPTPRTAV YLEKHQIMIRDVKSSRI	1		}	
ROPAETMMCAULTURANSFIRIOHEVEVSMSEETHALPLEDVLEI.  VSRDEINVSEEDUPEALAUVAT DREROFFIL\RILGSTRILL  FCR9GLSDRVQCDDLVRCCHKCEDLVDEARDYLLAPPERBHLE  AFRTRPRCCTS IAGLIYAVGGLNSAGDSLRVVLAPPERBHLE  AFRTRPRCCTS IAGLIYAVGGLNSAGDSLRVVLAPPERBHLE  AFRTRPRCTS IAGLIYAVGGLNSAGDSLRVVLAPPERBHLE  TOKUTVUTSMSSNRSAA, GVVTVEGGIVTGGLSTVQANTHETOT  WTRVSSMSKRSAMGTVVLDGQIYVCGGYDGNSISSVETYSEE  TOKUTVUTSMSSNRSAA, GVVTVEGGIVTGGLGLSTVQANTHETOT  WTRVSSMSKRSAMGTVVLDGQIYVCGGYDGNSISSVETYSEE  TOKUTVUTSMSSNRSAA, GVVTVEGGIVTGGLGLSSVETYSEE  ARMYSSV\ADQUCLIVPH\HTMR\SKSUGDAVGRLYAVWGVT  TGGSBL\SSVGDVLTPETTCTTM\APMACKEGGVEVGGLYAVWGVT  TGGSBL\SSVGDVLTPETTCTTM\APMACKEGGVEVGGLYAVWGVT  TGGSBL\SSVGDVLTPETTCTTM\APMACKEGGVEVGGLYALTI  1  5429  828  202  RREDALSSEGCLWPBESTVSGNGIPEPQVYAPPEPPDLAVPPF  ARREFHRIPPOTYPTVALDELDLPTISLSDGERPPPYGFOTLO-  LRIPEGQLEIANRSVVALPRITTEDDLMDSALLGGPQCPPSSNS  GISATCYGSGGRMEGPPP\TYSEVICHYPGSSPDPLAVPPG  GRARKRRRKIMMTIDFKNINSISWATPTGLAALCEPGOVVKS  GISATCYGSGGRMEGPPP\TYSEVICHYPGSSPDYGSGPPSS  GISATCYGSGGRMEGPPP\TYSEVICHYPGSSPDYGSGPPSSOPSIS  GORTFFKAMGNVVVLQOSATLACTIONEVRVALBINSTILLY  GNDKWGLDPRVVLLSNTQTOYSIELIQNDVVIDGBGPTVTGVQTVRS  GORTFFKAMGNVVVLQOSATLACTIONEVRVALBINSTILLY  HENGRVÄLLVQVSKIVLISSISIISMGNISLTCIATIONEPP  TVTWRHISPRAVGFVSEDEVLEIQGTTREGGGIYEGSSNIDV\A  APPV\VERVVLVVIYPPYSESSISIISMGNISLTCIATIONEPP  TVTWRHISPRAVGFVSEDEVLEIQGTTREGGGIYEGSSNIDVA  APPV\VERVVLVVIYPPYSEAKATOVYTOVSESSISIISMGUSLDLLLLLL  LLLKY   4AAAPGSRRRRPLPDRPHMAHGYEAPPPFARFSFAWRARSKFVV\  LPGITTINY\TLAGGSSP\TSEGASSANLVOLGKKLEELELDEGG  KKELBAFLTCKAKVGELKDDDFRRISLGAGNGGVVTVCHHRS  GLIMARKLIHLEIKPAIRNGLIREGLHSISSIGNINGVTVTCHHRS  FVGTRSYMAPBELGGTHYSVGSDINSMGLSLVELAVRGILA  YLEEKHQIMIRDVKSSGILLVINSKGEIKLCDFGGVVIKCHKRIPS  GLIMARKLIHLEIKPAIRNGLIREGLUHCSNSPITVGPTGAPY  SOGEISICMERMGGSSLDQVIKSAKRIPEELIGKVSIAVLRGILA  YLEEKHQIMIRDVKSNILVNSKGEIKLCDFGGVVIKCHRPS  GLIMARKLIHLEIKPAIRNGLIREGHAISSPRPEPPEPPAPRSFRAWRASKFVV  LPGITTINY\TIAGGSPVTGSBERBETJGHTPPPPAPRSFRAWRASKFVV  LPGTTINY\TIAGGSPVTGSBERBETJGHTPPPPAPRSFRAWRASKFVV  LPGTTINY\TIAGGSPVTGSBERBETJGHTPPPPAPRSFRAWRASKFVV  SOGEISICMERMGSSLDQVIK	i	J	]	
VSEDELMVESEGOVERALAMVENGEGTFLANNLGSNITRLI  FCRROFLSDRVQODLURCHKCRDLUPREAVDYLLMERRERHLE  AFRTRRCCTSIAGLIYAVGGINSAGDSLNUVEVPDPIANCHER  CRPHTTARSRVGVAVVALGGINYGGYDGNSSLSSVETYSEE  TDKWTVVTSMSSNSRAA\GVTVFEGRIYVSGGHOSSLSSVETYSEE  TDKWTVVTSMSSNSRAA\GVTVFEGRIYVSGGHOGSSLSSVETYSEE  TDKWTVVTSMSSNSRAA\GVTVFEGRIYVSGGHOGSSLSSVETYSEE  TDKWTVVTSMSSNSRAA\GVTVFEGRIYVSGGHOGSSLSSVETYSEE  TDKWTVVTSMSSNSRAA\GVTVFEGRIYVSGGHOGSSLSSVETYSEE  TDKWTVVTSMSSNSRAA\GVTVFEGRIYVSGGHOLGIFSSVEH  YNHHIATMIPAAGHINKRCRHAAASLSHKMPYGGYDDSGFLSI  ABMYSSV\ADOWCLIVPM\HTRR\SRVSLGGPAVGRLYAWGVT  TGQSEL\SSVGDVLTPFTDCWTFM\APMACHEGGGVOGCIPLLT  I  5429  628  202  REBEALSSEGCLMPSSETYGGGIFEPQVVAPPRFTDELAVPPF  AQRERFHRFQPTYPYLQHEIDLPPTISLSDGBEPPPYQGPCTLQ  LRDPEQQLEIARRSVRAPPNRTIFDSLDMDSARLGGCPPSSNS  GISATCTGSGGRMEGPP\TYSEVIGH YFOSSFGHOQSSGPPSL  LEGTRLHHTHIALLESAATWSREKOKKKGHBL  COKREKERRKIMKTIGGHEPQVVAPPRFTDLAVPPF  AQRERFHRHHIALLESAATWSREKOKKKGHBL  GERTPFKAMDRVTURGGSSATLRCTIDNRUTRVAHLINSTILVA  GDATFFKAMDRVTURGGSSATLRCTIDNRUTRVAHLINSTILVA  GDATFFKAMDRVTURGGSSATLRCTIDNRUTRVAHLINSTILVA  GDATFFKAMDRVTURGGSSATLRCTIDNRUTRVAHLINSTILVA  GDATFFKAMDRVTURGGPAVSEVSHSGOVFEGSNDV\A  APV\VRZVKVVTVNYPPYISEAKGTGVPVQGKGTLQCSSASVPSA  EFQWIKDDKRLI\FGGAVSEVSHGAGGGVYTKVSDUTN  HPKTSRVHLIVQVSPKIVSISSDISINGRNISLICTATGRPEP  TVVTRRIISFKAMGFVSEGGAVSEVSHRAFGSGOVFECSASVPSA  EFQWIKDDKRLI\FGGAVSEVSHGAGGGVYTKVGHTSB  GLIMRKLIHLEIKPAIRNGILRELQULHECNSPYIVGFYGAFY  SOGELSICHEHUNGGSLQQVIKKAKRIPELGKVSIAVLRGLA  YLREKG\UHHDLVKPSNITIVNSRGGELKLDFROVSGQLIDSMANS  FVGTRSYMAPBRLQGTHYSVQSDIWSGGLSGUVSTAVKLKNBARRA  DLAMILTNITFIKRSVERVPRABGLGVEARARVELKLKNBARRA  TVLFREHQTIMIRDVKPSNITIVNSRGGLKLKLDRFOVSGQLIDSMANS  FVGTRSYMAPBRLQGTHYSVQSDIWSGGLSGUVSTAVQHEPS  GLIMARKLIHLBIKPAIRNQIIRELGGRAGGGVVTKVQHRPS  GLIMARKLIHLBIKPAIRNQIIRELGGRAGGGVVTKVQHRPS  GLIMARKLIHLBIKPAIRNQIIRELGGRAGGGVVTKVQHRPS  GLIMARKLIHLBIKPAIRNQIIRELGGRAGGGVVTKVQHRPS  GLIMARKLIHLBIKPAIRNQIIRELGGRAGGGVVTKVQHRPS  GLIMARKLIHLBIKPAIRNGIIRELGGRAGGGVVTKVQHRPS  GLIMARKLIHLBIKPAIRNGIIRELGGRAGGGVVTKVQHRPS  GLIMARKLIHLBIKPAIRNGIIRELGGRAGGGVVTKVQHRPS  FVGTTSYMAPPRLQGTH	1	[	l	
### PCRPQFLSDRVQQDDLVRCCHKCRDLUDERARDYLLMPERRPHLP ### AFRCTRECTS IAGLI YAVQGIDASQUAVUSVEVED PLANCHER ### CRPMTTARSRVQVAVVNGLLYAIGGYDGVGUSSISSVETYSEE ### TOWNTVYTHASSNESSA, CVITYEER IT VYSGGHDGLQIFSSVEH ### TOWNTVYTHASSNESSA, CVITYEER IT VYSGGHDGLQIFSSVEH ### YNHHTATH# PAAGHLNKRCCHGASALGSKMFVCGGYDGSGFLSI ### AEMYSSV, ADQWCLIVPW HTRRY, SYRUGGAVORGLYAWGUT TGQSNL\SSVGDVLTPETDCWTFM\APMACHEGGVGVGCIPLLT I  5429  628  202  **REDALSSEGCLWPSESTVSGNGIPEPQVVAPPRPTDRLAVPPF AQRER PHREQET YSTLCHBIDLIPPTISLSDGESPPPTQGFCTLQ LRDPEQGLERRESVARAPNRTIFEDSJMDSARLGGPCDPSSNS GISATCYGSGGRMGGPPP\TYSEVIGHYDGSSFOHQOSGCPPSL LEGTRLWHHTAPLESSATUSKENGKGFD  5430  441  1507  GKRKRRRKKIMKTIQDKHINSISWALPTGLAALC-FGGVVVRS GDATPFKAMDWVTVGGGSSATLRCTIDAYTWAWALINSTILVA GNDKWCLDFRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDN HPKTSVYLLIVQSPKIVNSISSATISTICATGREFSP TVTWRHISPKAVGGVSEBSYLEIGGITRESSGDYECSASNDVA APV\VERVKVTVWYPPYISEAKGTGVVVGGKGTLQCSASAVPSA EFGWYKDDKRLI/BGKKGVVENNEPPSTREDSHOTEGSANDVA APV\VERVKVTVWYPPYISEAKGTGVVVGGKGTLQCSASAVPSA EFGWYKDDKRLI/BGKKGVVENNEPPSTRESSGDYECSASNDVA APV\VERVKVTVWYPPYISEAKGTGVVVGGKGTLQCSASAVPSA EFGWYKDDKRLI/BGKGVVENNEPPSTRESSGDYECSASNDVA APV\VERVKVTVWYPPYISEAKGTGVVVGGKGTLQCSASAVPSA EFGWYKDDKRLI/BGKGVVENNEPPSTRESSGDYECSASNDVA APV\VERVKVTVWYPPYISEAKGTGVVVGGKGTLQCSASAVPSA EFGWYKDDKRLI/BGKGVVENNEPPSTRESSGDVENGASAVPSA  **EFGWYKDDKRLI/BGKGVVENNEPPSTRESSGDVENGASAVPSA **EFGWYKDDKRLI/BGKGVVENNEPPSTRESSGNVVA APV\VERVKVTVWYPPYISEAKGTGVVVGGKGTLQCSASAVPSA **EFGWYKDDKRLI/BGKGVVENNEPPSTRAWRARSKEV\ LPGITINN\TTASGPSP\TSEGSASEANLVDLCKKLEBLELDEGQ KKELEAFLTQKAVGGLEDDDFREISELIGKVSIAVUGHRS GLIMARKLIHLBIKPAIRNQIIRELGVLECHSPYIVGFYGRPY SDGEISIGMEMDGGSGLOVLKEAKRIPELIGKVSIAVUGHSS GLIMARKLIHLBIKPAIRNQIIRELGVLEKLERUFTRAV **JREGKLQTHYSVQSDIMSMGLSLVELAVGRYPIPPP DAKELBAITGRAWGGLOVLKEAKRIPELIGKVSIAVUGFGPY SDGEISIGMEMDGGSLDQVLKEAKRIPELIGKVSIAVUGFGPY **SDGEISIGMEMGGSLDQVLKEAKRIPELIGKVSIAVUGFGPY SDGEISIGMEMGGSLDQVLKEAKRIPELIGKVSIAVUGFGPY **SDGEISIGMEMGGSLDQVLKEAKRIPELIGKVSIAVUGFGPY **SDGEISIGMEMGGSLDQVLKEAKRIPTYGFYGFFY **DDGEISIGMEMGGSLDQVLKEAKRIPETLIGKVSIAVUGFGPP **DDA	1		l	1 7
AFFTRERCCTS INGLIVANGGINAGGDELNVERUPDIANCWER CREMTTARSRUVANVINGLIVAIGGYDGURLSTVQAYNTETDT WTRYGSMINSKRAMSTVULDGITYUGGYDGURSTSUSTYSPE TDKWTVVTSMSSINSAA\GVTUPEGRITYUGGGDGUSSLSSUSTYSPE TDKWTVVTSMSSINSAA\GVTUPEGRITYUGGGDGUSSLSSUSTYSPE TDKWTVVTSMSSINSAA\GVTUPEGRITYUGGGDGUSGLSI AEMYSSV\ADQWCLIVPM\HTRR\SRVELGGPAVGRIYAVWGVT TGQSIL\SVGVGUTUPETCOTFM\ADGREGGGVUCTPLIT I  5429 628 202 RREDALSEGGLWFSESTVSGNGTEPQVVAPPRFTDRLAVPPF AQRER PHRROPTYPYLQHEIDLPPTISLSGSEPPPYQGPCTLQ LRDPEQQLELMRESVRAPPNRTTPDSDLMDSARLGGPCPPSSINS GISATCYGSGGRMEGPPYTYSTUGHFDSDLMDSARLGGPCPPSSINS GISATCYGSGGRMEGPPYTYSEVIGHFDGSRGRGGVUCTGVGS GDATFFKAMDNVTURQSSATLRCTIDNRVTRVAHLNSTILVA GDATFFKAMDNVTURQSSATLRCTIDNRVTRVAHLNSTILVA GDATFFKAMDNVTURQSSATLRCTIDNRVTRVAHLNSTILVA GNDKWCLDRPVULLSNTQTQSSISTINGGNISLICIATGRPEP TVTWRHISPKAUGVSERBYLEIGGITREDSGDYECSASNOV\A APV\VERVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSA EFQWKDDKALL\SGKKGVKURNFPLSKLIFFNVSSHDYGNT CVASNKLSHTTASIMLFGGGAVSEVSGRAFGAGCVELLFLLVL HLLLKF AAAAGGSRRRPLDDRFHHAHGYEAPPPPAPRSPAWRARSKPV\ LPGITTINY\TTASGPSP\TSGASGSANLVDLQKKLEELELDEQQ KKRLERFITQSKAYGGLIADDFERISAGGGGVVTKVGHRPS GLIMARKLIHLBIKDAIRNOIIRELGULGKSSPVIUGFYGAPY SDGEISICMEHMOGGSLDQVLKEAKRIPELIGKVSIAVURGLA YLREKGIMHEDVRSNILVNSRGGIKLCLDFOVSGQLIDSMANS FVOTRSYNAPERLQGTHYSVQSDLWSMGLSJUPLAVGRYPIPPP DAKELGAT FGGFVVOGEGEBPHSISTPPPPROFRVSHGMDGRP AMAIFELLDYIVNSPPPKLPMOYFTDFGEFVNKLIKNPBERA JLMMLTNITFIKRSCEBERDFSGEBPHSISTPPPPROFRVSHGMGRGF ANAIFELLDYIVNSPPPKLPMOYFTDFGEFVNKLIKNPBERA JLMMLTNITFIKRSCEBERDFSGEBHSISTPPPPRAFRSKEFYV LPGITINY\TIABGPSP\TSRGASEANLVDLQKKLEBLELDEQQ KKRLBRFLTGKAVGELGDULKEAKRIPELIGKVSIAVLRGIA YLREKGIMHEDVRSNILLVNSRGEIKLCDFGVSGQLIDSMANS FVOTRSYNAPERLQGTHYSVQSDLWSMGUSLUFLAVGRYPIPP DAKELGAIFTGRAVGGEBPHSISTPPPPROFRVSHGMGRGF YLDREHGGMGGSDDVAKCKKIPETELIGKVSIAVLRGIA YLREKGTMHEDVRSDILLVNSRGEIKLCDFGVSGCLIDSMANS FVOTRSYNAPERLGGTHYSVQSDLWSMGUSLUFLAVGRYPIPP DAKELGAIFTGRAVGERGEBPHSISTPPPPPROFRVSHGMGRGF AMAIFELLDYIVNDERPLOQUVLKEAKRIPETLIGKVSIAVLRGIA YLREKGTMHEDVRSDILLVNSRGEIKLCDFGVSGCLIDGUGRF AMAIFELLDYIVNDERPLOQUVLTGRAFGFFOWNCLIKNFRARG FVOTRSYNAPERLGGTHYSVQSDLWSMGUS		1		
CRPMTTARSRVSTAVVNICLLYALIGGYDGOLRLSTVQAYNTETDT WTRVGSWMKKRSAMTVVLDQI YCGGYDGNSSLSSVETYSPE TDKWTVVTSMSSNRSAA\GVTVFEGRIYVSGGHDGLJIFSSVEH YNHHTATWHFAAGMLNKKCKHRAASLGSMRWCGGYDGSGFLSI AEMYSSVADQWCLTVPM\THTR\SRVSLGGBAVGRLYAWGYT TGQSNL\SSUGPULTPETDCWTFM\APMACHEGGVGVGCIPLIT I  5429 628 202 RREDALSSEGCLWPSESTVSGNGIPEPQVYAPRFTDRLAVPPF AQRER PHRROPT?PYLQMEIDLPPTISLSDGEEPPPYVQGPCTLQ LRDPEQQLELARESVRAPPRRTIFDSDLWDGARLGGCCPPSSNS GISATCYGSGGRMEGPPP\TYSRVIGHYGESFGHQQSSGPPSL LEGTRLHHHTAPLESAATUSKKKOKGHBL  5430 441 1507 OKREKBRRKKIMKTIQPKHINSISWAIPFGLAALCLFGGVPVSS GDATFFKAMDNITVGQESATLRCTIDNRVTRVAWLINRSTILVA GNOKWCLDPRVVLISNTQTQYSIEIQNVDVDEGPYTCSVQTDN HPYTSRVHLIVQVSPKLVEISSDISINEGNISLTCIATGRPEP TVTWRHISPKAUGVVSPKLVEISSDISINEGNISLTCIATGRPEP TVTWRHISPKAUGVVSREPPLSKLIFFWSSHDYGNYT CVASNKLGHTMASIMLFGGAVSEVSNGTSRRAGCWWLLPLUL HLLKF  5431 2 1312 AAAAFGSRRRRFLDPRHMAHGYEAPPPARSDAWRANSKPV LPGITINP\TIAEGPSP\TSEGASEANLVDLQKKKLEELEDEQQ KRELEAFLTQKAKWGELKDDDFERISELGAGNGGVVTKVQHRPS GLIMARKLIHLEIKPAIRNOIIRELQVLHECNSPYIVGFYGAFY SOBEISICMEHMOGSLDQVLKEARGLSVELAWGYPYPIPT DAKELAIFGRPVVDGEEGEPHSISPRPPPGRPVSGCHIDNRANS FVOTRSYMAPERLQGTHYSVGSDINGLSVELAWGYPYPIPT DAKELAIFGRPVVDGEEGEPHSISPRPPPGRPVSGCHIDNRAR FVOTRSYMAPERLQGTHYSVGSDINGLSVELAWGYPYPIPT DAKELAIFGRPVVDGEEGEPHSISPRPPPGRPVSGCHIDNRAR FVOTRSYMAPERLGGTHYSVGSDINGLSVELAWGYPYPPP DAKELAIFGRPVDGEEGEPHSISPRPPPGRPVSGCHIDNRANS FVOTRSYMAPERLGGTHYSVGSDINGLSVELAWGYPYPPP DAKELAIFGRPVDGEEGEPHSISPRPPPGRPVSGCHIDNRANS FVOTRSYMAPERLGGTHYSVGSDINGLSVELAWGYPYPPP DAKELAIFGRPVDGEEGEPHSISPRPPPPGRPVSGCHIDNRANS FVOTRSYMAPERLGGTHYSVGSDINGLSVELAWGRYPIPPP DAKELAIFGRPVDGEEGEPHSISPRPPPPGRPVSGCHIDNRANS FVOTRSYMAPERLGGTHYSVGSDINGLSVELAWGRYPIPPP DAKELAIFGRPVDGEEGEPHSISPRPPPGRPVSGCHIDNRANS FVOTRSYMAPERLGGTHYSVGSDINGLSVELAWGRYPIPPP DAKELAIFGRPVDGEEGEPHSISPRPPPGRPVSGCHIDNSRP AMAIPELLDYIVNBPPPKLPNOYFPPDFGFPVKCLIKPPAFA SDGEISICMEHMOGGSLDQVLKEARRILSVELAWGRYPIPPP DAKELAIFGRPVDGEEGEPHSISPRPPPGPRPSVSGCHODSRP AMAIPELLDYIVNBPPPKLPNOYFPPDFGFPVKCLIKPPAFA SDGEHSIFPHPPPROFFFVKLOCGPGFTSTAV  SVGENGVFFFEDFIHLCSWARARCPCTFFFEC/CGGLECGFAGV LYGHCMFFFEDFIH	l	i	]	
#TRYGSMNSKRSAMGTVULDOQI TVCGGYDGNSSLSSVETTSEE #TDKWTVVTSMSSNRSAA\GVTVPEGRITVSGGHDGLQIFSSVEH YNHHTATWHPAAGHINKKCHGAASIGSKMFVCGGYDGSGFLSI AEMYSSV\ADQWCLIVZM\HTRR\SRVSIGGGAVGKLYAVWGVT TGQSBL\SSVGDVITPETDCATEM\APMACHEGGUGGCTPLIT I  5429 628 202 RREDALSSEGCLWPSESTVSGNGIPEPQVYAPPRFTDRLAVPPF AQRER FHRFQPTYPYLQHEIDLPPTISLSDGEEPPPYQGPCTLQ LRPPEQQLELMRESVRAPPRRTIFDSDLWDGSARIGGCPPSSNS GISATCYGSGGRMEDPPP\TYSSVIGHYBGSSFGHQGSGOPPSL LEGTRLHHTHIAPLESAAIUSKEKUKQKCHI  5430 441 1507 OKRRKRRKKIMKTOPNHINGISMATIFGLAAUCLFGGYPVRS GDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLMRSTILVA GNDKWCLDPRVVLLSNTQTQYSIBIQNVDVYDGBPYTCSVQTDN HPKTSRVHLIVQVSPKLVSISBISIBRGNNIGHTCHATGREPP TVTWRHISPKAVGFVSSBDEVLEIQGITREQSGDYCCSASNDVSA APV\VERVEVTVTNYPPYISEAKGTGPVGQKSTTQCSASNPSA EFGWYKDDKRLI/EKKKOVENRPPLSRLIFFFVSSHDYGNYT CVASNLUGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVL HLLLKP  5431 2 1312 AAAAFGSRRRRPLPDRHMAHGYEAPPPPAPRSBWRARSKEV\ LEGITINP\TTAEGFSY\TSGLGAGNGGVVTKVOHRPS GLMARKLHLBIRDAIRNOITBELJJECNSVIVYGYGAPY SDGEISICMEHMDGGSLDQVLKEAKRIPEELIGKVSIAVLRGLA YLREKQIMHRDVKPSNILVNSRGBIKLCDFGVSGQLIDSMANS FVOTRSYMAPERLQGTHSVGSDINGLSVELAVGRYPIPPP DAKELBAIFGRPVVDGESGEBHSISPRPPPGRPVSGHGMDSRP ANAFPELLDTYVNEPPFKLPNGVFDFDFOEFVINCLIKPBARA DLKMLTNHTFIKRSEVEEVDFAGWLCKTLRLNOPGTPTRTAV  5432 2 1312 AAAARGSRRRPLPDRRHMAHGYEAPPPPARFSRWRARSKEV\ LEGITINP\TTAEGFSP\TSGLSGARNLJOLQKKLBELBLDGQQ KKRLBAFLTQKAKVGELKDDFFRISELGAGNGGVVTKVQHRPS GLMARKLHLHLEIKPAFRNGITERCHLSVELSVELAVGFTGFFF SDGEISICMEHMDGGSLDQVLKEAKRIPEELIGKVSIAVLRGLA YLREKGUMHRDVFSNILVNSRGBIKLCDFGVSGQLIDSMANS FVOTRSYMAPERLQGTHSVGSDLIMECNSPIVYGYGAFY SDGEISICMEHMDGGSLDQVLKEAKRIPEELIGKVSIAVLRGLA YLREKGUMHRDVKPSNILVNSRGBIKLCDFGVSGQLIDSMANS FVOTRSYMAPERLQGTHTSVGSDLIMECNSPIVYGYGAFY SDGEISICMEHMDGGSLDQVLKEAKRIPEELIGKVSIAVLRGLA YLREKGUMHRDVKPSNILVNSRGBIKLCDFGVSGQLIDSMANS FVOTRSYMAPERLQGTHTSVGSDLIMECNSPIVGTGGGGGGGFG GLMARKLHHLINGTFIKRSEVEEVDPRAGMLCKTLRLNOPGTPTRTAV SDGEISICMEHMDGGSLDQVLKEAKRIPEELIGKVSIAVLRGLA YLREKGUMHRDVKPSNILVNSRGBIKLCDFGRPSGGGGGGGDGFF DAKELBAIFGVTGGGGGGGGGFGFGGGGGGGGGFGGGGGGGGGGGGG	I	!		AFRTRPRCCTSIAGLIYAVGGLNSAGDSLNVVEVFDPIANCWER
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AMAIFELLDYIVNEPPPKLPNGVFTPDFQEFVNKCLIKNPAERA DLKMLTNHTFIKRSEVEEVDFAGWLCKTLRLNQPGTPTRTAV  AAAAPGSRRRPLPDRPHMAHGYEAPPPPAPRSPAWRARSKPV\ LPGITINP\TIAEGPSP\TSEGASEANLVDLQKKLEELEDEQQ KKRLEAFLTQKAKVGELKDDFERISELGAGNGGVVTKVQHRFS GLIMARKLIHLEIKPATRNQIIRELQVLHECNSPYIVGFYGAFY SDGEISICMEHMDGGSLDQVLKEAKRIPEEILGKVSIAVLRGLA YLREKHQIMHRDVKPSNILVNSRGEIKLCDFGVSGQLIDSMANS FVGTRSYMAPERLQGTHYSVQSDINSMGLSLVELAVGRYPIPPP DAKELEAIFGRPVVDGEEGEPHSISPRPPPGPFVSGHGMDSRP AMAIFELLDYIVNEPPPKLPNGVFTPDFQEFVNKCLIKNPAERA DLKMLTNHTFIKRSEVEEVDFAGNLCKTLRLNQPGTPTRTAV  5433 360 1885 SVQEDKVGFEDPLHCSWRARACFCTWPHC/CTGLLECLGFAGV LFGWPSLVFVFKNEDYFKDLCGPDAGFIGNATGQADCKAQDERF	1 1			FVGTRSYMAPERLQGTHYSVQSDIWSMGLSLVELAVGRYPIPPP
AMAIFELLDYIVNEPPPKLPNGVFTPDFQEFVNKCLIKNPAERA DLKMLTNHTFIKRSEVEEVDFAGWLCKTLRLNQPGTPTRTAV  AAAAPGSRRRPLPDRPHMAHGYEAPPPPAPRSPAWRARSKPV\ LPGITINP\TIAEGPSP\TSEGASEANLVDLQKKLEELEDEQQ KKRLEAFLTQKAKVGELKDDFERISELGAGNGGVVTKVQHRFS GLIMARKLIHLEIKPATRNQIIRELQVLHECNSPYIVGFYGAFY SDGEISICMEHMDGGSLDQVLKEAKRIPEEILGKVSIAVLRGLA YLREKHQIMHRDVKPSNILVNSRGEIKLCDFGVSGQLIDSMANS FVGTRSYMAPERLQGTHYSVQSDINSMGLSLVELAVGRYPIPPP DAKELEAIFGRPVVDGEEGEPHSISPRPPPGPFVSGHGMDSRP AMAIFELLDYIVNEPPPKLPNGVFTPDFQEFVNKCLIKNPAERA DLKMLTNHTFIKRSEVEEVDFAGNLCKTLRLNQPGTPTRTAV  5433 360 1885 SVQEDKVGFEDPLHCSWRARACFCTWPHC/CTGLLECLGFAGV LFGWPSLVFVFKNEDYFKDLCGPDAGFIGNATGQADCKAQDERF	, , ,			DAKELEAIFGRPVVDGEEGEPHSISPRPRPPGRPVSGHGMDSRP
DLKMLTNHTFIKRSEVEEVDFAGWLCKTLRLNQPGTPTRTAV  5432  2 1312  AAAAPGSRRRRPLPDRPHMAHGYEAPPPPAPRSPAWRARSKPV\ LPGITINP\TIAEGPSP\TSBGASEANLVDLQKKLBELEDEQQ KKRLEAPLTQKAKVGELKDDFERISELGAGNGGVVTKVQHRPS GLIMARKLIHLEIKPAIRNQIIRELQVLHECNSPYIVGFYGAFY SDGEISICMEHMDGGSLDQVLKEAKRIPEEILGKVSIAVLRGLA YLREKHQIMHRDVKPSNILVNSRGEIKLCDFGVSGQLIDSMANS FVGTRSYMAPERLQGTHYSVQSDIWSMGLSLVELAVGRYPIPPP DAKELEAIFGRPVVDGEEGEPHSISPRPPPGRPVSGHGNDSRP AMAIFELLDYIVNEPPPKLPNGVFTPDFQEFVNKCLIKNPAERA DLKMLTNHTFIKRSEVEEVDFAGMLCKTLRLNQPGTPTRTAV  5433  360  1885  SVQEDKVGFEDPLHCSWRARACPCTWPHC/CTGLLECLGFAGV LFGWPSLVFVFKNEDYFKDLCGPDAGFIGNATGQADCKAQDERF	j i			
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LPGITINP\TIAEGPSP\TSEGASEANLVDLQKKLEELELDEQQ KKRLEAFLTQKAKVGELKDDDFERISELGAGNGGVVTKVQHRPS GLIMARKLIHLEIKPAIRNQIIRELQVUHECNSPYIVGFYGAFY SDGEISICMEHMDGGSLDQVLKEAKRIPEEILGKVSIAVLRGLA YLREKHQIMHRDVKPSNILVNSRGBIKLCDFGYSGQLIDSMANS FVGTRSYMAPERLQGTHYSVQSDIWSMGLSLVELAVGRYPIPPP DAKELEAIFGRPVVDGEEGEPHSISPRPPPGRPVSGHGMDSRP AMAIFELLDYIVNEPPPKLPNGVFTPDFQEFVNKCLIKNPAERA DLKMLTNHFIKRSEVEEVDFAGWLCKTLRLNQPGTPTRTAV DAKELSSTEVEEVDFAGWLCKTLRLNQPGTPTRTAV SVQEDKVGFEDPLHLCSWRARACPCTWPHC/CTGLLECLGFAGV LFGWPSLVFVFKNEDYFKDLCGPDAGFIGNATGQADCKAQDERF	5432	<del></del>	1310	
KKRLEAFLTQKAKVGELKDDDFERISELGAGNGGVVTKVQHRPS GLIMARKLIHLEIKPAIRNQIIRELQVLHECNSPYIVGFYGAFY SDGEISICMEHMDGGSLDQVLKEAKRIPEEILGKVSIAVLRGLA YLREKHQIMHRDVKPSNILVINSRGEIKLCDFGVSGQLIDSMANS FVGTRSYMAPERLQGTHYSVQSDIWSMGLSLVELAVGRYPIPP DAKELEAIFGRPVVDGSEGEPHSISPRPPGRPVSGHGMDSRP AMAIFELLDYIVNEPPPKLPNGVFTPDFQEFVNKCLIKNPAERA DLKMLTNHTFIKRSSVEEVDFAGNLCKTLRLNQPGTPTRTAV DLKMLTVHTFIKRSSVEEVDFAGNLCKTLRLNQPGTPTRTAV LFGWPSLVFVFKNEDYFKDLCGPDAGFIGNATGQADCKAQDERF		~	4344	)
GLIMARKLIHLEIKPAIRNQIIRELQVLHECNSPYIVGFYGAFY SDGEISICMEHMDGGSLDQVLKEAKRIPEEILGKVSIAVLRGLA YLREKHQIMHRDVKPSNILVNSRGEIKLCDFGYSGQLIDSMANS FVGTRSYMAPERLQGTHYSVQSDLWSMGLSLVELAVGRYPIPPP DAKELEAIFGRPVVDGEEGEPHSISPRPPPGPRVSGHGMDSRP AMAIFELLDYIVNEPPPKLPNGVFTPDFQEFVNKCLIKNPAERA DLKMLTNHTFIKRSVEEVDFAGNLCKTLRLNQPGTPTRTAV DLSMLTNHTFIKRSVEEVDFAGNLCKTLRLNQPGTPTRTAV LFGWPSLVFVFKNEDYFKDLCGPDAGFIGNATGQADCKAQDERF	1 1		•	
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YLREKHQIMHRDVKPSNILVNSRGEIKLCDFGVSGQLIDSMANS FVGTRSYMAPERLQGTHYSVQSDIWSMGLSLVELAVGRYPIPPP DAKELEAIFGRPVVDGEEGEPHSISPRPPPGRPVSGHGMDSRP AMAIFELLDYIVNEPPPKLPNGVFTPDFQEFVNKCLIKNPAERA DLKMLTNHFIKRSEVEEVDFAGNLCKTLRLNQPGTPTRTAV  5433 360 1885 SVQEDKVGFEDPLHLCSWRARACPCTWPHC/CTGLLECLGFAGV LFGWPSLVFVFKNEDYFKDLCGPDAGFIGNATGQADCKAQDERF	, ,			
FVGTRSYMAPERLQGTHYSVQSDIWSMGLSLVELAVGRYPIPPP  DAKELEAI FGRPVVDGEEGEPHS ISPRPRPPGRPVSGHGMDSRP  AMAIFELLDYIVNEPPPKLPNGVFTPDFQEFVNKCLIKNPAERA  DLKMLTNHTFIKRSEVEEVDFAGWLCKTLRLNQPGTPTRTAV  5433 360 1885 SVQEDKVGFEDPLHLCSWRARACPCTWPHC/CTGLLECLGFAGV LFGWPSLVFVFKNEDYFKDLCGPDAGPIGNATGQADCKAQDERF				SDGEISICMEHMDGGSLDQVLKEAKRIPEEILGKVSIAVLRGLA
FVGTRSYMAPERLQGTHYSVQSDIWSMGLSLVELAVGRYPIPPP  DAKELEAI FGRPVVDGEEGEPHS ISPRPRPPGRPVSGHGMDSRP  AMAIFELLDYIVNEPPPKLPNGVFTPDFQEFVNKCLIKNPAERA  DLKMLTNHTFIKRSEVEEVDFAGWLCKTLRLNQPGTPTRTAV  5433 360 1885 SVQEDKVGFEDPLHLCSWRARACPCTWPHC/CTGLLECLGFAGV LFGWPSLVFVFKNEDYFKDLCGPDAGPIGNATGQADCKAQDERF				YLREKHQIMHRDVKPSNILVNSRGEIKLCDFGVSGQLIDSMANS
DAKELEAI FGRPVVDGEEGEPHS ISPRPRPPGRPVSGHGMDSRP AMAI FELLDY I VNEPPPKLPNGV FTPDFQEFVNKCLI KNPAERA DLKMLTNHTFI KRSEVEEVDFAGWLCKTLRLNQFGTPTRTAV  5433 360 1885 SVQEDKVGFEDFLHLCSWRARACPCTWFHC/CTGLLECLGFAGV LFGWPSLVFVFKNEDYFKDLCGPDAGPIGNATGQADCKAQDERF	]		,	FVGTRSYMAPERLOGTHYSVOSDIWSMGLSLVELAVGRYPIPPP
AMAIFELLDYIVNEPPPKLPNGVFTPDFQEFVNKCLIKNPAERA DLKMLTNHTFIKRSEVEEVDFAGWLCKTLRLNQPGTPTRTAV  5433 360 1885 SVQEDKVGFEDPLHLCSWRARACPCTWPHC/CTGLLECLGFAGV LFGWPSLVFVFKNEDYFKDLCGPDAGPIGNATGQADCKAQDERF	[ [	1		
DLKMLTNHTFIKRSEVEEVDFAGWLCKTLRLNQPGTPTRTAV  5433 360 1885 SVQEDKVGFEDPLHLCSWRARACPCTWPHC/CTGLLECLGFAGV LFGWPSLVFVFKNEDYFKDLCGPDAGPIGNATGQADCKAQDERF		}		
5433 360 1885 SVQEDKVGFEDPLHLCSWRARACPCTWPHC/CTGLLECLGFAGV LFGWPSLVFVFKNEDYFKDLCGPDAGPIGNATGQADCKAQDERF	{			
LFGWPSLVFVFKNEDYFKDLCGPDAGPIGNATGQADCKAQDERF	5432	360	1005	
1 1	5=33	300	7082	
SLIFTLGSFMNNFMTFPTGYIFDRFKTTVARLIAIFFYTTATLI	ļ Į	ļ		
	<u> </u>	<u></u>		SLIFTLGSFMNNFMTFPTGYIFDRFKTTVARLIAIFFYTTATLI

SEQ	Predicted	Predicted end	Taming soid compat containing simple service
	1		Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ĺ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1			
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence	ł	\=possible nucleotide insertion)
			IAFTSAGSAVLLFLAMPMLTIGGILFLITNLQIGNLFGQHRSTI
		(	ITLYNGAFDSSSAVFLIIKLLYEKGISLR/VLLHLHLCLQYLAC
	İ	1	STHFPPDAPGAHPIPTAPQLQLWPVPWEWHHKGREG/QQLSMKT
	1	}	GSYSQRSSFQRRKRPQGQGRSRNSAPSGATL/CSRRFAWHLVWL
ł	Į.	1	1
1	Ī		SVIQLWHYLFIGTLNSLLTNMAGGDMARVSTYTNAFAFTQFGVL
1	i	ļ	CAPWNGLLMDRLKQKYQKEARKTGSSTLAVALCSTVPSLALTSL
	1		LCLGFALCASVPILPLQYLTFILQVISRSFLYGSNAAFLTLAFP
1	!	1	SEHFGKLFGLVMALSAVVSLLQFPIFTLIKGSLQNDPFYVNVMF
1	į.		MLAILLTFFHPFLVYRECRTWKESPSAIA
5434	66	652	RYAALIISLIQHKLLWRNQHCSRCVIMSPAQSAGLNWLF/GSGK
) 2424	, 88	034	
	Į.	1	HGPFLGCSQYPACDYVRPLKSSADGHIVKVLEGQVCPACGANLV
1		Į	LROGREGMEIGCINYPECENTELIDKPDETAITCPQCRTGHLVQ
1	1		RRSRYGKTFHSCDRYPECQFAINFKPIAGECPECHYPLLIEKKT
1	!		AQGVKHFCASKQCGKPVSAE
5435	4704	1597	PGDSSORLAEMSNAKERKHAKKMRNOPINVILSSGFVADRGVKH
1	1		HSGGEKPFQAQKQEPHPGTSRQRQTRVNPHSLPDPEVNEQSSSK
!	j		
i	1		GMFRKKGGWKAGPEGTSQEIPKYITASTFAQARAAEISAMLKAV
}	1	Ł	TOKSSNSLVFQTLPRHMRRRAMSHNVKRLPRRLQEIAQKEAEKA
i	ļ.	1	VHQKKEHSKNKCHKARRCHMNRTLEFNRRQKKNIWLETHIWHAK
1	1		RFHMVKKWGYCLGERPTVKSHRACYRAMTNRCLLQDLSYYCCLE
	1		LKGKEEEILKALSGMCNIDTGLTFAAVHCLSGKRQGSLVLYRVN
1	1	İ	KYPREMLGPVTFIWKSQRTPGDPSESRQLWIWLHPTLKQDILEE
1		1	IKAACOCVEPIKSAVCIADPLPTPSOEKSOTELPDEKIGKKRKR
1	1	1	
1	1		KDDGENAKPIKKIIGDGTRDPCLPYSWISPTTGIIISDLTMEMN
1	Ì	ļ	RFRLIGPLSHSILTEAIKAASVHTVGEDTEETPHRWWIETCKKP
1	ł		DSVSLHCRQEAIFELLGGITSPAEIPAGTILGLTVGDPRINLPQ
1	ļ		KKSKALPNPEKCQDNEKVRQLLLEGVPVECTHSFIWNQDICKSV
1		ł	TENKISDODLNRMRSELLVPGSQLILGPHESKIPILLIQQPGKV
1		1	TGEDRLGWGSGWDVLLPKGWGMAFWIPFIYRGVRVGGLKESAVH
1	(	Í	SQYKRSPNVPGDFPDCPAGMLFAEEQAKNLLEKYKRRPPAKRPN
1	į	ļ	
1	ļ ·	1	YVKLGTLAPFCCPWEQLTQDWESRVQAYEEPSVASSPNGKESDL
Į	]	· ·	RRSEVPCAPMPKKTHQPSDEVGTSIEHPREAEEVMDAGCQESAG
1			PERITDQEASENHVAATGSHLCVLRSRKLLKQLSAWCGPSSEDS
ì	ł		RGGRRAPGRGQQGLTREACLSILGHFPRALVWVSLSLLSKGSPE
i	1	1	PHTMICVPAKEDFLQLHEDWHYCGPQESKHSDPFRSKILKQKEK
1	ĺ		KKREKRQKP\GRASSDGPAGEEPVAGQEALTLGLWSGPLPRVTL
1	,		HCSRTLLGFVTQGDFSMAVGCGEALGFVSLTGLLDMLSSQPAAQ
1			RGLVLLRPPASLQYRFARIAIEV
F	170		
5436	1781	635	ASDS I PWSEARTTRKLAQRGCQWSLPERMPLVVFCGLPYSGKSR
ſ	1		RABELRVALAAEGRAVYVVDDAAVLGAEDPAVYGDSAREKALRG
1	ļ		ALRASVERRLSRHDVVILDSLNYIKGFRYELY\CLARAARTPLC
1			LVYCVRPGGPIAGPQVAGANENPGRNVSVSWRPRAEEDGRAQAA
ı			GSSVLRELHTADSVVNGSAQADVPKELEREESGAAESPALVTPD
1			SEKSAKHGSGAFYSPELLBALTLRFEAPDSRNRWDRPLFTLVGL
1 .			EEPLPLAGIRSALFENRAPPPHOSTOSOPLASGSFLHOLDOVTS
1			OVLAGLMEAOKSAVPGDLLTLPGTTEHLRFTRPLTMAELSRLRR
i	}		
			QFISYTKMHPNNENLPQLANMFLQYLSQSLH
5437	739	1672	CQEAASEFGGPLHTPAMFLRRLGGWLPRPWGRRKPMRPDPPYPE
j	]		PRRVDSSSENSGSDWDSAPETMEDVGHPKTKDSGALRVSRAASE
ł			PSKEEPQVEQLGSKRMDSLKWDQPISSTQESGRLEAGGASPKLR
]			WDHVDSGGTRRPGVSPEGGL\GVPGPGAPLEKPGRREKLLGWLR
ł			
ĺ	İ		GEPGAPSRYLGGPEECLQISTNLTLHLLELLASALLALCSRPLR
1		'	AALDTLGLRGPLGLWLHGLLSFLAALHGLHAVLSLLTAHPLHFA
[			CLFGLLQALVLAVSLREPNGDEAATDWBSEGLEREGEEQRGDPG
]			KGL
5438	2443	1152	TKPRKRRHQPASORORPWSSDSTGDLLARGKGRKEENKGSDRVS
1	227	1132	
			LAPPSLRRPMMCQSEARQGPBLRAAKWLHFPQLALRRRLGQLSC
1 .			MSRPALKLRSWPLTVLYYLLPFGALRPLSRVGWRPVSRVALYKS
1			VPTRLLSRAWGRLNQVELPHWLRRPVYSLYIWTFGVNMKEAAVE
1		•	DLHHYRNLSEFFRRKLKPQARPVCGLHSVISPSDGRILNFGQVK
1	!		NCEVEQVKGVTYSLESFLGPRMCTEDLPFPPAASCDSFKNQLVT

	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ			(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
j	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ĺ	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			REGNELYHCVIYLAPGDYHCFHSPTDWTVSHRRHFPGSLMSVNP
)	j	1	GMARWIKELFCHNERVVLTGDWKHGFFSLTAVGAT\NWGSIRIY
		i	FDRDLHTNSPRHSKGSYNDFSFVTHTNREGVPMALRGEHLG/QS
ł		ł	FNLGSTIVLIFEAPKDFNFQLKTGQKIRFGEALGSL
5439	2443	1152	TKPRKRHQPASQRQRPWSSDSTGDLLARGKGRKEENKGSDRVS
1		1	LAPPSLRRPMMCQSEARQGPELRAAKWLHFPQLALRRRLGQLSC
l .		Į.	MSRPALKLRSWPLTVLYYLLPFGALRPLSRVGWRPVSRVALYKS
i	1		VFTRLLSRAWGRLNQVELPHWLRRPVYSLYIWTFGVNMKEAAVE
Ĭ	[	1	DLHHYRNLSEFFRRKLKPQARPVCGLHSVISPSDGRILNFGQVK
1	\{	1	
i	(	Í	NCEVEQVKGVTYSLESFLGPRMCTEDLPFPPAASCDSFKNQLVT
J			REGNELYHCVIYLAPGDYHCFHSPTDWTVSHRRHFPGSLMSVNP
1			GMARWIKELFCHNERVVLTGDWKHGFFSLTAVGAT\NWGSIRIY
}	}	Į.	FDRDLHTNSPRHSKGSYNDFSFVTHTNREGVPMALRGEHLG/QS
1			FNLGSTIVLIFEAPKDFNFQLKTGQKIRFGEALGSL
	<del> </del>		
5440	693	253	EPIPVTPDHRLVTMTHIV\QTFSPVNS\GQPPNYEMLKEEQEVA
1	}		MLGAPHNPAPPMSTVIHIRSETSVPDHVVWSLFNTLFMNTCCLG
1			FIAFAYSVKSRDRKMVGDVTGAQAYASTAKCLNIWALILGIFMT
1		[	ILLIIIPVLVVQAQR
5441	2	2054	CRDGGKNGFMVSPMKPLEIKTQCSGPRMDPKICPADPAFFSFIN
1 3	-	1	NSDLWVANIETGEERRLTFCHQGLSNVLDDPKSAGVATFVIQEE
1	<u> </u>	ļ	FDRFTGYWWCPTASWEGSEGLKTLRILYEEVDESEVEVIHVPSP
		1	
J	}	1	ALEERKTDSYRYPRTGSKNPKIALKLAEFQTDSQGKIVSTQEKE
1			LVQPFSSLFPKVEYIARAGWTRDGKYAWAMFLDRPQQWLQLVLL
į.	1	ł	PPALPIPSTENEEQ\RLASARAVPRNVQPYVVYEEVTNVWINVH
ł	1	1	DIFYPFPQSEGEDELCFLRANECKTGFCHLYKVTAVLKSQGYDW
İ	1		SEPFSPGEGEOSLINAIWVNEETKLVYFQGTKDTPLEHHLYVVS
i .		1	YEAAGEIVRLTTPGFSHSCSMSQNFDMFVSHYSSVSTPPCVHVY
ł	l	1	
			KLSGPDDDPLHKQPRFWASMMEAAKIFHFHTRSDVRLYGMIYKP
1	í	1	HALQPGKKHPTVLFVYGGPQVQLVNNSFKGIKYLRLNTLASLGY
1	}	}	AVVVIDGRGSCQRGLRFEGALKNQMGQVEIEDQVEGLQFVAEKY
1	1	1	GFIDLSRVAIHGWSYGGFLSLMGLIHKPQVFKVAIAGAPVTVWM
J		ŀ	AYDTGYTERYMDVPENNQHGYEAGSVALHVEKLPNEPNRLLILH
1	•		GFLDENVHFFHTNFLVSQLIRAGKPYQLQVALPPVSPQIYPNER
l	1	i	
			HSIRCPESGEHYEVTLLHFLQEYL
5442	1	3474	CGQRSRRSPDMPEAKPAAKKAPKGKDAPKGAPKEAPPKEAPAE
	· ·	1	APKEAPPEDQSPTAEEPTGVFLKKPDSVSVETGKDAVVVAKVNG
1	(	1	KELPDKPTIKWFKGKWLELGSKSGARFSFKESHNSASNVYTVEL
1	}	j	HIGKVVLGDRGYYRLEVKAKDTCDSCGFNIDVEAPRQDASGQSL
1			ESFKRTSEKKSDTAGELDFSGLLKKREVVEEEKKKKKKDDDDLG
}	]		IPPEIWELLKGAKKSEYEKIAFOYGITDLRGMLKRLKKAKVEVK
I	l		
1	}	ł.	KSAAFTKKI,DPAYQVDRGNKIKLMVEISDPDLTLKWFKNGQEIK
			PSSKYVFENVGKKRILTINKCTLADDAAYEVAVKDEKCFTELFV
1			KEPPVLIVTPLEDQQVFVGDRVEMAVEVSEEGAQVMWMKDGVEL
1		1	TREDSFKARYRFKKDGKRHILIFSDVVQEDRGRYQVITNGGQCE
ł			AELIVEEKQLEVLQDIADLTVKASEQAVFKCEVSDEKVTGKWYK
	1	1	NGVEVRPSKRITISHVGRFHKLVIDDVRPEDEGDYTFVPDGYAL
Ī		,	
1			GSLSAKLNFLEIKVEYVPKQ\EPPKIPLGFASGGKTSENAD/IV
i			VVAGNKLRLDV\SITGEAPSPFAT\WLKG\DEVFTTTEGRTRIE
ļ	}	ì	KRVDCSSFVIESAQREDEGRYTIKVTNPIGEDVASIFLQVVDVP
l .		Į.	DPPEAVRITSVGEDWAILVWEPPMYDGGKPVTGYLVERKKKGSQ
1	1	1	RWMKLNFEVFTETTYESTKMIEGILYEMRVFAVNAIGVSQPSMN
1			TKPFMPIAPTSEPLHLIVEDVTDTTTTLKWRPPNRIGAGGIDGY
ì		i	
1		1	LVEYCLEGSEEWVPANTEPVERCGFTVKNLPTGARILFRVVGVN
ł	İ		IAGRSEPATLAQPVTIREIAEPPKIRLPRHLRQTYIRKVGEQLN
1			LVVPFQGKPRPQVVWTKGGAPLDTSRVHVRTSDFDTVFFVRQAA
1	ì		RSDSGEYELSVQIENMKDTATIRIRVVEKAGPPINVMVKEVWGT
l			NALVEWOAPKDDGNSEIMGYFVQKADKKTMEWFNVYERNRHTSC
{		i .	
1	ļ	1	TVSDLIVGNEYYFRVYTENICGLSDSPGVSKNTARILKTGITFK
i .	1	1	PPEYKEHDFRMAPKFLTPLIDRVVVAGYSAALNCAVRGHPKPKV
1			VWMKNKMEIREDPKFLITNYQGVLTLNIRRPSPFDAGTYTCRAV
1			NELGEALAECKLEVRVPQ
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* *PDMGDRRPNGQVATGLPELMGARGPAGLEPRICQVMFSQAPAH QGGGCGYGQSQGPSGRPRGGAGSRB  5445  2364  486  ILSRGFLGSVEICIQDPLBASEPVLLTWARRAWRETESREEPT TLRAGSVCPWMI* *BTKMRSIPVEVDESEPYSQLLKPIPPYSP EERSEPPARNIRMANNSLSAPTHLHNSSGDFSQAHSTLKLANH QRPVSRQVTCLRTQVLEDBESDFCRENFGGASFSCRAVSEP ASRSVVGALPARHOFSFMEKRNGILVSGLSAASPDFGHDSDKSD QSLPNASADSLGGSGGMVQROPRIRHSGLDLPTITUTYDSQPQ DVLGIRQLERPLPLTSVCYPQDLRPLRSREPPQEPPGRYPACA QMIPPHILSPHAPHNYHYHCPGSPDHQVPYGHDYPRAAYQQVIQP ALBEQDLBGASVRGLHPVGXVILMYFSPMDQEERPAGRDCSFPG LPHHQDQDPHHQPFNRAGAGGSLBCPARSLRQVPGPPSPAAVRR PFSNPPARGTLKTSNIP_DEBLRKVPITYSKGSMNFPFIPVLF PNAKKEHVPTWLQNTHVYSWPKNKNILLRLEEBYVAPPRGB LPHLQVVPL  5446  972  161  SSMSWCTGRMRKTRLWGLHMLFVSELRAATKLTEEKYELKEGQ TLDVKCDYTLEKFASSGRAWGI IRDGEMPKTLACTERPSKNSHP VOWGRI LIEDYHDHGLKURVRMNLQVEDSGLVQCUTQPPKEPH MLPDRIRLVVTKGPSGTPGSNENSTQNVYKIPPTTTKALCPLYT TPRTVTQAPPRSTADVETDDESILLTVITLRUPVRNIVLLLA GGFLSKSLVFSVLFAVTLRSFVP*AHEPTHMSSDPQPHPSGSCA KGGGRR  5447  207  617  MTARTISLMASLVAYDDSDERAFTEHAGSFNATGOOKDTSGVAR PFGQDFASGTLDVPKAGAOPTKHGSCEDPGGYRLPLAQLGRSDR GCCPSGRLQWWGKEGVTFP IKEBSCSLMTSHVPAAHMPLAAA RFKQVLLSRNIPFKSSPHAQSBSTVGKNGSSDVALFLPLAQLGRSDR GCCPSGRLQWWGKEGVTFP IKEBSCSLMTSHVPAAHMPLAAA RFKQVLLSRNIPFKSSPHAQSBSTVGKNGSSDVALFLPRGSFSSTD ASTRDSADRTIIANDFRTSAKISQLIPLERGSSPFSSSTD ASTRDSADRTIIANDFRTSAKISQLIPLERGRSPFSSTD ASTRDSADRTIIANDFRTSAKISQLIPLERGRSPFSSTD ASTRDSADRTIIANDFRTSAKISQLIPLERGRSPFSSTD ASTRDSADRTIIANDFRTSAKISQLIPLERGRSPFSSSTD ASTRDSADRTIIANDFRTSAKISQLIPLERGRSPFSSTD ASTRDSADRTIIANDFRTSAKISQLIPLERGRSPFSSTD ASTRDSADRTIIANDFRTSAKISQLIPLERGRSPFSSTD ASTRDSADRTIIANDFRTSAKISQLIPLERGRSPFSSTD ASTRDSADRTIIANDFRTSAKISQLIPLERGRSPFSSTD ASTRDSADRTIIANDFRTSAKISQLIPLERGRSPFSSTD ASTRDSADRTIIANDFRTSAKISQLIPLERGRSPFSSTD ASTRDSADRTIIANDFRTSAKISQLIPLERGRSPFSSTD ASTRDSADRTIIANDFRTSAKISQLIPLERGRSPFSSTD ASTRDSADRTIIANDFRTSAKISQLIPLERGRSPFSSTD ASTRDSADRTIIANDFRTSAKISQLIPLERGRSPFSSTD ASTRDSADRTIIANDFRTSAKISQTVTFDLEHAFFFPSFFFF RWMLQVTSKVIFFDLEMINSFFTSSFHSSTDLTEVIU GPJMMLLLGTVHQLVSSTTTKPGPLSTGSSFHSILTEVIU GPJMMLLLGTVHQLVSSTTTKPGPLSTGSSFHSILTEVIU GPJMMLLLGTVHQQLVSTTTKFDLETGL	1			
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11. SEGFIGSVETCIQLEDASEPVLLLYMÄRRRWEETESKREET TLRAQSVCPWWW * ETRNWRS IPVESEPYPSQLLYD IPPYSB EBSSEPPARNIRNBRIPVESEPYPSQLLYD IPPYSB EBSSEPPARNIRNBRIPVESEPYPSQLLYD IPPYSB EBSSEPPARNIRNBAPSLSAPTMLHNSSGDFSQAHSTLKLANH QRPVSRQVTCLRTQVLEDSBGSCRHHEGLGKAFPSCGSAVSEP ASSSVUGALPARHOFSPMERKROWLVSQLSAASPDTHDSDKSD QSLPNASADSLGGSQBMVQPPQHRNRAGLDLPTITGYDSQPQ DVLGIRQLBRPLPLTGVCYPQDLPBRLRSRFPQFBPQRPACAC QMLPPNLSPHAPMNYHYHCGSPDHQVPYGHUYPRAAYQQVIQP ALPGQPLGGASVRGLHPVQVXLNTYSSWDQEERPAQRDCSFPG LPHAQDPHHQPPHRAGAGPGSBLECPASLRPQVSQPPSPAAVRR PFSNPPARGTLKTSNLPEELRKVFTTYSNDTMEVVKFVMFLUV NGCYTAIDIFFERIR GID II KMMERYLRDKTMI IVAISPKYKQ DVEGABSQLDEDEHGLHTKYTHRMMGIEFIKQGSMNFRFIPULP PNAKKENPUTWLQNTHVYSWPKNKKNI LIRLLREERYVAPPRGP LPTLQVVVL  5446  972  161 SSMSWCTGRMRKTRLWGLWMLFVSELRAATKLTEEKYELKEGQ TLDVKCOTYTLEFFASSQKAWQI IRDGEMPKTLACTERPSKNSHP VQVGRI ILBDYNDHGLRPVKMVLQVEDSGLYQCU TQOPPKEPH MLFDRIRLVTKGFSGFTGSNENSTONYVKI PPTTTKALGCL VT TPRTVYQAPPKSTADVSTPDSEINLTNVTDI IRUPVRNI VILLA GGPLSKSLVPSVLPAVTLRSPVP*AHEPTRMSSDFQPHPSGSCA KGGGRR  5447  207  617  MTARTISLMASLVAYDDSDSEAETEHAGSFNATGQQKDTSGVAR PFGQDFASGTLDVPRAGAQPTKHGSCEDPGGYRLPLAQLGRSDR GSCPSQRLQWHGKEFQVTFPIKEPSCSSLWTSHVPASHMPLAAA REKOVLKISNPPKSSPHAQESSTVIXKNGSFQKKKCEDCVVPP TPRRLRQRQALSTETGKGKDVEPQGPPAGRAPALLYVQFGVSEF IQPYLMSHKKETTVPRKVLPHLRGIRGPVNTI QWCPVLSKSHML LSTSMKKTKVMNANDGSGCLOTYSI SHTEAWAARMAPCGRI L SGGFBPALHLTDLETGTQLFSGRSPFRI TTLKFFFK VHNIFEPV PLAQTINGNYLALFSTVWPYRMSRRRT YEHKVFCYSLALHPREPV PLAQTINGNYLALFSTVWPYRMSRRRT YEHKVFCYSLALHPREPV PLAQTINGNYLALFSTVWPYRMSRRRT YEHKVFCYSLALHPREPV PLAQTINGNYLALFSTVWPYRMSRRRT YEHKVFCYSLALHPREPV PLAQTINGNYLALFSTVWPYRMSRRRT YEHKVFCYSLALHPREPV PLAQTINGNYLALFSTVWPYRMSRRRT YEHKVFCYSVCCCCSPG GGLLVTGSADGRUMYSFRTARRACTLQGHCTGCTTHPVLP SVLATCSWGGDMKWH*AFFRWSLGEAGIGDLAPARGYSGFGRSL KSPSPSKSLIVLLICGRAMFQPATCYGGLAPARGYSGFGRSL KSPSPSKSLIVLLICGRAMFQPATCYGGLAPARGYSGFGRSL KSPSPSKSLIVLLICGRAMFQPATCYGGLAPARGYSGFGRSL KSPSPSKSLIVLLICGRAMFQPATCYTGDLUHAAFFICS GPWLMALLLGTTHQUVARATVFCSTSSPHSIPLTEVU GPWLMLLLGTTHQUVARATURFCSTSSPHSIPLTEVU	1	1	1	
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GATIA ODDIA DE VINTE TIDUMANO A E DOOD TITUE A STATE OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF T	1	1	1	GVLVELEVLPAAIPLEAQNFSVPEGGSLTLAPPLLRVSGPYFPT

	, <u> </u>		
SEQ	Predicted beginning	Predicted end nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	203	\=possible nucleotide insertion)
		<del>  </del>	LLGLSLOVLEPPQHGPLQKEDGPQARTLSAFSWRMVEEQLIRYV
ł		ł	HDGSETLTDSFVLMANASEMDRQSHPVAFTVTVLPVNDQPPILT
		Į.	TNTGLOMWEGATAPIPAEALRSTDGDSGSEDLVYTIEQPSNGRV
			VLRGAPGTEVRSFTQAQLDGGLVLFSHRGTLDGGFPFRLSDGEH
ļ		}	TSPGHFFRVTAQKQVLLSLKGSQTLTVCPGSVQPLSSQTLRASS
			SAGTDPQLLLYRVVRGPQLGRLFHAQQDSTGEALVNFTQAEVYA
ĺ			GNILYEHEMPPEPFWEAHDTLELQLSSPPARDVAATLAVAVSFE
			AACPQRPSHLWKNKGLWVPEGQRARITVAALDASNLLASVPSPQ
j		]	RSEHDVLFQVTQFPSRGQLLVSEEPLHAGQPHFLQSQLAAGQLV
			YAHGGGGTQQDGFHFRAHLQGPAGASVAGPQTSEAFAITVRDVN
		1	ERPPQPQASVPLRLTRGSRAPISRAQLSVVDPDSAPGEIEYEVQ
İ		)	RAPHNGFLSLVGGGLGPVTRFTQADVDSGRLAFVANGSSVAGIF
	ļ	1	QLSMSDGASPPLPMSLAVDILPSAIEVQLRAPLEVPQALGRSSL
			SQQQLRVVSDREEPEAAYRLIQGPQYGHLLVGGRPTSAFSQFQI
	*	}	DOGEVVFAFTNFSSSHDHFRVLALARGVNASAVVNVTVRALLHV
		l .	WAGGPWPQGATLRLDPTVLDAGELANRTGSVPRFRLLEGPRHGR VVRVPRARTEPGGSQLVEQFTQQDLEDGRLGLEVGRPEGRAPGP
		İ	AGDSLTLELWAQGVPPAVASLDFATEPYNAARPYSVALLSVPEA
		,	ARTEAGKPESSTPTGEPGPMASSPEPAVAKGGFLSFLEANMFSV
			IIPMCLVLLLALILPLLFYLRKRNKTGKHDVOVLTAKPRNGLA
		ļ.	GDTETFRKVEPGQAIPLTAVPGQGPPPGGQPDPELLQFCRTPNP
			ALKNGQYWV
5451	1	2274	RDSSEOGRTGDTLGRPSACMDALKPPCLWRNHERGKKDRDSCGR
	}		KNSEPGSPHSLEALRDAAPSQGLNFLLLFTKMLFIFNFLFSPLP
		}	TPALICILTFGAAIFLWLITRPQPVLPLLDLNNQSVGIEGGARK
			GVSQKNNDLTSCCFSDAKTMYEVFQRGLAVSDNGPCLGYRKPNQ
			PYRWLSYKQVSDRAEYLGSCLLHKGYKSSPDQFVGIFAQNRPEW
	}		IISELACYTYSMVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQ
			KALVLIGNVEKGFTPSLKVIILMDPFDDDLKQRGEKSGIEILSL
			YDAENLGKEHFRKPVPPSPEDLSVICFTSGTTGDPKGAMITHQN
			IVSNAAAFLKCVEHAYEPTPDDVAISYLPLAHMFERIVQAVVYS
			CGARVGFFQGDIRLLADDMKTLKPTLFPAVPRLLNRIYDKVQNE AKTPLKKFLLKLAVSSKFKELQKGIIRHDSFWDKLIFAKIQDSL
		1	GGRVRVIVTGAAPMSTSVMTFFRAAMGCQVYEAYGQTECTGGCT
		<b>)</b> '	FTLPGDWTSGHVGVPLACNYVKLEDVADMNYFTVNNEGEVCIKG
		1	TNVFKGYLKDPEKTQEALDSDGWLHTGDIGRWLPNGTLKIIDRK
		1	KNIFKLAQGEYIAPEKIENIYNRSQFVLQIFVHGESLRSSLVGV
		ł	VVPDTDVLPSFAAKLGVKGSFEELCQNQVVRBAILEDLQKIGKE
		l	SGLKTFEQVKAIFLHPEPFSIENGLLTPTLKAKRGELSKYFRTQ
			IDSLYEHIQD
5452	1833	1138	SRVPSLCLSLSLSPSREPVAGAPGCGTAGPPAMATLWGGLLR
		}	LGSLLSLSCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENSG
ļ			HIYNKNISQKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERSS
	}	ł	VTIKVTIIIYLSILGLLLLYMVYLTLVEPILKRRLFGHAQLIQS
	1	ł	DDDIGDHQPFANAHDVLARSRSRANVLNKVEYAQQRWKLQVQEQ
			RKSVFDRHVVLS
5453	111	1520	PSIPAAVPQSAPPEPHREETVTATATSQVAQQPPAAAAPGEQAV
	ļ	ł	AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAKE
			PQEERSQQQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTVY KGLDTETTVEVAWCELODRKLTKSERORFKEEAEMLKGLQHPNI
		1	VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKVMKIKVL
		ļ	RSWCRQILKGLQFLHTRTPPIIHRDLKCDNIFITGPTGSVKIGD
		1	LGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCM
		}	LEMATSEYPYSECONAAQIYRRVTSGVKPASFDKVAIPEVKEII
	,		EGCIRONKDERYSIKDLLNHAFFQEETGVRVELAEEDDGEKIAI
		I	KLWLRIEDIKKLKGKYKDNEAIEFSFDLERNVPEDVAQEMVESG
		<u> </u>	
		j	
5454	111	1520	YVCEGDHKTMAKAIKDRVSLIKRKREQRQL*
5454	111	1520	YVCEGDHKTMAKAIKDRVSLIKRKREQRQL* PSIPAAVPQSAPPEPHREETVTATATSQVAQQPPAAAAPGEQAV
5454	111	1520	YVCEGDHKTMAKAIKDRVSLIKRKREQRQL* PSIPAAVPQSAPPEPHREETVTATATSQVAQQPPAAAAPGEQAV AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAKE
5454	111	1520	YVCEGDHKTMAKAIKDRVSLIKRKREQRQL* PSIPAAVPQSAPPEPHREETVTATATSQVAQQPPAAAAPGEQAV

	1 32 - 37		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}	amiro acid	residue of	S=Serine, T=Threonine, V=Valine,
]	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	· ·	Codon, /=possible nucleotide deletion,
į		sequence	
	sequence	L	\=possible nucleotide insertion)
]	i	J	VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKVMKIKVL
(	(	•	RSWCRQILKGLQFLHTRTPPIIHRDLKCDNIFITGPTGSVKIGD
}	1	1	LGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCM
1	Į.	{	LEMATSEYPYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEII
1	1	j	EGCIRONKDERYSIKDLLNHAFFQEETGVRVELAEEDDGEKIAI
1	1	ţ	KLWLRIEDIKKLKGKYKDNEAIEFSFDLERNVPEDVAQEMVESG
1	}	]	YVCEGDHKTMAKAIKDRVSLIKRKREQRQL*
		1 222	
5455	1359	377	LTMVSPATRKSLPKVKAMDFITSTAILPLLFGCLGVFGLFRLLQ
1		1	WVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGAKLVLCGRNG
J	j	1	GALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEIL
1	Ļ	!	QCFGYVDILVNNAGISYRGTIMDTTVDVDKRVMEINYFGPVALT
1	J		KALLPSMIKRROGHIVAISSIQGKMSIPFRSAYAASKHATQAFF
I		1	DCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTT
l	1	J	TAOGRSPVEVAQDVLAAVGKKKKDVILADLLPSLAVYLRTLAPG
	ļ		1
			LFFSLMASRARKERKSKNS
5456	2	2332	CGAGLVAAGAVLVLYPASRAGERTRVPGSPAPSSLPLHSPGACG
1	1	1	TEVDMDPQRSPLLEVKGNIELKRPLIKAPSQLPLSGSRLKRRPD
İ			QMEDGLEPEKKRTRGLGATTKITTSHPRVPSLTTVPQTQGQTTA
1	}	}	QKVSKKTGPRCSTAIATGLKNQKPVPAVPVQKSGTSGVPPMAGG
-	<b>{</b>	1	KKPSKRPAWDLKGQLCDLNAELKRCRERTQTLDQENQQLQDQLR
1	į.	i	DAQQQVKALGTERTTLEGHLAKVQAQAEQGQQELKNLRACVLEL
	ļ		EERLSTOEGLVOELOKKOVELOEERRGLMSQLEEKERRLOTSEA
}	l	1	ALSSSQAEVASLRQETVAQAALLTEREERLHGLEMERRRLHNQL
ļ	1		OELKGNIRVFCRVRPVLPGEPTPPPGLLLFPSGPGGPSDPPTRL
}	ţ	}	1 **
1	ł		SLSRSDERRGTLSGAPAPPTRHDFSFDRVFPPGSGQDEVFEEIA
ì	1	i	MLVQSALDGYPVCIFAYGQTGSGKTFTMEGGPGGDPQLEGLIPR
,	}	ł	ALRHLFSVAQELSGQGWTYSFVASYVEIYNETVRDLLATGTRKG
i	· ·		QGGECEIRRAGPGSEELTVTNARYVPVSCEKEVDALLHLARQNR
1	1	1	AVARTAQNERSSRSHSVFQLQISGEHSSRGLQCGAPLSLVDLAG
1	[	ĺ	SERLDPGLALGPGERERLRETQAINSSLSTLGLVIMALSNKESH
1		1	VPYRNSKLTYLLQNSLGG\$AKMLMFVNISPLEENV3ESLNSLRF
ŀ		j	ASKVEPSVLFGTAQSNRKWKTDPDLCVCVCVCVCVCVCVCVCV
}		ļ	MSMYRVRGGRVAGGCFIGWRAPCPRAIK
5457	2	1540	DDFVERRRWTRTTCLVRSPPHVPVCGHACSWNGGSLDPLKGTPA
1 3.37	1 ~	1 -5-0	LLRSAERLMRKVKKLRLDKENTGSWRSFSLNSEGAERMATTGTP
l			1
į.	ļ		TADRGDAAATDDPAARFQVQKHSWDGLRSIIHGSRKYSGLIVNK
1	1		APHDFQFVQKTDESGPHSHRLYYLGMPYGSRENSLLYSEIPKKV
1	l		RKEALLLLSWKQMLDHFQATPHHGVYSREEELLRERKRLGVFGI
1			TSYDFHSESGLFLFQASNSLFHCRDGGKNGFMVSPGPGCVSPMK
l	ł		PLEIKTQCSGPRMDPKICPADPAFFSFINNSDLWVANIETGEER
	i '		RLTFCHQGLSNVLDDPKSAGVATFVIQEEFDRFTGYWWCPTASW
ł	ł		EGSEGLKTLRILYEEVDESEVEVIHVPSPALEERKTDSYRYPRT
l	}		GSKNPKIALKLAEFQTDSQGKIVSTQEKELVQPFSSLFPKVEYI
f	1		ARAGWTRDGKYAWAMFLDRPQOWLQLVLLPPALFIPSTENEEQA
]	j		ASLCOSCPOECPAVCGVRGGHORLDQCS
	CCAO	4000	FVPGLREPOWEPAOPSATMSAPSEEEEYARLVMEAOPEWLRAEV
5458	6642	4022	
Į.			KRLSHELAETTREKIQAAEYGLAVLEEKHQLKLQFEELEVDYEA
			IRSEMEQLKEAFGQAHTNHKKVAADGESREESLIQESASKEQYY
			VRKVLELQTELKQLRNVLTNTQSENERLASVAQBLKEINQNVEI
j			QRGRLRDDIKEYKFREARLLQDYSELEEENISLQKQVSVLRQNQ
[			VEFEGLKHEIKRLEEETEYLNSQLEDAIRLKEISERQLEEALET
1			LKTEREOKNSLRKELSHYMSINDSFYTSHLHVSLDGLKFSDDAA
1			EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS
}			DLLSELNISEIQKLKQQLMQMEREKAGLLATLQDTQKQLEHTRG
1			
J			SLSEQQEKVTRLTENLSALRRLQASKERQTALDNEKDRDSHEDG
1			DYYEVDINGPEILACKYHVAVAEAGELREQLKALRSTHEAREAQ
1			HAEEKGRYEAEGQALTEKVSLLEKASRQDRELLARLEKELKKVS
	1		DVAGETQGSLSVAQDELVTFSEELANLYHHVCMCNNETPNRVML
			DYYREGQGGAGRTSPGGRTSPEARGRRSPILLPKGLLAPEAGRA
			DGGTGDSSPSPGSSLPSPLSDPRREPMNIYNLIAIIRDQIKHLQ
1			AAVDRTTELSRORIASOELGPAVDKDKEALMEEILKLKSLLSTK
L	L		CONTROL OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE

SEQ	Predicted	Predicted end	Dring gold
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	1	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i		to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Į.	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	I	\=possible nucleotide insertion)
		<del> </del>	REQITTLRTVLKANKQTAEVALANLKSKYENEKAMVTETMMKLR
	ļ		NELKALKEDAATFSSLRAMFATRCDEYITQLDEMQRQLAAAEDE
ĺ	f	1	VYTI NCLI DWA TOOKY AL TOOL DE LOT DE DEMORQUADA DE
i	Į.	1 .	KKTLNSLLRMAIQQKLALTQRLELLELDHEQTRRGRAKAAPKTK
5459	316		PATPSVSHTCACASDRAEGTGLANQVFCSEKHSIYCD
3439	316	1262	RGGHRLSGMASNFNDIVKQGYVRIRSRRLGIYQRCWLVFKKASS
			KGPKRLEKFSDERAAYFRCYHKVTELNNVKNVARLPKSTKKHAI
1			GIYFNDDTSKTFACESDLEADEWCKVLQMECVGTRINDISLGEP
			DLLATGVEREQSERFNVYLMPSPNLGCYMGECALQITYEYICLW
}	}		DVQNPRVKLISWPLSALRRYGRDTTWFTFEAGRMCETGEGLFIF
			QTRDGEAIYQKVHSAALAIAEQHERLLQSVKNSMLQMKMSERAA
1	]		SLSTMVPLPRSAYWQHITRQHSTGQLYRLQDVSSPLKLHRTETF
			PAYRSEH
5460	45	2097	
1	1	207/	RPGCRAGELSTGSRARERVRNRVSAPCGQDSRRCDPEVLRGRSP
	1		GLGLAEMPSCGACTCGAAAVRLITSSLASAQRGISGGRIHMSVL
	1		GRLGTFETQILQRAPLRSFTETPAYFASKDGISKDGSGDGNKKS
1	1		ASEGSSKKSGSGNSGKGGNQLRCPKCGDLCTHVETFVSSTRFVK
1			CEKCHHFFVVLSEADSKKSIIKEPESAAEAVKLAFQQKPPPPPK
1	1		KIYNYLDKYVVGQSFAKKVLSVAVYNHYKRIYNNIPANLRQQAE
1			VEKQTSLTPRELEIRRREDEYRFTKLLQIAGISPHGNALGASMQ
1	1.		QQVNQQIPQEKRGGEVLDSSHDDIKLEKSNILLLGPTGSGKTLL
	i		AQTLAKCLDVPFAICDCTTLTQAGYVGEDIESVIAKLLQDANYN
1	1		VEKAQQGIVFLDEVDKIGSVPGIHQLRDVGGEGVQQGLLKLLEG
1			
1			TIVNVPEKNSRKLRGETVQVDTTNILFVASGAFNGLDRIISRRK
1			NEKYLGFGTPSNLGKGRRAAAAADLANRSGESNTHQDIEEKDRL
1 1	1		LRHVEARDLIEFGMIPEFVGRLPVVVPLHSLDEKTLVQILTEPR
		*	NAVIPQYQALFSMDKCELNVTEDALKAIARLALERKTGARGLRS
1 .	1		IMEKLLLEPMFEVPNSDIVCVEVDKEVVEGKKEPGYIRAPTKES
<b></b>			SEEEYDSGVEEEGWPRQADAANS
5461	1481	160	INPPPPPKSPCGRARKWRRRRRPGAPEAAVMELPSGPGPERLFD
ł .			SHRLPGDCFLLLVLLLYAPVGPCLLVLRLFLGIHVFLVSCALPD
1 1	(		SVLRRFVVRTMCAVLGLVARQEDSGLRDHSVRVLISNHVTPFDH
1 1			NIVNLLTTCSTPLLNSPPSFVCWSRGFMEMNGRGELVESLKRFC
1 1	ľ		ASTRLPPTPLLLFPEEEATNGREGLLRFSSWPFSIQDVVQPLTL
1 1			UNDBINGALACTOR SERVINGED THE EMBERGADA PARTIES CO.
1 1			QVQRPLVSVTVSDASWVSELLWSLFVPFTVYQVRWLRPVHRQLG
1	į		EANBEFALRVQQLVAKELGQTGTRLTPADKAEHMKRQRHPRLRP
	i i		QSAQSSFPPSPGPSPDVQLATLAQRVKEVLPHVPLGVIQRDLAK
1 1	i		TGCVDLTITNLLEGAVAFMPEDITKGTQSLPTASASKFPSSGPV
-			TPQPTALTFAKSSWARQESLQERKQALYEYARRRFTERRAQEAD
5462	663	3353	KIKEROMSANNSPPSAOKSVLPTAIPAVLPAASPCSSPKTGLSA
1 1	ĺ		RLSNGSFSAPSLTNSRGSVHTVSFLLQIGLTRESVTIEAQELSL
į l	}		SAVKDLVCSIVYQKFPECGFFGMYDKILLFRHDMNSENILOLIT
1	j		SADEIHEGDLVEVVLSALATVEDFQIRPHTLYVHSYKAPTFCDY
1	ł	j	CGEMLWGLVRQGLKCEGCGLNYHKRCAFKIPNNCSGVRKRRLSN
			VSLPGPGLSVPRPLQPEYVALPSEESHVHQEPSKRIPSWSGRPI
[ ]	ļ	1	WMEKMVMCRVKVPHTFAVHSYTRPTICQYCKRLLKGLFRQGMQC
	ł	1	KDCKFNCHKRCASKVPRDCLGEVTFNGEPSSLGTDTDIPMDIDN
1	ł		NOTING DESCRIPTION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROP
1	j		NDINSDSSRGLDDTEEPSPPEDKMFFLDPSDLDVERDEEAVKTI
1	ł		SPSTSNNIPLMRVVQSIKHTKRKSSTMVKEGWMVHYTSRDNLRK
1 1	i		RHYWRLDSKCLTLFQNESGSKYYKEIPLSEILRISSPRDFTNIS
	į	İ	QGSNPHCFEIITDTMVYFVGENNGDSSHNPVLAATGVGLDVAQS
1			WEKAIRQALMPVTPQASVCTSPGQGKDHKDLSTSISVSNCQIQE
1 1	1	Į	NVDISTVYQIFADEVLGSGQFGIVYGGKHRKTGRDVAIKVIDKM
ļ Ì			RFPTKQESQLRNEVAILQNLHHPGIVNLECMFETPERVFVVMEK
; !	ļ	1	LHGDMLEMILSSEKSRLPERITKFMVTQILVALRNLHFKNIVHC
į 1		}	
( )	Į.	í	DLKPENVLLASAEPFPQVKLCDFGFARIIGEKSFRRSVVGTPAY
}	1	l	LAPEVLRSKGYNRSLDMWSVGVIIYVSLSGTFPFNEDEDINDQI
(	1	1	QNAAFMYPPNPWREISGEAIDLINNLLQVKMRKRYSVDKSLSHP
			WLQDYQTWLDLREFETRIGERYITHESDDARWEIHAYTHNLVYP
			KHFIMAPNPDDMEEDP
5463	237	1012	LLSVTMTTSRCSHLPEVLPDCTSSAAPVVKTVEDCGSLVNGQPQ
<u> </u>			YVMQVSAKDGQLLSTVVRTLATQSPFNDRPMCRICHEGSSQEDL

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Ī	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
			LSPCECTGTLGTIHRSCLEHWLSSSNTSYCELCHFRFAVERKPR
	1	į.	PLVEWLRNPGPQHEKRTLFGDMVCFLFITPLATISGWLCLRGAV
	İ		DHLHFSSRLEAVGLIALTVALFTIYLFWTLVSFRYHCRLYNEWR
L	<u></u>	}	RTNQRVILLIPKSVNVPSNQPSLLGLHSVKRNSKETVV
5464	195	677	SPSMNPRKKVDLKLIIVGAIGVGKTSLLHQYVHKTFYEEYQTTL
j			GASILSKIIILGDTTLKLQIWDTGGQERVRSMVSTFYKGSDGCI
1	ļ		LAFDVTDLESFEALDIWRGDVLAKIVPMEQSYPMVLLGNKIDLA
			DRKYQSILENHLTESIKLSPDQSRSRCC
5465	5278	3348	KGDPREFIRVHREALECDYVSAHLHEWIDLIFGYKQQGPAAVEA
			VNVFHHLFYEGQVDIYNINDPLKETATIGFINNFGQIPKQLFKK
			PHPPKRVRSRLNGDNAGISVLPGSTSDKIFFHHLDNLRPSLTPV
1			KELKEPVGQIVCTDKGILAVEQNKVLIPPTWNKTFAWGYADLSC
1			RLGTYESDKAMTVYECLSEWGQILCAICPNPKLVITGGTSTVVC
[			VWEMGTSKEKAKTVTLKQALLGHTDTVTCATASLAYHIIVSGSR
,			DRTCIIWDLNKLSFLTQLRGHRAPVSALCINELTGDIVSCAGTY
			IHVWSINGNPIVSVNTFTGRSQQIICCCMSEMNEWDTQNVIVTG
ĺ			HSDGVVRFWRMEFLQVPETPAPEPAEVLEMQEDCPEAQIGQEAQ
ļ			DEDSSDSEADEQSISQDPKDTPSQPSSTSHRPRAASCRATAAWC
j .			TDSGSDDSRRWSDQLSLDEKDGFIFVNYSEGQTRAHLQGPLSHP
			HPNPIEVRNYSRLKPGYRWERQLVFRSKLTMHTAFDRKDNAHFA
i i			EVTALGISKDHSRILVGDSRGRVFSWSVSDQPGRSAADHWVKDE
1 1			GGDSCSGCSVRFSLTERRHHCRNCGQLFCQKCSRFQSEIKRLKI
5466			SSPVRVCQNCYYNLQHERGSEDGPRNC
3466	3	992	HACAHASAHASGRLVRWWRKRRSVMGIQTSPVLLASLGVGLVTL
i i			LGLAVGSYLVRRSRRPQVTLLDPNEKYLLRLLDKTTVSHNTKRF
, ,			RFALPTAHHTLGLPVGKHIYLSTRIDGSLVIRPYTPVTSDEDQG
			YVDLVIKVYLKGVHPKFPEGGKMSQYLDSLKVGDVVEFRGPSGL
1 1			LTYTGKGHFNIQPNKKSPPEPRVAKKLGMIAGGTGITPMLQLIR
1 1			AILKVPEDPTQCFLLFANQTEKDIILREDLEELQARYPNRFKLW FTLDHPPKDWAYSKGFVTADMIREHLPAPGDDVLVLLCGPPPMV
			QLACHPNLDKLGYSQKMRFTY
5467	2103	4	GEALRYGTRGCRRDLPDPQARIFIQKKDLEEDESVTAAHLKSRG
1 !		-	RSPRKIDQFCNSSNMVHGSVTFRDVAIDFSQREWECLQPDQRTL
}	}		YRDVMLENYSHLISLAGSSISKPDVITLLEQBKEPWMVVRKETS
[ ]			RRYPDLELKYGPEKVSPENDTSEVNLPKQVIKQISTTLGIEAFY
1 1	1		FRNDSEYROFEGLOGYQEGNINQKMISYEKLPTHTPHASLICHT
]	ì		HKPYECKECGKYFSCGSNLIQHQSIHTGEKPYKCKECGKAFQLH
	:		IQLTRHQKFHTGEKTFECKECGKAFNLPTOLNRHKNIHTVKKLF
} }			ECKECGKSFNRSSNLTQHQSIHAGVKPYQCKECGKAFNRGSNLI
l l			QHQKIHSNEKPFVCKECGMAFRYHYQLIEHCQIHTGEKPFECKE
] 1	ļ		CGKAFTLLTKLVRHQKIHTGEKPFECRECGKAFSLLNQLNRHKN
	i		IHTGEKPFECKECGKSFNRSSNLVQHQSIHAGIKPYECKECGKG
1 1	1		FNRGAHLIQHQKIHSNEKPFVCRECEMAFRYHCQLIEHSRIHTG
1	ŀ	i	DKPFECQDCGKAFNRGSSLVQHQSIHTGEKPYECKECGKAFRLY
	ĺ		LQLSQHQKTHTGEKPFECKECGKFFRRGSNLNQHRSIHTGKKPF
1 1	4		ECKECGKAFRLHMHLIRHQKLHTGEKPFECKECGKAFRLHMQLI
<u> </u>			RHQKLHTGEKPFECKECGKVFSLPTQLNRHKNIHTGEKAS
5468	225	2976	SFLTDLFQSLAQLENLCKQLYETTDTTTRLQAEKALVEFTNSPD
[			CLSKCQLLLERGSSSYSQLLAATCLTKLVSRTNNPLPLEQRIDI
]			RNYVLNYLATRPKLATFVTQALIQLYARITKLGWFDCQKDDYVF
] ].			RNAITDVTRFLQDSVEYCIIGVTILSQLTNEINQVSATAFLIEA
1	ĺ	1	DTTHPLTKHRKIASSFRDSSLFDIFTLSCNLLKQASGKNLNLND
j		Ì	ESQHGLLMQLLKLTHNCLNFDFIGTSTDESSDDLCTVQIPTSWR
		}	SAFLDSSTLQLSTIGRCEYEKTCALLVQLFDQSAQSYQELLQSA
	1	ſ	SASPMDIAVQEGRLTWLVYIIGAVIGGRVSFASTDEQDAMDGEL
<u> </u>	1		VCRVLQLMNLTDSRLAQAGNEKLELAMLSFFEQFRKIYIGDQVQ
]	j		KSSKLYRRLSEVLGLNDETMVLSVFIGKIITNLKYWGRCEPITS
	1		KTLQLLNDLSIGYSSVRKLVKLSAVQFMLNNHTSEHFSFLGINN
			QSNLTDMRCRTTFYTALGRLLMVDLGEDEDQYEQFMLPLTAAFE
	İ	1	AVAQMFSTNSFNEQEAKRTLVGLVRDLRGIAFAFNAKTSFMMLF
	<del></del>		EWIYPSYMPILQRAIELWYHDPACTTPVLKLMAELVHNRSQRLQ

680	Dendistra	Dec 21 at a 2 and	
SEQ	Predicted beginning	Predicted end nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
No.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ľ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
		<del> </del>	FDVSSPNGILLFRETSKMITMYGNRILTLGEVPKDQVYALKLKG
į.	1		ISICFSMLKAALSGSYVNFGVFRLYGDDALDNALOTFIKLLLSI
İ	ļ	İ	PHSDLLDYPKLSQSYYSLLEVLTQDHMNFIASLEPHVIMYILSS
1		j	ISEGLTALDTMVCTGCCSCLDHIVTYLFKOLSRSTKKRTTPLNO
İ			ESDRFLHIMOOHPEMIQOMLSTVLNIIIFEDCRNOWSMSRPLLG
			LILLNEKYFSDLRNSIVNSQPPEKQQAMHLCFENLMEGIERNLL
i .	ł		TKNRDRFTQNLSAFRREVNDSMKNSTYGVNSNDMMS
5469	134	2653	DQEFETSLVPWHLPMGWLCSGLLFPVSCLVLLQVASSGNMKVLQ
			EPTCVSDYMSISTCEWKMNGPTNCSTELRLLYQLVFLLSEAHTC
1	l	1	VPENNGGAGCVCHLLMDDVVSADNYTLDLWAGQQLLWKGSFKPS
		j	EHVKPRAPGNLTVHTNVSDTLLLTWSNPYPPDNYLYNHLTYAVN
}		ŀ	IWSENDPADFRIYNVTYLEPSLRIAASTLKSGISYRARVRAWAQ
1	[		CYNTTWSEWSPSTKWHNSYREPFEQHLLLGVSVSCIVILAVCLL
1	i	}	CYVSITKIKKEWWDQIPNPARSRLVAIIIQDAQGSQWEKRSRGQ
}	1		EPAKCPHWKNCLTKLLPCFLEHNMKRDEDPHKAAKEMPFQGSGK
1			SAWCPVEISKTVLWPESISVVRCVEL?EAPVECEZEEEVEEEKG
	1		SFCASPESSRDDFQEGREGIVARLTESLFLDLLGEENGGFCQQD
ł			MGESCLLPPSGSTSAHMPWDEFPSAGPKEAPPWGKEQPLHLEPS
	1		PPASPTQSPDNLTCTETPLVIAGNPAYRSFSNSLSQSPCPRELG
1 .			PDPLLARHLEEVEPEMPCVPQLSEPTTVPQPEPETWEQILRRNV
1			LOHGAAAAPVSAPTSGYQEFVHAVEQGGTQASAVVGLGPPGEAG
}			YKAFSSLLASSAVSPEKCGFGASSGEEGYKPFQDLIPGCPGDPA PVPVPLFTFGLDREPPRSPOSSHLPSSSPEHLGLEPGEKVEDMP
1			KPPLPQEQATDPLVDSLGSGIVYSALTCHLCGHLKQCHGQEDGG
			QTPVMASPCCGCCCGDRASPPTTPLRAPDPSPGGVPLEASLCPA
ľ			SLAPSGISEKSKSSSSFHPAPGNAQSSSQTPKIVNFVSVGPTYM
ł			RVS
5470	17	1418	TACRIRTSLNRGIAAVKRDAVEMLASYGLAYSLMKFFTGPMSDF
			KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI
İ			INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY
1			SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA
			LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA
1			LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP
1			YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA
}			LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF
l			PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYL
l		i	GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKKMENESAT
			EGEDSAMTDMPPTEEVTDIVEMREENE
5471	1868	658	RSSAPPGPQRAAAATAAAAAAGVEMAAAAAQGGGGGEPRRTEGV
l			GPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVR
	İ		KTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILR
	İ		ASTLEAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR
1 .	,	ı	GLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHD
]			HTGFLTEYVATRWYRAPEINLNSKGYTKSIDIWSVGCILAEMLS NRPIFPGKHYLDQLNHILGILGSPSQBDLNCIINMKARNYLQSL
[			PSKTKVAWAKLFPKSDSKALDLLDRMLTFNPNKRITVEEALAHP
1	.		YLEQYYDPTDEPVAEEPFTFAMELDDLPKERLKELIFQETARFO
]			PGVLEAP
5472	1469	753	LYVMARYLSDEEVAVSIDRLCKANGRSPSIPFGTVRIPGRARVR
		, 55	DPOALWIFGYGSLVWRPDFAYSDSRVGFVRGYSRRFWQGDTFHR
	i		GSDKMPGRVVTLLEDHEGCTWGVAYQVQGEQVSKALKYLNVREA
			VLGGYDTKEVTFYPODAPDOPLKALAYVATPONPGYLGPAPEEA
1			IATOILACRGFSGHNLEYLLRVRDVMOLCGPQAQDEHLAAIVDA
1			VGTMLPCFCPTEQALALV
5473	3	2119	FMNVKLLIQDLEDIEQRVPVMDAQYKIITKTAHLITKESPQEEG
	=		KEMFATMSKLKEOLTKVKECYSPLLYESOOLLIPLBELEKOMTS
			FYDSLGKINEIITVLEREAGSSALFKOKHQELLACQENCKKTLT
			LIEKGSQSVQKFVTLSNVLKHFDQTRLQRQIADIHVAFQSMVKK
			TGDWKKHVETNSRLMKKFEESRAELEKVLRIAQEGLEEKGDPEE
			LLRRHTEFFSQLDQRVLNAFLKACDELTDILPEQEQQGLQEAVR
[			KLHKQWKDLQGEAPYHLLHLKIDVEKNRFLASAEECRTELDRET

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
j	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	bequence	\=possible nucleotide insertion)
		<del>                                     </del>	KLMPQEGSEKIIKEHRVFFSDKGPHHLCEKRLQLIBELCVKLPV
			RDPVRDTPGTCHVTLKELRAAIDSTYRKLMEDPDKWKDYTSRFS
ı			EFSSWISTNETQLKGIKGEAIDTANHGEVKRAVEEIRNGVTKRG
1	1	ĺ	ETLSWLKSRLKVLTEVSSENEAQKQGDELAKLSSSFKALVTLLS
1			EVEKMLSNFGDCVQYKEIVKNSLEELISGSKEVQEQAEKILDTE
	1 .	İ	NLFEAQQLLLHHQQKTKRISAKKRDVQQQIAQAQQGEGGLPDRG
ĺ			HEELRKLESTLDGLERSRERQERRIQVTLRKWERFETNKETVVR
Ì	ł	}	YLFQTGSSHERFLSFSSLESLSSELEQTKEFSKRTESIAVQAEN
ł		}	LVKEASEIPLGPQNKQLLQQQAKSIKEQVKKLEDTLEEEYVIDK
			S S
5474	2	780	TPDVRQLQASRRGIAVASWCSPRWFAGEEMAFVKSGWLLRQSTI
1	i -		LKRWKKNWFDLWSDGHLIYYDDQTRQNIEDKVHMPMDCINIRTG
1	ļ		QECRDTQPPDGKSKDCMLQIVCRDGKTISLCAESTDDCLAWKFT
1			LQDSRTNTAYVGSAVMTDETSVVSSPPPYTAYAA?APEVGRTLS
1			LQQAYGYGPYGGAYPPGTQVVYAANGQAYAVPYQYPYAGLYGQQ
1			PANQVIIRERYRDNDSDLALGMLAGAATGMALGSLFWVF
5475	2	506	ARGWLESLSLTCQTTPPPSSPCLLHSPETFIHTMPPNLTGYYRF
1			VSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTL
1			STFRNYTVQFDVGVEFEEDLRSVDGRKCQTIVTWEEEHLVCVQK
1			GEVPNRGWRHWLEGEMLYLELTARDAVCEQVFRKVR
5476	192	1457	SDSMSLLDCFCTSRTQVESLRPEKQSETSIHQYLVDEPTLSWSR
			PSTRASEVLCSTNVSHYELQVEIGRGFDNLTSVHLARHTPTGTL
[			VTIKITNLENCNEERLKALQKAVILSHFFRHPNITTYWTVFTVG
1 1			SWLWVISPFMAYGSASQLLRTYFPEGMSETLIRNILFGAVRGLN
[			YLHQNGCIHRSIKASHILISGDGLVTLSGLSHLHSLVKHGQRHR
]			AVYDFPQFSTSVQPWLSPELLRQDLHGYNVKSDIYSVGITACEL
1			ASGQVPFQDMHRTQMLLQKLKGPPYSPLDISIFPQSESRMKNSQ
			SGVDSGIGESVLVSSGTHTVNSDRLHTPSSKTFSPAFFSLVQLC
1 1			LQQDPEKRPSASSLLSHVFFKQMKEESQDSILSLLPPAYNKPSI
			SLPPVLPWTEPECDFPDEKDSYWEF
5477	3	1044	RGNSRLRYSHEDELQLPRLPELFETGRQLLDEVEVATEPAGSRI
1 /			VQEKVFKGLDLLEKAAEMLSQLDLFSRNEDLEEIASTDLKYLLV
1 1			PAFQGALTMKQVNPSKRLDHLQRAREHFINYLTQCHCYHVAEFE
1 1			LPKTMNNSAENHTANSSMAYPSLVAMASQRQAKIQRYKQKKELE
1 [	[		HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLEEIESIDQ
1 1			EIKILRERDSSREASTSNSSRQERPPVKPFILTRNMAQAKVFGA
1	]	ļ	GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPEEFRKAAQQQE
5478			EQEEKEEEDDEQTLHRAREWDDWKDTHPRGYGNRQNMG
34/0	2	835	KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT
1	1	ł	VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK
	l		LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW
		į	DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL
[	į	i	MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF
	i		DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC
5479	2	835	LENQQLIMQRATP
j	~	033	KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT
]		1	VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK
(	ĺ		LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW
1 1	1	j	DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MFGPLLYTLUGUGDATTE/ARSPTGRYFRSGGDDOWN
	ļ	Ì	MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF
	İ		DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP
5480	444	1952	
	***	1932	LSITSRMEEAELVKGRLQAITDKRKIQEEISQKRLKIEEDKLKH QHLKKKALREKWLLDGISSGKEQEEMKKQNQQDQHQIQVLEQSI
) 1		1	T.DI.FYFTODI.FYAFI OTOTYPPATT PUT YOTAPHATATA
[	j	[	LRLEKEIQDLEKAELQISTKEEAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR
1 1		i	KALVAMETKVEKDI. KUCEGUULGOTDI DODDENOGGI MENDEQNR
! [			KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEFILDOASEDNEKSDTEVH
, i			KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYANPFYRPTTPQRETVTPGPNFQERIKIKTNGLGIGVNESI
ĺ	1	İ	HNMGNGLSEERGNNFNHISPIPPVPHPRSVIQQAEEKLHTPQKR
			THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VEHICLE OF THE VE

Designating	SEQ	Predicted	Predicted end	
Notation   Corresponding				Amino acid segment containing signal peptide
Corresponding				Gluramic Acid Rephenylalanian Columbia
COTTEMPORATION  to first amino acid residue of amino acid residue of amino acid sequence  Seguence  DEPUNTATION  THYPODINE, "CHURATION, VAVILINE," SEGINE, THYPODINE, VAVILINE, WINKNOWN, "SEGO COCO," "PODSIBLE MUCLECTIC de deletion," Lapossible mucleotide deletion," Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible mucleotide deletion, Lapossible deletion,	1			H-Histidine I-Tsoleugine Multimine, G-Glycine,
To first   maino acid   residue of		1		L-Leucine M-Methionine M-X
### amino acid residue of ### amino acid sequence	1		ł .	P=Proline O=Glutamine P=Argining
# Tryptophan, Y=Tyzosine, X=Dixinown, *stop amino acid sequence  # Tryptophan, Y=Tyzosine, X=Dixinown, *stop coden, /=possible nucleotide deletion.    Poposible nucleotide deletion   Poposible nucleotide deletion   Poposible nucleotide deletion   Poposible nucleotide insertion   Poposible nucleotide insertion   Poposible nucleotide insertion   Poposible nucleotide insertion   Poposible nucleotide insertion   Poposible nucleotide insertion   Poposible nucleotide insertion   Poposible nucleotide insertion   Poposible nucleotide insertion   Poposible nucleotide insertion   Poposible nucleotide insertion   Poposible nucleotide insertion   Poposible nucleotide insertion   Poposible nucleotide insertion   Poposible nucleotide insertion   Poposible nucleotide insertion   Poposible nucleotide insertion   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotide   Poposible nucleotid	1	amino acid		
Sequence   Codon, /-possible nucleotide deletion,	Į.	residue of		W=Tryptophan, Y=Tyrosine X-Unknown +-crom
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5482  1492  528  THOWMINGVARHOULEY INGUTTS KEPOZALVISHDERNILEL EGIQEKDSGPYSCS VINVQDKQGKSRGHS IKTLELAVLIVPPAPPS CRIGGOPHYGANVILSCOSPRSKPAVQYQWDROJLSFGTFFAPA LDVIRGSLSLINLSSSMAGVYVCKHAVEVSTAGCAVILSVENGE GAAVVAGAVVAGIAVGILAGULLAGUVLIYHRGKALBEPANDIKEDA LAPRILIPPHYSSDTISKMGTUSSVINSALPPHOEPHPEPALTT TPSLSSQALPSPRIPTTDGAHPQPISPIPGGVSSGLSRMGAVP WWPADSQAGSLV  S483  1 788  FFFFKGCRAGKGNESDYRKLEEMHQRFLVSERSKDDLQLRLITRA ENRIKQLETDSSERIGRVP WWPADSQAGSLV  KLQCENKQURRITESJRKITALBAQKKAKWISTMEHPSI KERG FEVQLSRRMEDSNRRSIVELRHLLATQGKAANRWKETKKLTESA KLQCENKQURRITESJRKITALBAQKKAKWISTMEHPSI KERG FEVQLSRRMEDSNRRSIVELRHLLATQGKAANRWKETKKLTESA KRIKINNLKSELSRGKURKLTELSLAGURAVVAGVESGRIL KLAQENKGURRITESJRKIKALBAQKKAKWISTMEHPSI KERG FEVQLSRRMEDSNRRSIVELRHLLATQGKAANRWKETKKLTESA KRIKINNLKSELSRGKURTHELLSQLERKVASDSGSDEDGNAASGSNESSELSGDDERGASGSNESSELSGENGEN KARRLORRLSGABERAASASQALSVITVQRRKAASGSNAGSS ESDQDERGBSGQPSNRSIFODDERAASGSNAGSSSARGSSENDENDASSGSBENDERAASGSNAGSSENDERAASGSNAGSSELSGDDERAASGSNAGSSELSGDDERAASGSNAGSSELSGDDERAASGSNAGSSELSGDDERAASGSNAGSSELSGDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNAGSSELSGDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDERAASGSNEKSDDER				CIMNAVEWNKKEELVAEQALKHLKQYAPLLAVFSSQGQSELILL
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EGIQEROSGPYSCSVINVODROGISSRHSIKTIELIVTUVPPAPPS CRLOGVPHYGANVTLSCQSPRSHAVCYCWDNOGLPSTGTFFAPA LDVIRGSLSITHLISSSSMAGYVYCKANNEWGTACOLVTLEWSTGG GAAVVAGAVVGTUVGLGILAGLULIVHRIRGKALEEPANDIKEDA LDVIRGSLSITHLISSSSMAGYVYCKANNEWGTACOLVTLEWSTGG GAAVVAGAVVGTUVGLGILAGLULIVHRIRGKALEEPANDIKEDA LAPRTLIPWKSSDTISKINGTLSSVTSARALRPPHOPPEGALTP TPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSRMGAVP VWVPAQSQAGSLV  S483  1 788 FFFFKGCRAGRONESDYRKLEEMHQRFLVSERSKDDLQLRLITRA ENRIKQLETDSSEELSYQEMIQKLQNVLJSEERSNCGLVSSQAL KLQQENKQLRKSTESLAKILLEHOGLKAKKKKKISTMEHPESIKEKG FEVGLREMEDSNRNSIVELRHLLATQOKAANNWEETKKLITESA RIKINLKSELSGAGKHTYGELSQLAMANBKVASPEKLILEHOG KAMRLQRELSQAERAASASQQLSVITVQRRKAASLNNLENI  S484 3 1997 IMADMEDLEGSBADSERERKOSDSGSBSDSDDFORAASGSNAGGS ESDQDERGGSGQPGNKELFODDESGASHHSGSDNISERSDNR SRASERSHENDDPSDVDQHSGSEAPNDDEDGHRAASGSNAGGS ESDQDERGGSGQPGNKELFODDESGASHHSGSDNISERSDNR SRASERSHENDDPSDVDQHSGSEAPNDDEDGHRAASGSNAGGS AGSGEKAHSDDEKKGRSDKSGDSGDBGASHNGSDDRERPAN SCHABEKGNSDDEERQPLSDERROGSBERHSGD SERANSDEKGNSDDEERQPLSDERROGSBERHSG SARGHSDEKGNDDEERQPLSDERROGSBEHHSGD EERQDHKSESARGSDSDEVKTONDDERRAGGSBEHK LQNSDDDEKGNSDAERGDLSDERKONNSDDERPQAN SDEEHHSDD EERQDHKSESARGSBEDVLRMKRKNALASDSEADSDTEVPKD NSGTMDLEGGADDISGSGENKPTFGQFVDENGLEQQQEEE P1PETRIEVEIPKWTDLGNDLIFVKLSPNETSVEPREFDPQYYE DEFEDEEMLDEERGTELKLKVENTITWELSVEPREFDPQYYE DEFEDEEMLDEERGTELKLKVENTITWELSVEPREFDPQYEE DEFEDEEMLDEERGTELKLKVENTITWELSVEPREFDPQYEE DEFEDEEMLDEERGTELKLKVENTITWELSVEPREFDPQYEE DEFEDEEMLDEERGTELKKLKTSDEVGRAREKONGLASAYLE PDDYNEBEEGGESISLAAIKNRYKGGIREERARIYSSDSDEGSE EDKAQRLLKAKKLTSDEVGRIFKGNOMERKHYLCG CCAARNNVATITFJOKJENKFTNTQAKARALKCHGI GEYYGGLVPILMRKTTLAMFGLYSDLSCLLHKNVSAPEFATSGVAA VLAGTTERIFPTERVYTLLDOHKSVETNTVQAKARALKCHGI GEYYGGLVPILMRKTTLAMFGLYSDLSCLLHKNVSAPEFATSGVAA VLAGTTERIFPTERVYTLLDOHKSVETNTVQAKARALKCHGI GEYYGGLVPILFRNGLSNVLPFGLRGPIKEHLPTATTHSAHLVN DPICCGLLGAMLGFLFFPTINVVKTRIOSGIGGFGFFFNVFQKI WEERDRKLLNILFRSAGANGKFENDGGELLEDDLPPASSGDS GSLATSISWSPAAARGGSVCCCCLHFSSAMDLFGDLPFEERSFP FAAGKEARLKGFEREMQDAHVILUNITRFFKGDVISVEKTVKCL LDTFKHTOEEFIKQASSOKPAMKOGSTATCULAVDNILTIANLG DSRALLCK				
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to first amino acid sequence    Note	1			
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residue of amino acid sequence (codon, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide insertion)  5487 538 182 AVSIEGURGYPPENPISCOPTESKYQTREKISADDRYRAC NRLANKAVQRSGANNTYMVURIGR LEANDPFANNDDPFYYDMKNLQLSGLICOGLIAIAGIAAVLSGK (CKCKSQNQHSPVPENPISCOPTSCHARVTIALLLLAGUTA LEANDPFANNDDPFYYDMKNLQLSGLICOGLIAIAGIAAVLSGK (CKCKSQNQHSPVPENKATPLITTGSGATTC CKCKSQNQHSPVPENKATPLITTGSGATTC CKCKSQNQHSPVPENKATPLITTGSGATTC CKCKSQNQHSPVPENKATPLITTGSGATTC CKCKSQNQHSPVPENKATPLITTGSGATTC CKCKSQNQHSPVPENKATPLITTGSGATTC CKCKSQNQHSPVPENKATPLITTGSGATTC CKCKSQNQHSPVPENKATPLITTGSGATTC CKCKSQNQHSPVPENKATPLITTGSGATTC CKCKSQNQHSPVPENKATPLITTGSGATTC CKCKSQNQHSPVPENKATPLITTGSGATTC CKCKSQNQHSPVPENKATPLITTGATTSGATTC CKCKSQNQHSPVPENKATPLITTGATTSGATTC CKCKSQNQHSPVPENKATPLITTGATTSGATTC CKCKSQNAPATPLITTGATTCATTCATTCATTCATTCATTCATTCATTCATTCA			***************************************	
amino acid sequence    Codon, /=possible nucleotide deletion,   Lepassible nucleotide insertion	[	· ·		
Sequence	1			Welryptopnan, Yelyrosine, Asunkhown, **Stop
ACOGLEKYTPEEAWFILISCLEDERKIGTREGKSADDARVEDAC   RILLANKANGROSANDVIAWVIG BR   SAST   182		1	sequence	
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HERPTIGEGIGANCCUQARALGAMTSWCKVGKESGENDYIEN LKQMDISTEPTYQTOKDANTGAS IIVANGGALIUVAGANILL NTEDLRAARHVIGRAKWWCQLEITPARSLEALTMARRSGVKTL FREADARADLDOPYTLSDUPCCNESBAEILTGLTVGSAADAGE RALVLKRGCQVVIITLGASGCVVLSQTEPERHIPTEKVRAVY TTUSFRI  5489 81 893 GKGFVARFIDGSNIFLTDPKIFLGQWREEPRMFLLLIGETEPLK LERDCRSDVERWAASSPDLALACLCHCQDLSSGAPFRKGVLGGV LFPTVEMVIKVFVATSGSGIARKKQGEVVGJERNKIDFKELD LAGDEDNRRMRENVEGKKPONGIPLPPGIFNEGQVGDFDFS FRAKEENIIYSFIGLAPPPDSKGSKKAGGGFTEAQKEGSEDVG NLPFAQGKREEGETATETEELAMEGAGEGEAEEEETARGEEP GEDEDS  5490 81 693 GKGFVARFIDGSNIFLITDPKIFLGQWREEPKMFLLLLGETEPLK LERDCRSDVEBWAAASPDLALACLCHCQDLSSGAPPNRGVLGGV LFPTVEMVIKVFVATSSGSIALACLCHCQDLSSGAPPNRGVLGGV LFPTVEMVIKVFVATSSGSIALACLCHCQDLSSGAPPNRGVLGGV LFPTVEMVIKVFVATSSGSIALACHCQDLSSGAPPNRGVLGGV LFPTVEMVIKVFVATSSGSIALACHCQDLSSGAPPNRGVLGGV LFPTVEMVIKVFVATSSGSIALRKKQGBVVGFLEANKIDFKELD IAGDEDNRRMRENVPGSKKPORGIPLPPGSVGGFDFSF FRAKEENIIYSFIGLAPPDBKSSEKABEGGTERAQKESSEDVG NLPFAQGKNEEGEGTATTETELAMEGAGEGAEEEETARGEEP GEDEDS  5491 204 1194 GGAPRISLEDPTGARAEDPBDKSSEKABEGGTERAQKESSEDVG NLPFAQGKNEEGEGTATTETETELAMEGAGEGAEEEETARGEEP GEDEDS  5492 5491 204 1194 GGAPRISLEDPTGARAEDPBDKSSEKABEGGTERAQKESBUVG NLPFAQGKNEEGEGTATTETETELAMEGAGEGAEEEETARGEEP GEDEDS  5492 5492 5493 1696 ASKRIPLSAVTCTTGIMSSLAVRDPRGVLSVAVVKLDPGGRNDQI PEKKOKEANTGFGGPVISSLAVTCTGIMSSLAVVVKLDPGGRNDQI PEKKOKEANTGFGGPVISSLAVTCTGIMSSLAVVVKLDPGGRNDQI PEKKOKEANTGFGGPVISSLAVTCTGIMSSLAVVVKLDPGGRNDQI PEKKOKEANTGFGGPVISSLAVTCTGTRETGKRYGFGCTQDGCTALSAM RNLNGGEFSGRALRVANASEEKKELGFARFITDSFVDP UNCHTPTOGGTARGPUTPAMAGERGKKEKELKSLGFARFITDSFVDP UNCHTPTOGGTARGPUTPAMAGERGKKEKELKSLGFARFITDSFVDP UNCHTPTOGGTARAFUNDALAGERGKEKEKELKSLGFARFITDSFVDP UNCHTPTOGGTARAFUNDALAGGRAFTERAFTERATE GGTLLSVTGEVEFRGTLUPHQGPPMHLAGGDARAFTRAMFTE ULTRVMERRAMTCAMFTRAMFRAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	i	1	ļ	CKCKSSQKQHSPVPEKAIPLITPGSATTC
LKOMDISTEFTYQTKURATGTSI ITVNNEGONI LUTUAGANILLI NTEDLARAANUSRAWWOCQUE ITPARSEGUETHARRAGSGUETH PRAPAJALDEDOPTYLEDUYCCNESSAEILYGLIYGSAADAGE AALVYLKRGCQVYLTITGABGCVVLSQTEFEPRHIPTEKVKAVD TTVSFKI  5489 81 893 GKGFVARFIDGSNIFLTDPKIFLGQWREEPRHPLLLLGETEPLK LERDCRSVDRWRAASSDIALACLCHCQDLSSGAFPNRGVLGGV LFPTVEMVIKYFVATSSGSIAIRKKQQSVVGHLRAKKIDFKKLD LAGDENNRRWRRNVPGSKRYGNGI PLPPGIPNEGVCGDFDSF FSAKEENI YSFIGLAPPPDSKGSEKABEGGTERAQKGSGSDVG NLPFAQEKNEEGEGTATTEFTE IAMEGAGGTERAQKGSGSDVG NLPFAQEKNEEGEGTATTEFTE IAMEGAGGTERAQKGSGSDVG NLPFAGENBEEGETATTEFTE IAMEGAGGTERAQKGSGSDVG NLPFAGENBEEGETATTEFTE IAMEGAGGTERAQKGSGSDVG NLPFAGENBEEGETATTEFTE IAMEGAGGABEEETATGGEEP LERDCRSPVEBWAAASDDIALACLCHCQDLSSGAPPNRGVLGGV LEPPTWEMIKYPVATSSGSIATRKKQGDVGFDRSP FSAKEENI YSFIGLAPPPDGKSEKABGGTERAQKGSGSDVG NLPFAGENBEAGGATTATEFTE IAMEGAGGABEEETATGGEEP SAKEENI YSFIGLAPPPDGKSEKKABGGGATARANIDFKELD LAGDEDNRRMRENVEGKKPQMGI PLPPGIFNEGVCGDFDSP FSAKEENI YSFIGLAPPPDGKSEKKABGGABEEEETABGEEP GEBEDS  5491 204 1194 GSAPRISLGFTGAQARDPDWWARPFSRPYTGSKEDRPDTEGRSE QCDMASSFLPAGAITGDGGCELSSGIDSGEVEFRSPEIEETSC LAELFEKAARALGGIJOVASREGLIYLYAAYVUVKNICKTEKP SFPFFFGKQKKABWKALGDSDGGELSSGIDSGEVEFRSPEIEETSC LAELFEKAARALGGIJOVASREGLIYLYAAYVUVKNICKTEKP SFPFFFGKQKKABWKALGDSDGGELSSGIDSGEVEFRSPEIEETSC LAELFEKAARALGGIJOVASREGLIYLYATVUVKLDPGKMPQI PEKKGEANTGGGVISSLYHEETIREEDHYCRGENITD ITKA I KSKQUVUVNVKOBEGBALLHWACCRGHKELVTULQHRAD INCOMEGGTALHYSAGCETIJUVELILLGGGATICHCOGGNDG TITKA I KSKQUVUVNVKOBEGBALLHWACCRGHKELVTULLGHRAD INCOMEGGTALHYSAGCETIJUVELILLGGAGGAT ILKGGLOVGKTOSHAD PLOVENTOKA SKRPLLARTGIN SAKERKELKISLGYOKONTOKANO UNDERGTALHYSAGCETIJUVELILLGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	5488	1072	259	AMAASGEPQRQWQEEVAAVVVVGSCMTDLVSLTSRLPKTGETIH
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VLETRVMERRGMETCAMETRGMEARGMDARGLEMRGPVPSSRGP MTGGIQGPGPINIGAGGPPQGPRQVPGISGVGNPGAGMQGTGIQ GTGMQGAGIQGGMQGAGIQGYSIQGGGIQGASKQGGSQ PSSFSFGQSQVTPQDQEKAALIMQVLQLTADQIAMLPPEQRQSI LILKEQIQKSTGAS  1 1876 RAPMMTKAVPEEPRKPGRLTQALMSPLTWEHVWICVPGGTPDCL TDTFRVKRPHLRRSASNGHVPGTPVYREKEDMYDEIIELKKSLH VQKSDVDLMRTKLRRLEEENSRKDRQIEQLLDPSRGTDFVRTLA EKRPDASWVINGLKQRILKLEQQCKEKDGTISKLQTDMKTTNLE EMRIAMETYYEEVHRLQTLLASSETTGKKPLGEKKTGAKRQKKM GSALLSLSRSVQELTEENQSLKEDLDRVLSTSPTISKTQGYVEW SKPRLLRRIVELEKKLSVMESSKSHAAEPVRSHPPACLASSSAL HRQPRGDRNKDHERLGAVROLKEERTALQEQLLQRDLEVKQLL QAKADLEKBLECARBGEEERREREVLRERIQTLTSKLQELQEM KKBEKEDCPEVPHKAQELPAPTPSSRHCEQDWPPDSSBEGLPRP	i	ľ		
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GTGMQGAGIQGGMQGAGIQGVSIQGGGIQGASKQGGSQ PSSFSPGQSQVTPQDQEKAALIMQVLQLTADQIAMLPPEQRQSI LILKEQIQKSTGAS  1 1876 RAPMMTKAVPEEPRKPGRLTQALNSPLTWEHVWICVPGGTPDCL TDTFRVKRPHLRRSASNGHVPGTPVYREKEDMYDEIIELKKSLH VQKSDVDLMRTKLRRLEEENSRKDRQIEQLLDPSRGTDFVRTLA EKRPDASWVINGLKQRILKLEQQCKEKDGTISKLQTDMKTTNLE EMRIAMETYYEEVHRLQTLLASSETTGKKPLGEKKTGAKRQKKM GSALLSLSRSVQELTEENQSLKEDLDRVLSTSPTISKTQGYVEW SKPRLLRRIVELEKKLSVMESSKSHAAEPVRSHPACLASSSAL HRQPRGDRNKDHERLBGAVRDLKEERTALQEQLLQRDLEVKQLL QAKADLEKBLECARBGEEERREREVLRERIQTLTSKLQELQEM KKBEKEDCPEVPHKAQELPAPTPSSRHCEQDWPPDSSBEGLPRP	1	1		
PSSFSPGQSQVTPQDQEKAALIMQVLQLTADQIAMLPPEQRQSI LILKEQIQKSTGAS  1 1876 RAPMMTKAVPEEPRKPGRLTQALNSPLTWEHVWICVPGGTPDCL TDTFRVKRPHLRRSASNGHVPGTPVYREKEDMYDEIIELKKSLH VQKSDVDLMRTKLRRLEEENSRKDRQIEQLLDPSRGTDFVRTLA EKRPDASWVINGLKQRILKLEQQCKEKDGTISKLQTDMKTTNLE EMRIAMETYYEEVHRLQTLLASSETTGKKPLGEKKTGAKRQKKM GSALLSLSRSVQELTEENQSLKEDLDRVLSTSPTISKTQGVVEW SKPRLLRRIVELEKKLSVMESSKSHAAEPVRSHPACLASSSAL HRQPRGDRNKDHERLRGAVRDLKEERTALQEQLLQRDLEVKQLL QAKADLEKBLECAREGEEERREREVLRERIQTLTSKLQELQEM KKBEKEDCPEVPHKAQELPAPTPSSRHCEQDWPPDSSBEGLPRP	1	i		
LILKEQIQKSTGAS  5493 1 1876 RAPMMTKAVPEEPRKPGRLTQALNSPLTWEHVWICVPGGTPDCL TDTFRVKRPHLRRSASNGHVPGTPVYREKEDMYDEIIELKKSLH VQKSDVDLMRTKLRRLEEENSRKDRQIEQLLDPSRGTDFVRTLA EKRPDASWVINGLKQRILKLEQQCKEKDGTISKLQTDMKTTNLE EMRIAMETYYEEVHRLQTLLASSETTGKKPLGEKKTGAKRQKKM GSALLSLSRSVQELTEENQSLKEDLDRVLSTSPTISKTQGYVEW SKPRLLRRIVELEKKLSVMESSKSHAAEPVRSHPPACLASSSAL HRQPRGDRNKDHERLRGAVRDLKEERTALQELQRDLEVKQLL QAKADLEKBLECAREGEEERREEEVLRERIQTLTSKLQELQEM KKBEKEDCPEVPHKAQELPAPTPSSRHCEQDWPPDSSBEGLPRP	1	1		
1 1876 RAPMMTKAVPEEPRKPGRLTQALMSPLTWEHVWICVPGGTPDCL TDTFRVKRPHLRRSASNGHVPGTPVYREKEDMYDEIIELKKSLH VQKSDVDLMRTKLRRLEEENSRKDRQIEQLLDPSRGTDFVRTLA EKRPDASWVINGLKQRILKLEQQCKEKDGTISKLQTDMKTTNLB EMRIAMETYYEEVHRLQTLLASSETTGKKPLGEKKTGAKRQKKM GSALLSLSRSVQELTEENQSLKEDLDRVLSTSPTISKTQGYVEW SKPRLLRRIVELEKKLSVMESSKSHAAEPVRSHPPACLASSSAL HRQPRGDRNKDHERLRGAVRDLKEERTALQEQLLQRDLEVKQLL QAKADLEKBLECAREGEEERREREEVLREBIQTLTSKLQELQEM KKBEKEDCPEVPHKAQELPAPTPSSRHCEQDWPPDSSBEGLPRP				
TDTFRVKRPHLRRSASNGHVPGTPVYREKEDMYDEIIELKKSLH VQKSDVDLMRTKLRRLEEENSRKDRQIEQLLDPSRGTDFVRTLA EKRPDASWVINGLKQRILKLEQQCKEKDGTISKLQTDMKTTNLE EMRIAMETYYEEVHRLQTLLASSETTGKKPLGEKKTGAKRQKKM GSALLSLSRSVQELTEENQSLKEDLDRVLSTSPTISKTQGVVEW SKPRLLRRIVELEKKLSVMESSKSHAAEPVRSHPPACLASSSAL HRQPRGDRNKDHERLRGAVRDLKEERTALQEQLLQRDLEVKQLL QAKADLEKBLECAREGEEERREREEVLREEIQTLTSKLQELQEM KKBEKEDCPEVPHKAQELPAPTPSSRHCEQDWPPDSSBEGLPRP	5/02	<del> </del>	1076	
VQKSDVDLMRTXLRRLEEENSRKDRQIEQLLDPSRGTDFVRTLA EKRPDASWVINGLKQRILKLEQQCKEKDGTISKLQTDMKTTNLE EMRIAMETYYEEVHRLQTLLASSETTGKKPLGEKKTGAKRQKKM GSALLSLSRSVGELTEENQSLKEDLDRVLSTSPTJSKTQGYVEW SKPRLLRRIVELEKKLSVMESSKSHAAEPVRSHPPACLASSSAL HRQPRGDRNKDHERLRGAVRDLKEERTALQEQLLQRDLEVKQLL QAKADLEKBLECAREGEBERREREVLREBIQTLTSKLQELQEM KKBEKEDCPEVPHKAQELPAPTPSSRHCEQDWPPDSSBEGLPRP	2433	1 1	19/9	WASHIITWAAREEKKERMIIONINGEADUMAHELLEI KAGI R KASHIITWAAREEKKERMIIONINGEADUMAHIOAEGISOOF
EKRPDASWVINGLKQRILKLEQQCKEKDGTISKLQTDMKTTNLE EMRIAMETYYEEVHRLQTLLASSETTGKKPLGEKKTGAKKQKKM GSALLSLSRSVQELTEENQSLKEDLDRVLSTSPTISKTQGYVEW SKPRLLRRIVELEKKLSVMESSKSHAAEPVRSHPPACLASSSAL HRQPRGDRNKDHERLRGAVRDLKEERTALQEQLLQRDLEVKQLL QAKADLEKBLECARBGEEERREREVLRERIQTLTSKLQELQEM KKBEKEDCPEVPHKAQELPAPTPSSRHCEQDWPPDSSBEGLPRP	1	Í		
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GSALLSLSRSVQELTEENQSLKEDLDRVLSTSPTISKTQGYVEW SKPRLIRRIVELEKKLSVMESSKSHAAEPVRSHPPACLASSSAL HRQPRGDRNKDHERLRGAVRDLKEERTALQEQLLQRDLEVKQLL QAKADLEKBLECAREGEERREEVLRERIQTLTSKLQEM KKEEKEDCPEVPHKAQELPAPTPSSRHCEQDWPPDSSBEGLPRP	1	1		EKKYDASWYINGLKQRILKLEQQCKEKDGTISKLQIDMKTTNLE
SKPRLLRRIVELEKKLSVMESSKSHAAEPVRSHPPACLASSSAL HRQPRGDRNKDHERLRGAVRDLKEERTALQEQLLQRDLEVKQLL QAKADLEKBLECAREGEERREREEVLREEIQTLTSKLQELQEM KKBEKEDCPEVPHKAQELPAPTPSSRHCEQDWPPDSSBEGLPRP	1	ŀ	1	
HRQPRGDRNKDHERLRGAVRDLKEERTALQEQLLQRDLEVKQLL QAKADLEKBLECAREGEERREREEVLREEIQTLTSKLQELQEM KKBEKEDCPEVPHKAQELPAPTPSSRHCEQDWPPDSSBEGLPRP	1	1		GSALLSLSRSVQELTEENQSLKEDLDRVLSTSFTISKTQGYVEW
QAKADLEKBLECAREGEERREREEVLREEIQTLTSKLQELQEM KKBEKEDCPEVPHKAQELPAPTPSSRHCEQDWPPDSSBEGLPRP	1	[		SKPRLLRRIVELEKKLSVMESSKSHAAEPVRSHPPACLASSSAL
KKBEKEDCPEVPHKAQELPAPTPSSRHCEQDWPPDSSBEGLPRP	1			HRQPRGDRNKDHERLRGAVRDLKEERTALQEQLLQRDLEVKQLL
KKBEKEDCPEVPHKAQELPAPTPSSRHCEQDWPPDSSBEGLPRP RSPCSDGRRDAAARVLQAQWKVYKHKKKKAVLDEAAVVLQAAFR	1		]	QAKADLEKBLECAREGEEERREREEVLREEIQTLTSKLQELQEM
RSPCSDGRRDAAARVLQAQWKVYKHKKKKAVLDEAAVVLQAAFR	I			KKBEKEDCPBVPHKAQELPAPTPSSRHCEQDWPPDSSBEGLPRP
	L		<u> </u>	RSPCSDGRRDAAARVLQAQWKVYKHKKKKAVLDEAAVVLQAAFR

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
j	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Į.	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Ī	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W-Tweeterbas W Towns of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the Sta
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
<del> </del>	- Jodgeonec		\=possible nucleotide insertion)
	]		GHLTRTKLLASKAHGSEPPSVPGLPDQSSPVPRVPSPIAQATGS
1	ł		PVQEEAIVIIQSALRAHLARARHSATGKRTTTAASTRRRSASAT
1			HGDASSPPFLAALPDPSPSGPQAVAPLPGDDVNSDDSDDIVIAP
5494	71		SLPTKNFPV
3494	) '±	536	RSKAKIGTPTREVPSTDMKVRRESSSSLTHRPAPSPATPRLIGT
}	1		RRVLLGVSEGTGCADAMELVLVFLCSLLAPMVLASAAEKEKEMD
			PFHYDYQTLRIGGLVFAVVLFSVGILLILSRRCKCSFNQKPRAP
5495			GDEEAQVENLITANATEPQKAEN
3435	273	21.68	DSLLLIQVDTMPFTLHLRSRLPSAIRSLILQKKPNIRNTSSMAG
į.			ELRPASLVVLPRSLAPAFERFCQVNTGPLPLLGQSEPEKWMLPP
1	}		QGAISETRMGHPQFWKYEFGACTGSLASLEQYSEQLKDMVAFFL
}			GCSFSLEEALEKAGLPRRDPAGHSQAGAYKTTVPCVTHAGFCCP
i			LVVTMRPIPKDKLEGLVRACCSLGGEQGQPVHMGDPELLGIKEL
			SKPAYGDAMVCPPGEVPVFWPSPLTSLGAVSSCETPLAFASIPG
			CTVMTDLKDAKAPPGCLTPERIPEVHHISQDPLHYSIASVSASQ
			KIRELESMIGIDPGNRGIGHLLCKDELLKASLSLSHARSVLITT
1			GFPTHFNHEPPEETDGPPGAVALVAFLQALEKEVAIIVDQRAWN
			LHQKIVEDAVEQGVLKTQIPILTYQGGSVEAAQAFLCKNGDPQT
1			PRFDHLVAIERAGRAADGNYYNARKMNIKHLVDPIDDLFLAAKK
1 :			IPGISSTGVGDGGNELGMGKVKEAVRRHIRHGDVIACDVEADFA
}			VIAGVSNWGGYALACALYILYSCAVHSQYLRKAVGPSRAPGDQA
			WTQALPSVIKEEKMLGILVQHKVRSGVSGIVGMEVDGLPFHNTH
5406			AEMIQKLVDVTTAQV
5496	3	2408	QDTKMHEIYKGNITPQLNKNTLKTSAATDVWAVYFSQFWIDYEG
1 1			MKSGKGRPISPVDSFPLSIWICQPTRYAESQKEPQTCNQVSLNT
1 1			SQSBSSDLAGRLKRKKLLKEYYSTESEPLTNGGQKPSSSDTFFR
)			FSFSSSEADIHLLVHVHKHVSMQINHYQYLLLLFLHESLILLSE
			NLRKDVEAVTGSPASQTSICIGILLRSAELALLLHPVDQANTLK
( )			SPVSESVSPVVPDYLPTENGDFLSSKRKQISRDINRIRSVTVNH
1 1	}		MSDNRSMSVDLSHIPLKDPLLFKSASDTNLQKGISFMDYLSDKH
1 1	. 1		LGKISEDESSGLVYKSGSGEIGSETSDKKDSFYTDSSSVLNYRE
1 1			DSNILSFDSDGNQNILSSTLTSKGNETIESIFKAEDLLPEAASL
1 1	]		SENLDISKEETPPVRTLKSQSSLSGKPKERCPPNLAPLCVSYXN
1 1	1		MKRSSSQMSLDTISLDSMILEEQLLESDGSDSHMFLEKGNKKNS
1 1	1		TTNYRGTAESVNAGANLQNYGETSPDAISTNSEGAQENHDDLMS
j j			VVVFKITGVNGEIDIRGEDTEICLQVNQVTPDQLGNISLRHYLC
1 1			NRPVGSDQKAVIHSKSSPEISLRFESGPGAVIHSLLAEKNGFLQ
1 1	i	i	CHIKNFSTEFLTSSLMNIQHFLEDETVATVMPMKIQVSNTKINL
į į	j	j	KDDSPRSSTVSLEPAPVTVHIDHLVVERSDDGSFHIRDSHMLNT
1			GNDLKENVKSDSVLLTSGKYDLKKQRSVTQATQTSPGVPWPSQS
1	ł		ANFPEFSFDFTREQLMEENESLKQELAKAKMALAEAHLEKDALL
5497	1821	3308	HHIKKMTVE
] ""	1061	2208	SISKLLKRRSNIDAYLLSNSCAFFAPRLFSLASQIIREQQSPNV
1	ĺ	ſ	CFIYKYSGFPSLECQCHFVSPHSSCYINFFSFPPPFFVCFQLSN
1			GFSHYSLSSESHVGPTGAGLFPHCLPASRLLPRVTSVHLPDYAH
1 1		ļ	YYTIGPGMFPSSQIPSWKDWAKPGPYDQPLVNTLQRRKEKREPD
1			PNGGGPTTASGPPAAAEEAQRPRSMTVSAATRPGEEMEACEELA
1 1		1	LALSRGLQLDTQRSSRDSLQCSSGYSTQTTTPCCSEDTIPSQVS
1			DYDYFSVSGDQEADQQEFDKSSTIPRNSDISQSYRRMFQAKRPA
1 1		(	STAGLPTTLGPAMVTPGVATIRRTPSTKPSVRRGTIGAGPIPIK
1	1	1	TPVIPVKTPTVPDLPGVLPAPPDGPEERGEHSPESPSVGEGPQG
1 1	1	ļ	VTSMPSSMWSGQASVNPPLPGPKPSIPEEHRQAIPESEAEDQER
1	1	ĺ	EPPSATVSPGQIPESDPADLSPRDTPQGEDMLNAIRRGVKLKKT
5498			TTNDRSAPRFS
2436	2434	1492	ILTHQEIFTGEKPCECGKASIQMSHLSQQKIYSGENPFACKVCG
[	•		KVFSHKSNLTEHEHFHTREKPFECNECGKAFSQKQYVIKHQNTH
			TGEKLFBCNECGKSFSQKENLLTHQKIHTGEKPFECKDCGKAFI
	İ	1	QKSNLIRHQRTHTGEKPFVCKECGKTFSGKSNLTEHEKIHIGEK
		1	PFKCSECGTAFGQKKYLIKHQNIHTGEKPYECNECGKAFSQRTS
1	į		LIVHVRIHSGDKPYECNVCGKAFSQSSSLTVHVRSHTGEKPYGC
			NECGKAFSQFSTLALHLRIHTGKKPYQCSECGKAFSQKSHHIRH

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G-Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
i	seguence	] -	\=possible nucleotide insertion)
	<del> </del>	<del>                                     </del>	QKIHTH
5499	324	926	GFGQIGRGHKITTYPFSPRKSGRKGMAQSQGWVKRYIKAFCKGF
	1	}	FVAVPVAVTFLDRVACVARVEGASMQPSLNPGGSQSSDVVLLNH
ì	i		WKVRNFEVHRGDIVSLVSPKNPEQKIIKRVIALEGDIVRTIGHK
ł	l	ł	NRYVKVPRGHIWVEGDHHGHSFDSNSFGPVSLGLLHAHATHILW
1	1		PPERWQKLESVLPPERLPVQREEE
5500	1978	1286	KPDWRLQNLPPRLYLWRSSRFGFGHLKKRLQMDFKIEHTWDGFP
		1	VKHEPVFIRLNPGDRGVMMDISAPFFRDPPAPLGEPGKPFNELW
			DYEVVEAFFLNDITEQYLEVELCPHGQHLVLLLSGRRNVWKQEL
Ì	į	1	PLSFRVSRGETKWEGKAYLPWSYFPPNVTKFNSFAIHGSKDKRS
-		ì	YEALYPVPQHELQQGQKPDFHCLEYFKSFNFNTLLGEEWKQPES
			DLWLIEKCDI
5501	2927	2226	1_
	]		CRPPVSARVAPGHQGAVGGSGRRPARVEVVDAAARPSSRPFSLP
			AAIMLALISRLLDWFRSLFWKEEMELTLVGLQYSGKTTFVNVIA
}			SGQFSEDMIPTVGFNMRKVTKGNVTIKIWDIGGQPRFRSMWERY
			CRGVNAIVYMIDAADREKIEASRNELHNLLDKPQLQGIPVLVLG
1			NKRDLPNALDEKQLIEKMNLSAIQDREICCYSISCKEKDNIDIT LQWLIQHSKSRRS
5502	3	824	
3302	٠	524	NSAFPVWVPERTALLTCPLGAAPGSSREAPGIAGPPNSTAMSKL
	1		GKFFKGGGSSKSRAAPSPQEALVRLRETEEMLGKKQEYLENRIQ
1			REIALAKKHGTQNKRAALQALKRKKRFEKQLTQIDGTLSTIEFQ
			REALENSHTNTEVLRNMGFAAKAMKSVHENMDLNKIDDLMQEIT
1 1	i		EQQDIAQEISEAFSQRVGFGDDFDEDELMAELEELEQEELNKKM
j l			TNIRLPNVPSSSLPAQPNRKPGMSSTARRSRAASSQRAEEEDDD IKOLAAWAT
5503	216	654	
3303	240,	034	KGVRRGRVRSDSEDSHLGYFKMSFLLPKLTSKKEVDQAIKSTA
	1	,	EKVLVLRFGRDEDPVCLQLDDILSKTSSDLSKMAAIYLVDVDQT
			AVYTQYFDISYIPSTVFFFNGQHMKVDYGGEDPALRSIKAVRRT SPAGTLGEKPVNS
5504	58	3563	QLSFSFQAPVTFDDITVYLLQEEWVLLSQQQKELCGSNKLVAPL
		3303	GPTVANPELFRKFGRGPEPWLGSVQGQRSLLEHHPGKKQMGYMG
1 1			EMEVQGPTRESGQSLPPQKKAYLSHLSTGSGHIEGDWAGRNRKL
1 1	ļ		LKPRSIQKSWFVQFPWLIMNEEQTALFCSACREYPSIRDKRSRL
1			IEGYTGPFKVETLKYHAKSKAHMFCVNALAARDPIWAARFRSIR
			DPPGDVLASPEPLFTADCPIFYPPGPLGGFDSMAELLPSSRAEL
1 !	J		EDPGGDGAIPAMYLDCISDLRQKEITDGIHSSSDINILYNDAVE
1			SCIQDPSAEGLSEEVPVVFBELPVVFEDVAVYFTREEWGMLDKR
1 1			QKELYRDVMRMNYELLASLGPAAAKPDLISKLERRAAPWIKDPN
] ]			GPKWGKGRPPGNKKMVAVREADTQASAADSALLPGSPVEARASC
1 1			CSSSICEEGDGPRRIKRTYRPRSIQRSWFGQFPWLVIDPKETKL
1			FCSACIERPNLHDKSSRLVRGYTGPFKVETLKYHEVSKAHRLCV
} [	İ		NTVEIKEDTPHTALVPEISSDLMANMEHFFNAAYSIAYHSRPLN
1	ľ		DFEKILQLLQSTGTVILGKYRNRTACTQFIKYISETLKREILED
1	}		VRNSPCVSVLLDSSTDASEOACVGIYIRYFKOMEVKESYITLAP
1	İ		LYSETADGYFETIVSALDELDIPFRKPGWVVGLGTDGSAMLSCR
	Į.		GGLVEKFQEVIPQLLPVHCVAHRLHLAVVDACGSIDLVKKCDRH
, ,	J		IRTVFXFYQSSNKRLNELQEGAAPLEQEIIRLKDLNAVRWVASR
ļ 1	ł		RRTLHALLVSWPALARHLQRVAEAGGQIGHRAKGMLKLMRGFHF
, ,	Ì		VKFCHFLLDFLSIYRPLSEVCQKEIVLITEVNATLGRAYVALES
, I			LRHQAGPKEEEFNASFKDGRLHGICLDKLEVAEQRFQADRERTV
J. I		ĺ	LTGIEYLQQRFDADRPPQLKNMEVFDTMAWPSGIELASFGNDDI
1 1	į	İ	LNLARYFECSLPTGYSEEALLEEWLGLKTIAQHLPFSMLCKNAL
]		i	AQHCRFPLLSKLMAVVVCVPISTSCCERGFKAMNRIRTDERTKL
1 1	1		SNEVLNMLMMTAVNGVAVTEYDPQPAIQHWYLTSSGRRFSHVYT
]		j	CAQVPARSPASARLRKEEMGALYVEEPRTQKPPILPSREAAEVL
1 1	,		KDCIMEPPERLLYPHTSQEAPGMS KDCIMEPPERLLYPHTSQEAPGMS
5505	3312	1219	NCSPRSLSAAKMSNRNNNKLPSNLPQLQNLIKRDPPAYIEEFLQ
]		****	QYNHYKSNVEIFKLQPNKPSKELAELVMFMAQISHCYPEYLSNF
		ľ	PQEVKDLLSCNHTVLDPDLRMTFCKALILLRNKNLINPSSLLEL
1	ł	ł	FFELFRCHDKLLRKTLYTHIVTDIKNINAKHKNNKVNVVLQNFM
L			T TO THE TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOT

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1 2,0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ŀ	to first	amino acid	P-Proline, Q-Glutamine, R-Arginine,
1	amino acid	residue of	Partoline, Qadiutamine, Kaarginine,
1	ľ		S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u></u>	sequence		\=possible nucleotide insertion)
			YTMLRDSNATAAKMSLDVMIELYRRNIWNDAKTVNVITTACFSK
1	·		VTKILVAALTFFLGKDEDEKQDSDSESEDDGPTARDLLVQYATG
1			KKSSKNKKKLEKAMKVLKKHRKKKKPEVFNFSAIHLIHDPQDFA
1			EKLLKQLECCKERFEVKMMLMNLISRLVGIHELFLFNFYPFLQR
	1		FLQPHQREVTKILLFAAQASHHLVPPEIIQSLLMTVANNFVTDK
	Į.		NSGEVMTVGINAIKEITARCPLAMTEELLQDLAQYKTHKDKNVM
	1		MSARTLIHLFRTLNPQMLQKKFRGKPTEASIEARVQEYGELDAK
			DYIPGAEVLEVEKEENAENDEDGWESTSLSEEEDADGEWIDVOH
1	l		SSDEEQQEISKKLNSMPMBERKAKAAAISTSRVLTQBDFQKIRM
1			AQMRKELDAAPGKSQKRKYIEIDSDEEPRGELLSLRDIERLHKK
1			
}	]		PKSDKETRLATAMAGKTDRKEFVRKKTKTNPFSSSTNKEKKKQK
5506		1531	NFMMMRYSQNVRSKNKRSFREKQLALRDALLKKKKRMK
3300	1	1237	FREDLCGORGSAPGEGGSSAWPAPAHPLPEREREALCPGRS
1			CSGGGGEETPGTTPVWSPLEGGGDEELRPNPYVRFPYRWWAVVV
1			LAAFPSLGAGGETPEAPPESWTQLWFFRFVVNAAGYASFMVPGY
1		1	LLVQYFRRKNYLETGRGLCFPLVKACVFGNEPKASDEVPLAPRT
1			EAAETTPMWQALKLLFCATGLQVSYLTWGVLQERVMTRSYGATA
ſ		9	TSPGERFTDSQFLVLMNRVLALIVAGLSCVLCKQPRHGAPMYRY
J	}		SFASLSNVLSSWCQYEALKFVSFPTQVLAKASKVIPVMLMGKLV
			SRRSYEHWEYLTATLISIGVSMFLLSSGPEPRSSPATTLSGLIL
1			LAGYIAFDSFTSNWQDALFAYKMSSVQMMFGVNFFSCLFTVGSL
			LEQGALLEGTRFMGRHSEFAAHALLLSICSACGQLFIFYTIGQF
1			GAAVFTIIMTLRQAFAILLSCLLYGHTVTVVGGLGVAVVFAALL
			LRVYARGRLKQRGKKAVPVESPVQKV
5507	3704	1271	PRGTRRCRPAGRASRRARRRPPCPGPAAPGSLEIGGFGTAAGKK
1			VAVADVQFGPMRFHQDQLQVLLVFTKEDNQCNGFCRACEKAGFK
1			CTVTKEAQAVLACFLDKHHDIIIIDHRNPRQLDAEALCRSIRSS
	1		KLSENTVIVGVVRRVDREELSVMPFISAGFTRRYVENPNIMACY
			NELLQLEFGEVRSQLKLRACNSVFTALENSEDAIBITSEDRFIQ
			YANPAFETTMGYQSGELIGKELGEVPINEKKADLLDTINSCIRI
1			GKEWQGIYYAKKKNGDNIQQNVKIIPVIGQGGKIRHYVSIIRVC
1			NGNNKAEKISECVQSDTHTDNQTGKHKDRRKGSLDVKAVASRAT
1	' I		EVSSQRRHSSMARIHSMTIEAPITKVINIINAAQESSPMPVTEA
			LDRVLEILRTTELYSPQFGAKDDDPHANDLVGGLMSDGLRRLSG
			NEYVLSTKNTQMVSSNIITPISLDDVPPRIARAMENEEYWDFDI
			FELEAATHNRPLIYLGLKMFARFGICEFLHCSESTLRSWLQIIE
1			ANYHSSNPYHNSTHSADVLHATAYFLSKERIKETLDPIDEVAAL
			IAATIHDVDHPGRTNSFLCNAGSELAILYNDTAVLESHHAALAF
1 1	•	•	QLTTGDDKCNIFKNMERNDYRTLRQGIIDMVLATEMTKHFEHVN
į	į		KPVNSINKPLATLEENGETDKNQEVINTMLRTPENRTLIKRMLI
1			KCADVSNPCRPLQYCIEWAARISEEYFSQTDEEKQQGLPVVMPV
( I			FDRNTCSIPKSQISFIDYFITDMFDAWDAFVDLPDLMQHLDNNF
			KYWKGLDEMKLRNLRPPPB
5508	1151	691	LSSVFSRRSASMFAVGCSMGPFLHYWYLSLDRLFPASGLRGFPN
1 1	1		VLKKVLVDQLVASPLLGVWYFLGLGCLEGQTVGESCQELREKFW
	i		EFYKADWCVWPAAQFVNFLFVPPQFRVTYINGLTLGWDTYLSYL
L			KYRSPVPLTPPGCVALDTRAD
5509	1238	619	RKSRGCQNALSASGPAAAAAAIMVRKLKFHEQKLLKQVDFLNWE
	1		VTDHNLHELRVLRRYRLQRREDYTRYNQLSRAVRELARRLRDLP
1	!		ERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRRR
j !	Ì		LPTVLLKLRMAOHLOAAVAFVEOGHVRVGPDVVTDPAFLVTRSM
1 1	ľ		EDFVTWVDSSKIKRHVLEYNEERDDFDLEA
5510	96	1195	PAGAHLSSGSSEPLVEPGRGRVGARVKGERGLQASGSAPGRSKM
	,,,	1732	
] }	J		AEGERQPPPDSSEEAPPATQNFIIPKKEIHTVPDMGKWKRSQAY
Į į	ļ		ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRWID
1 1	j	1	ETPPVDQPSRFGNKAYRTWYAKLDEEAENLVATVVPTHLAAAVP
·		1	EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ
1 /	1	ľ	IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI
, 1		]	WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLECILFITEMKT
( l		i	GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF
<u> </u>			KFGSLLPIHPVTSG

SEO	1 Dwg 34 24 - 3	T	
ID	Predicted	Predicted end	Amino acid segment containing signal peptide
30:	beginning	nucleotide	(A=Alanine, C≂Cysteine, D=Aspartic Acid, E=
30:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	} _	\=possible nucleotide insertion)
5511	276	1980	KLSRVLNLPPENLITSISAVPISQKEEVADFQLSVDSLLEKDND
1	1	1	HSRPDIQVQAKRLAEKLRCDTVVSEISTGQRTVNFKINRELLTK
ļ			TVLQQVIEDGSKYGLKSELFSGLPQKKIVVEFSSPNVAKKFHVG
1		ì	
	)		HLRSTIIGNFIANLKEALGHQVIRINYLGDWGMQFGLLGTGFQL
1	1	ł	FGYEEKLQSNPLQHLFEVYVQVNKEAADDKSVAKAAQEFFQRLE
	ĺ	ł .	LGDVQALSLWQKFRDLSIEEYIRVYKRLGVYFDEYSGESFYREK
1	1		SQEVLKLLESKGLLLKTIKGTAVVDLSGNGDPSSICTVMRSDGT
1	Į.		SLYATRDLAAAIDRMDKYNFDTMIYVTDKGQKKHFQQVFQMLKI
	í	1	MGYDWAERCQHVPFGVVQGMKTRRGDVTFLEDVLNEIQLRMLQN
	l		MASIKTTKELKNPQETAERVGLAALIIQDFKGLLLSDYKFSWDR
	ĺ		VFQSRGDTGVFLQYTHARLHSLEETFGCGYLNDFNTACLQEPQS
			VSILQHLLRFDEVLYKSSQDFQPRHIVSYLLTLSHLAAVAHKTL
1	1	ĺ	QIKDSPPEVAGARLHLFKAVRSVLANGMKLLGITPVCRM
5512	120	1015	
1 3342	120	1013	DPSLLLTITVTGVTVLVLVLKSMNSRRREPITLQDPEAKYPLPL
1	<b>\</b>	-	IEKEKISHNTRRFRFGLPSPDHVLGLPVGNYVQLLAKIDNELVV
			RAYTPVSSDDDRGFVDLIIKIYFKNVHPQYPEGGKMTQYLENMK
}	ļ		IGETIFFRGPRGRLFYNGPGNLGIRPDQTSEPKKTLADHLGMIA
	•		GGTGITPMLQLIRHITKDPSDRTRMSLIFANQTEEDILVRKELE
Į.	ļ		EIARTHPDQFDLWYTLDRPPIGWKYSSGFVTADMIKEHLPPPAK
	L		STLILVCGPPPLIQTAAHPNLEKLGYTQDMIFTY
5513	2	837	ARWRLPSDSPRIPPAGAETPGRGSCRNYLPSSSPPPPEPSSFPS
ł	1		PPTSRGGPGSRDTMSDSEEESQDRQLKIVVLGDGASGKTSLTTC
1	1		FAQETFGKQYKQTIGLDFFLRRITLPGNLNVTLQIWDIGGQTIG
			GKMLDKYIYGAQGVLLVYDITXYQSFENLEDWYTVVKKVSEESE
1	1		TOPLVALVGNKIDLEHMRTIKPEKHLRFCQENGFSSHFVSAKTG
1	}		DSVFLCFQKVAAEILGIKLNKABIEQSQRVVKADIVNYNQEPMS
1			RTVNPPRSSMCAVO
5514	1295	449	
	1 1	442	VNRPSWIMGNFRGHALPGTFFFIIGLWWCTKSILKYICKKOKRT
1	1		CYLGSKTLFYRLEILEGITIVGMALTGMAGEQFIPGGPHLMLYD
1	Į l		YKQGHWNQLLGWHHFTMYFFFGLLGVADILCFTISSLPVSLTKL
ì	ł		MLSNALFVEAFIFYNHTHGREMLDIFVHQLLVLVVFLTGLVAFL
1			EFLVRNNVLLELLRSSLILLQGSWFFQIGFVLYPPSGGPAWDLM
1	, ,	•	DHENILFLTICFCWHYAVTIVIVGMNYAFITWLVKSRLKRLCSS
			EVGLLKNAEREQESEEEM
5515	1572	260	FVRLVGRGDCDPLLSVCLTTMPLYEGLGSGGEKTAVVIDLGEAP
1	ł 1		TKCGFAGETGPRCIIPSVIKRAGMPKPVRVVQYNINTEELYSYL
1			KEFIHILYFRHLLVNPRDRRVVIIESVLCPSHFRETLTRVLFKY
			FEVPSVLLAPSHLMALLTLGINSAMVLDCGYRESLVLPIYEGIP
			VINCWGALPLGGKALHKELETQLLEQCTVDTSVAKEQSLPSVMG
] .	ļ		SVPEGVLEDIKARTCFVSDLKRGLKIQAAKFNIDGNNERPSPPP
1			NVDYPLDGEKILHILGSIRDSVVEILFEQDNEEQSVATLILDSL
1			IQCPIDTRKQLAENLVVIGGTSMLPGFLHRLLAEIRYLVEKPKY
1			
1			KKALGTKTFRIHTPPAKANCVAWLGGAIFGALQDILGSRSVSKE
5516			YYNQTGRIPDWCSLNNPPLEMMFDVGKTQPPLMKRAFSTEK
1 070	3	73.5	NSREPPQAGPGPSPRKSPTASSFLFPWRPLASSFWMGAQGAQES
1			IKAMWRVPGTTRRPVTGESPGMHRPRAMLLLLTLALLGGFTWAG
1 1	1		KMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSVQVKLGDSW
1	' <b>!</b>		DVKLGALGGNTQEVTLQPGEYITKVFVAFQAFLRGMVMYTSKDR
1	1	i	YFYFGKLDGQISSAYPSQEGQVLVGIYGQYQLLGIKSIGFEWNY
L i	. [		PLEEPTTEPPVNLTYSANSPVGR
5517	246	499	SEIYVAMRTDSSKMTDVESGVANFASSARAGRRNALPDIQSSAA
			TDGTSDLPLKLEALSVKEDAKEKDEKTTQDQLEKPQNEEK
5518	3	1375	
	· /	49/3	DAWADAWVRAWDLIMDFPCLWLGLLLPLVAALDFNYHRQEGMEA
1 1			FLKTVAQNYSSVTHLHSIGKSVKGRNLWVLVVGRFPKEHRIGIP
1	ŀ		EFKYVANMHGDETVGRELLLHLIDYLVTSDGKDPEITNLINSTR
			IHIMPSMNPDGFEAVKKPDCYYSIGRENYNQYDLNRNFPDAFRY
1 1	ı	l	NNVSRQPETVAVMKWLKTETFVLSANLHGGALVASYPFDNGVQA
, I			TGALYSRSLTPDDDVFQYLAHTYASRNPNMKKGDECKNKMNFPN
1 1		}	GVTNGYSWYPLQGGMQDYNYIWAQCFEITLELSCCKYPREEKLP
L			SFWNNNKASLIEYIKQVHLGVKGQVFDQNGNPLPNVIVEVQDRK

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ì	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	SeSerine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	
i	sequence	sequence	Codon, /=possible nucleotide deletion,
	sequence	ļ	\=possible nucleotide insertion)
ł	<u> </u>		HICPYRTNKYGEYYLLLLPGSYIINVTVPGHDPHITKVIIPEKS
}			QNFSALKKDILLPFQGQLDSIPVSNPSCPMIPLYRNLPDHSAAT
5519	<u> </u>		KPSLFLFLVSLLHIFFK
5519	87	477	IKSKLNQQVEVQESEWRLTEAKGPTMGKESGWDSGRAAVAAVVG
		1	GVVAVGTVLVALSAMGFTSVGIAASSIAAKMMSTAAIANGGGVA
		<del></del>	AGSLVAILQSVGAAGLSVTSKVIGGFAGTALGAWLGSPPSS
5520	117	943	PTEGROKVLKTFTVPRSALAMIKTSTCIYHFLVLSWYTFLNYYI
ſ		1	SQEGKDEVKPKILANGARWKYMTLLNLLLQTIFYGVTCLDDVLK
ł			RTKGGKDIKFLTAFRDLLFTTLAFPVSTFVFLAFWILFLYNRDL
1	į	ĺ	IYPKVLDTVIPVWLNHAMHTFIFPITLAEVVLRPHSYPSKKTGL
1			TLLAAASIAYISRILWLYFETGTWVYPVFAKLSLLGLAAFFSLS
-			YVFIASIYLLGEKLNHWKWVSVQILQRWRLESVGICFQWPDWKS
			PAKHQLVKNIR
5521	546	911	KILNMQKSCEENEGKPQNMPKAEEDRPLEDVPQEAEGNPQPSEE
1		ł	GVSQEAEGNPRGGPNQPGQGFKEDTPVRHLDPEEMIRGVDELER
L			LREEIRRVRNKFVMMHWKQRHSRSRPYPVCFRP
5522	1224	637	GSRPLGQRSREKMWVFGYGSLIWKVDFPYQDKLVGYITNYSRRF
	}		WQGSTDHRGVPGKPGRVVTLVEDPAGCVWGVAYRLPVGKEEEVK
(	,		AYLDFREKGGYRTTTVIFYPKDPTTKPFSVLLYIGTCDNPDYLG
		i	PAPLEDIAEQIFNAAGPSGRNTEYLFELANSIRNLVPEKADEHL
			FALEKLVKERLEGKQNLNCI
5523	3	1280	SKGKKRMGSSMSAATARRPVFDDKEDVNFDHFQILRAIGKGSFG
		÷	KVCIVQKRDTEKMYAMKYMNKQQCIERDEVRNVFRELEILQEIE
1 1			HVFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVQFSEDTV
1 '			RLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI
1 1			ATIIKDGERATALSGTKPYMAPEIFHSFVNGGTGYSFEVDWWSV
]			GVMAYELLRGWRPYDIHSSNAVESLVQLFSTVSVQYVPTWSKEM
1 1			VALLRKLLTVNPEHRLSSLQDVQAAPALAGVLWDHLSEKRVEPG
			FVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRD
1 1			SSQSENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPES
L			RDAAEPVEDEAERSALPMCGPICPSAGSG
5524	85	2318	RERERDHRPGESSQGQSGAGGCFPSPTMELRCGGLLFSSRFDSG
1 1			NLAHVEKVESLSSDGEGVGGGASALTSGIASSPDYEFNVWTRPD
[			CARTEFENGNRSWFYFSVRGGMPGKLIKINIMNMNKQSKLYSQG
1 1			MAPFVRTLPTRPRWERIRDRPTFEMTETQFVLSFVHRFVEGRGA
1			TTFFAFCYPFSYSDCQELLNQLDQRFPENHPTHSSPLDTIYYHR
1 1			ELLCYSLDGLRVDLLTITSCHGLREDREPRLEQLFPDTSTPRPF
1 1	ļ		RFAGKRIFFLSSRVHPGETPSSFVFNGFLDFILRPDDPRAQTLR
1 1	}		RLFVFKLIPMLNPDGVVRGHYRTDSRGVNLNRQYLKPDAVLHPA
1 1	Į		IYGAKAVLLYHHVHSRLNSQSSSEHQPSSCLPPDAPVSDLEKAN
1	Í		NLQNEAQCGHSADRHNAEAWKQTEPAEQKLNSVWIMPQQSAGLE
]			ESAPDTIPPKESGVAYYVDLHGHASKRGCFMYGNSFSDESTQVE
) [			NMLYPKLISLNSAHFDFQGCNFSEKNMYARDRRDGQSKEGSGRV
1	İ		AIYKASGIIHSYTLECNYNTGRSVNSIPAACHDNGRASPPPPPPA
] [		•	FPSRYTVELFEQVGRAMAIAALDMAECNPWPRIVLSEHSSLTNL
1 1	j	l	RAWMLKHVRNSRGLSSTLNVGVNKKRGLRTPPKSHNGLPVSCSE
1			ntlsrarsfstgtsaggssssqqnspqmknspsfpfhgsrpagl
L			PGLGSSTQKVTHRVLGPVRGKPVWEPLQHVFGCLGHCWGK
5525	105	834	SNTLDFERHLFIMGQQISDQTQLVINKLPEKVAKHVTLVRESGS
[ /	ľ	1	LTYEEFLGRVAELNDVTAKVASGQEKHLLFEVQPGSDSSAFWKV
1 1	į	1	VVRVVCTKINKSSGIVEASRIMNLYQFIQLYKDITSQAAGVLAQ
1 [	1	1	SSTSEEPDENSSSVTSCQASLWMGRVKQLTDEEECCICMDGRAD
1	j		LILPCAHSFCQKCIDKWSDRHRNCPICRLQMTGANESWVVSDAP
[ [	1	j	TEDDMANYILNMADEAGOPHRP
5526	3	853	RRPCNPVRAAKRTGAAARAPRGLEVTMLRVAWRTLSLIRTRAVT
1			QVLVPGLPGGGSAKFPFNQWGLQPRSLLLQAARGYVVRKPAQSR
1			LDDDPPPSTLLKDYQNVPGIEKVDDVVKRLLSLEMANKKEMLKI
1	ļ		KQEQFMKKIVANPEDTRSLEARIIALSVKIRSYEEHLEKHRKDK
1 1	1		AHKRYLLMSIDQRKKMLKNLRNTNYDVFEKICWGLGIEYTFPPL
ļ	ļ	j	YYRRAHRRFVTKKALCIRVPQETQKLKKRRRALKAAAAAQKQAK
	<u></u>		TIME THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO T

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
]	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	-	\=possible nucleotide insertion)
	<del></del>		RRNPDSPAKAIPKTLKDSQ
5527	3225	565	LLRKYLLHONPLLLRHOPNRTCISFSATMKLKDTKSRPKOSSCG
			KFQTKGIKVVGKWKEVKIDPNMFADGQMDDLVCFEELTDYQLVS
1	Ì		PAKNPSSLFSKEAPKRKAQAVSEEEBEEEGKSSSPKKKIKLKKS
1			KNVATEGTSTOKEFEVKDPELEAOGDDMVCDDPEAGEMTSENLV
i	1		QTAPKKKKNKGKKGLEPSQSTAAKVPKKAKTWIPEVHDQKADVS
1	ĺ		AWKDLFVPRPVLRALSFLGFSAPTPIOALTLAPAIRDKLDILGA
1	1		AETGSGKTLAFAIPMIHAVLQWQKRNAAPPPSNTEAPPGETRTE
			AGAETRSPGKAEAESDALPDDTVIESEALPSDIAAEARAKTGGT
			VSDQALLFGDDDAGEGPSSLIREKPVPKQNENEEENLDKEQTGN
1			LKQELDDKSATCKAYPKRPLLGLVLTPTRELAVQVKQHIDAVAR
1			FTGIKTAILVGGMSTQKQQRMLNRRPEIVVATPGRLWELIKEKH
			YHLRNLRQLRCLVVDEADRMVEKGHFAELSQLLEMLNDSQYNPK
1	ł		ROTLVFSATLTLVHQAPARILHKKHTKKMDKTAKLDLLMQKIGM
ļ			RGKPKVIDLTRNEATVETLTETKIHCETDEKDFYLYYFLMQYPG
			RSLVFANSISCIKRLSGLLKVLDIMPLTLHACMHQKQRLRNLEQ
			FARLEDCVLLATDVAARGLDIPKVQHVIHYQVPRTSEIYVHRSG
1			RTARATNEGLSLMLIGPEDVINFKKIYKTLKKDEDIPLFPVQTK
			YMDVVKERIRLARQIEKSEYRNFQACLHNSWIEQAAAALEIELE
1			EDMYKGGKADQQEERRRQKQMKVLKKELRHLLSQPLFTESQKTK
[			YPTQSGKPPLLVSAPSKSESALSCLSKQKKKKTKKPKEPQPEQP
			QPSTSAN
5528	3	895	GPFLSACRMWGACKVKVHDSLATISITLRRYLRLGATMAKSKFE
1			YVRDFEADDTCLAHCWVVVRLDGRNFHRFAEKHNFAKPNDSRAL
			QLMTKCAQTVMEELEDIVIAYGQSDEYSFVFKRKTNWFKRRASK
			FMTHVASQFASSYVFYWRDYFEDQPLLYPPGFDGRVVVYPSNQT
1 !			LKDYLSWRQADCHINNLYNTVFWALIQQSGLTPVQAQGRLQGTL
			AADKNEILFSEFNINYNNEPPMYRKGTVLIWQKVDEVMTKEIKL
			PTEMEGKKMAVTRTRTKPCKPSHLPRAPCLRWL
5529	48	640	TFRLVSAHLKTRKLINPEAAERRWRDWDSRQGWLSVKMQRVSGL
ł I		i	LSWTLSRVLWLSGLSEPGAARQPRIMEEKALEVYDLIRTIRDPE
1			KPNTLEELEVVSESCVEVQEINEEEYLVIIRFTPTVPHCSLATL
			IGLCLRVKLQRCLPFKHKLEIYISEGTHSTEEDINKQINDKERV
			AAAMENPNLREIVEQCVLEPD
5530	4541	2606	AQIVHAISYCHKLHVGHRDLKPENVVFFEKQGLVKLTDFGFSNK
]			FQPGKKLTTSCGSLAYSAPEILLGDEYDAPAVDIWSLGVILFML
1 1			VCGQPPFQEANDSETLTMIMDCKYTVPSHVSKECKDLITRMLQR
1 1			DPKRRASLEEIENHPWLQGVDPSPATKYNIPLVSYKNLSEEEHN
			SIIQRMVLGDIADRDAIVEALETNRYNHITATYFLLAERILREK
1	ľ		QEKEIQTRSASPSNIKAQFRQSWPTKIDVPQDLEDDLTATPLSH
1 1			ATVPQSPARADSVLNGHRSKGLCDSAKKDDLPELAGPALSTVP
{			PASLKPTASGRKCLFRVEEDEEEDEEDKKPMSLSTQVVLRRKPS
[ [	ļ		VTNRLTSRKSAPVLNQIFEEGESDDEFDMDENLPPKLSRLKMNI
1 1	j		ASPGTVHKRYHRRKSQGRGSSCSSSETSDDDSESRRRLDKDSGF
]	]		TYSWHRRDSSEGPPGSEGDGGGQSKPSNASGGVDKASPSENNAG
1			GGSPSSGSGGNPTNTSGTTRRCAGPSNSMQLASRSAGELVESLK
1 1			LMSLCLGSQLHGSTKYIIDPQNGLSFSSVKVQEKSTWKMCISST
j l			GNAGQVPAVGGIKFFSDHMADTTTELERIKSKNLKNNVLQLPLC
5531		E15	EKTISVNIQRNPKEGLLCASSPASCCHVI GSOPRAPRPRDSMERPEPELIROSWRAVSRSPLEHGTVLFARLF
1 2227	24	515	
1	]		ALEPDLLPLFQYNCRQFSSPEDCI.SSPEFLDHIRKVMLVIDAAV
, ,			TNVEDLSSLEEYLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC
FE33- 1	2205	1405	LGPAFTPATRAAWSQLYGAVVQAMSRGWDGE
5532	3395	1402	SDWMVVGKRKMI I EDETEFCGEELLHSVLQCKSVFDVLDGEEMR
1 1			RARTRANPYEMIRGVFFLNRAAMKMANMDFVFDRMFTNPRDSYG
1	1	{	KPLVKDREAELLYFADVCAGPGGFSEYVLWRKKWHAKGFGMTLK
, I	}		GPNDFKLEDFYSASSELFEPYYGEGGIDGDGDITRPENISAFRN
} I	1		FVLDNTDRKGVHFLMADGGFSVEGQENLQEILSKQLLLCQFLMA
[ [	ſ	ĺ	LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFERVCLFKPITS
			RPANSERYVVCKGLKVGIDDVRDYLFAVNIKLNQLRNTDSDVNL

C 656	T 70-32-6-3	Predicted end	
SEQ	Predicted		Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ì	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first		
1		amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
[	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
<b>{</b>		Sequence	•
L	sequence	<u> </u>	\=possible nucleotide insertion)
			VVPLEVIKGDHEFTDYMIRSNESHCSLQIKALAKIHAFVQDTTL
	1	ì	SEPRQAEIRKECLRLWGIPDQARVAPSSSDPKSKFFELIQGTEI
1	1	1	DIFSYKPTLLTSKTLEKIRPVFDYRCMVSGSEQKFLIGLGKSQI
i	1	1	1
1	]	1	YTWDGRQSDRWIKLDLKTELPRDTLLSVEIVHELKGEGKAQRKI
1	Į.		SAIHILDVLVLNGTDVREQHFNQRIQLAEKFVKAVSKPSRPDMN
j	j	1	PIRVKEVYRLEEMEKIFVRLEMKIIKGSSGTPKLSYTGRDDRHF
1	į.	1	VPMGLYIVRTVNEPWTMGFSKSFKKKFFYNKKTKDSTFDLPADS
1	) .	1	
i	[		IAPFHICYYGRLFWEWGDGIRVHDSQKPQDQDKLSKEDVLSFIQ
i	1	Į.	MHRA
5533	94	789	MKERRAPQPVVARCKLVLVGDVQCGKTAMLQVLAKDCYPETYVP
1 -333	1	1	-
1	I	l	TVFENYTACLETEEQRVELSLWDTSGSPYYDNVRPLCYSDSDAV
1	1		LLCFDISRPETVDSALKKWRTEILDYCPSTRVLLIGCKTDLRTD
1	1	1	LSTLMELSHQKQAPISYEQGCAIAKQLGPEIYLEGSAFTSEKSI
	1	ļ	HSIFRTASMLCLNKPSPLPQKSPVRSLSKRLLHLPSRSBLISPT
I	1	ĺ	FKKEKAKXCSIM
5534	3	605	LVRGRARAANPGRVGAMDGLRQRVEHFLEQRNLVTEVLGALEAK
ŀ	i	l	TGVEKRYLAAGAVTLLSLYLLFGYGASLLCNLIGFVYPAYASIK
I	I	1	AIESPSKDDDTVWLTYWVVYALFGLAEFFSDLLLSWFPFYYVGK
1	ł	!	CAFLLFCMAPRPWNGALMLYORVVRPLFLRHHGAVDRIMNDLSG
1	ì	l	
		ł	RALDAAAGITRNVKPSQTPQPKDK
5535	1029	332	KSFMDSEARLCSLVELSDTQDETQKSDSENEDLKIDCLQESQEL
1	i	İ	NLQKLKNSERILTEAKQKMRELTVNIKMKEDLIKELIKTGNDAK
	1	ł	SVSKQYTLKVTKLEHDABQAKVELTETOKQLQELENKDLSDVAM
1			
1	)	}	KVKLQKEFRKKVDAAKLRVQVLQKKQQDSKKLASLSIQNEKRAN
	Į.		ELEQSVDHMKYQKIQLQRKLQEENEKRKQLDAVIKRDQQKIKVI
	Į		LSYIPAKYNMKC
5536	942	282	AAATAASLSPRGCRLRTPSSDVSPSRAPPPSAAPLPTGRAOMSP
2226	342	202	1
1		i	SGRLCLLTIVGLILPTRGQTLKDTTSSSSADATIMDIQVPTRAP
1			DAVYTELQPTSPTPTWPADETPQPQTQTQQLEGTDGPLVTDPET
l			HKSTKAAHPTDDTTTLSERPSPSTDVQTDPQTLKPSGFHEDDPF
1	!		FYDEHTLRKRGLLVAAVLFITGIIILTSGKCRQLSRLCRNHCR
5537			
223/	3	2391	RARVSSPQLRVFRSGRPRRLRVLRINRTSVALRLAGTGRFVAKT
1	1		PGHPGSWEMGLLTFRDVAVEFSLEEWEHLEPAQKNLYQDVMLEN
ļ			YRNLVSLGLVVSKPDLITFLEQRKEPWNVKSEETVAIQPDVFSH
	!		YNKDLLTEHCTBASFOKVISRRHGSCDLENLHLRKRWKREECEG
1	J .		HNGCYDEKTFKYDQFDESSVESLFHQQILSSCAKSYNFDQYRKV
}	]	•	FTHSSLLNQQEEIDIWGKHHIYDKTSVLFRQVSTLNSYRNVFIG
1	1		EKNYHCNNSEKTLNQSSSPKNHQENYFLEKQYKCKEFEEVFLQS
1			MHGQEKQEQSYKCNKCVEVCTQSLKHIQHQTIHIRENSYSYNKY
			DKDLSQSSNLRKQIIHNEEKPYKCEKCGDSLNHSLHLTOHQIIP
1	]		TEEKPYKWKECGKVFNLNCSLYLTKOOOIDTGENLYKCKACSKS
l '	1		,
]			FTRSSNLIVHQRIHTGEKPYKCKECGKAFRCSSYLTKHKRIHTG
1			EKPYKCKECGKAFNRSSCLTQHQTTHTGEKLYKCKVCSKSYARS
]	·	i e	SNLIMHQRVHTGEKPYKCKECGKVFSRSSCLTQHRKIHTGENLY
			KCKVCAKPFTCFSNLIVHERIHTGEKPYKCKECGKAFPYSSHLI
1 .	]	i	RHHRIHTGEKPYKCKACSKSFSDSSGLTVHRRTHTGEKPYTCKE
i !			
			CGKAFSYSSDVIQHRRIHTGQRPYKCEECGKAFNYRSYLTTHQR
<u> </u>		•	SHTGERPYKCEECGKAFNSRSYLTTHRRRHTGERPYKCDECGKA
j	•		FSYRSYLTTHRRSHSGERPYKCEECGKAFNSRSYLIAHORSHTR
			EKL
FESS			
5538	926	161	HSMMMKIPWGSIPVLMLLLLLGLIDISQAQLSCTGPPAIPGIPG
1			IPGTPGPDGQPGTPGIKGEKGLPGLAGDHGEFGEKGDPGIPGNP
1	1	1	GKVGPKGPMGPKGGPGAPGAPGPKGESGDYKATOKIAFSATRTI
]			NVPLRRDOTIRFDHVITNMNNNYEPRSGKFTCKVPGLYYFTYHA
(			
1	]		SSRGNLCVNLMRGRERAQKVVTFCDYAYNTFQVTTGGMVLKLEQ
/ I	· · · · · · · · · · · · · · · · · · ·		GENVFLQATDKNSLLGMEGANS I FSGFLLFPDMEA
5539	38	1258	HRGPSGAAAPGCALPRGOALEGPRSCRRPOPMARRYDELPHYPG
1 1	[	i	IVDGPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREK
1	¦ 1		DEIYGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCS
, l	<b>!</b>	1	SDSFNEDIAAFAKQVRSERPLFSSNPELDNLVIQAIQVLRFHLL

SEQ Predicted Predicted end Amino acid segment containing some production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production production pro	rtic Acid, E= . G=Glycine.
NO: nucleotide location Glutamic Acid, F=Phenylalanine, location corresponding H=Histidine, I=Isoleucine, K=Ly	. G=Glvcine.
location   corresponding   H=Histidine, I=Isoleucine, K=Ly	
corresponding   to final   v v	ysine,
corresponding to first L-Leucine, M-Methionine, N-Aspa	aragine,
to first amino acid P=Proline, Q=Glutamine, R=Argin	nine,
amino acid residue of S=Serine, T=Threonine, V=Valine residue of amino acid W=Tryptophan, Y=Tyrosine X=Th	2,
" I I I I I I I I I I I I I I I I I I I	cnown, *=Stop
amino acid sequence Codon, /=possible nucleotide de sequence \ =possible nucleotide insertion	eletion,
CLEKVHDLCDNFCHRYITCLKGKMPIDLVIE	
PASCPSLPDQNNMWIRDHEDSGSVHLGTPGE	
SDQGDGLDTSVASPSSGGEDEDLDQERRRNK	K DCT EDKNYALITM
RAWLFQHLSHPYPSEEQKKQLAQDTGLTILC	WWWELNYBOBIA
QPMIDQSNRTGQGAAFSPEGQPIGGYTETQP	HVAVRPPGSVGMS
LNLEGEWHYL	
5540 148 1440 PPLGAGAGVHARSPHPARRLPLTTAGVGGRA	APDLLPTPWROHRG
PSGAAAPGCALPRGQALEGPRSCRRPQPMAR	RYDELPHYPGIVD
GPAALASFPETVPAVPGPYGPHRPPQPLPPG	LDSDGLKREKDEI
YGHPLFPLLALVFEKCELATCSPRDGAGAGL	GTPPGGDVCSSDS
FNEDNTAFAKQVRSERPLFSSNPELDNLMIQ	
KGKMPIDLVIEDRDGGCREDFEDYPASCPSL	
SGSVHLGTPGPSSGGLASQSGDNSSDQGVGL	
EDLDQEPRRNKKRGIFPKVATNIMRAWLFQH	
LAQDTGLTILQVNNWFINARRRIVQPMIDQS	
QPIGGYTETEPHVAFRAPASVGDEFGTRKEE 5541 148 1440 PPLGAGAGVHARSPHPARRLPLTTAGVGGRA	
PSGAAAPGCALPRGQALEGPRSCRRPQPMAR	
GPAALASFPETVPAVPGPYGPHRPPQPLPPG	
YGHPLFPLLALVFEKCELATCSPRDGAGAGL	
FNEDNTAFAKQVRSERPLFSSNPELDNLMIQ	
KGKMPIDLVIEDRDGGCREDFEDYPASCPSL	
SGSVHLGTPGPSSGGLASQSGDNSSDQGVGL	DTSVASPSSGGED
EDLDQEPRRNKKRGIFPKVATNIMRAWLFQH	
LAQDTGLTILQVNNWFINAKRRIVQPMIDQS	
QPIGGYTETEPHVAFRAPASVGDEFGTRKEE  5542 148 1440 PPIGAGAGVHARSPHDARRIPLTTAGVGGRA	
5542 148 1440 PPLGAGAGVHARSPHPARRLPLTTAGVGGRA PSGAAAPGCALPRGQALEGPRSCRRPQPMAR	
GPAALASFPETVPAVPGPYGPHRPPQPLPPG	KIDERLHIEGIAN
YGHPLFPLLALVFEKCELATCSPRDGAGAGLG	GTPPGGDVCSSDS
FNEDNTAFAKQVRSERPLFSSNPELDNLMIQ	
KGKMPIDLVIEDRDGGCREDFEDYPASCPSL	PDQNNIWIRDHED
SGSVHLGTPGPSSGGLASQSGDNSSDQGVGLI	
EDLDQEPRRNKKRGIFPKVATNIMRAWLFQHI	
LAQDTGLTILQVNNWFINARRRIVQPMIDQSI	
QPIGGYTETEPHVAFRAPASVGDEFGTRKEEV 5543 2405 665 RWVREOPWPLRTSEAVKTPALRPFPGPRGVS	
5543 2405 665 RWVREQPWPLRTSEAVKTPALRPFFGPRGVSI KRPFSDSGAFWSPERRPGVLEAPRRRPVPASI	
SSASRDRVLARTMIVADSECRAELKDYLRFAI	
RESRARRGPRGPSAFIPVEEVLREGAESLEQI	
DNLAVVMGLHPDYFTSFWRLHYLLLHTDGPLF	
ARHQCSYLVGSHMAEFLQTGGDPEWLLGLHR	
LLAHRPWLITKEHIQALLKTGEHTWSLABLIC	QALVLLTHCHSLS
SFVFGCGILPEGDADGSPAPQAPTPPSEQSSF	
ESARDVEALMERMQQLQESLLRDEGTSQEEME	
VTPSADILEPSPHPDMLCFVEDPTFGYEDPTR	
DYTWEDHGYSLIQRLYPEGGQLLDEKFQAAYS	
DTSVLRRAIWNYIHCVFGIRYDDYDYGEVNQL	
ACYPEKTTRRMYNLFWRHFRHSEKVHVNLLLL RAITRYMT	DAYLLAADMAAA
5544 1895 514 LGGLLGRQRLLLRMGAGRLGAPMERHGRASAT	CUSCACEONAGO
PEGRRQEPLRRRASSASVPAVGASAEGTRRDR	
QRVESLRKKRPLFPWFGLDIGGTLVKLYYFEP	
ESLKSIRKYLTSNVAYGSTGIRDVHLELKDLT	
FPTHDMPAFIQMGRDKNFSSLHTVFCATGGGA	
LQLCKLDELDCLIKGILYIDSVGFNGRSQCYY	
LPFDLKNPYPLLLVNIGSGVSILAVYSKDNYK	
FGLCCLLTGCTTPEEALEMASRGDSTKVDKLV	RDIYGGDYERFG
LPGWAVASSFGNMMSKEKREAVSKEDLARATL	ITITNNIGSIAR
MCALNENINQVVFVGNFLRINTIAMRLLAYAL	DYWSKGQLKALF
SEHEGYFGAVGALLELLKIP	

Deginning   Not   location   corresponding   corresponding   cofirst   amino acid   cofirst   amino acid   cofirst   amino acid   more   corresponding   cofirst   amino acid   cofirst   amino acid   cofirst   common   corresponding   cofirst   amino acid   common   corresponding   cofirst   amino acid   common   corresponding   cofirst   common   corresponding   cofirst   common   corresponding   common   corresponding   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:   nucleotide   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   correspondi		1		
Location   Corresponding   Lofirst   amino acid   Amino acid   English   Laleucine, M-Metholonie, M-Magapragine,   Paproline,   Calulamine, R-Arginine,   Paproline,   Calulamine, R-Arginine,   Paproline,   Calulamine, R-Arginine,   Paproline,   Calulamine, R-Arginine,   Paproline,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine,   Calulamine, R-Arginine, R-Arginine,   Calulamine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine	NO:		location	
corresponding to first amino acid residue of amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequen	1	1	1	
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residue of amino acid sequence sequence sequence sequence 131 GAMASAGRGANAPULGILLALLUPEGGARATOABLYTCSSYL (Com. /=possible nucleotide deletion) GAMASAGRGANAPULGILLALLUPEGGARATOABLYTCSSYL (KLIATHHRVELHSIDIKYGSGGQASTOABLYTCSSYL) KILIATHHRVELHSIDIKYGSGGQGYTGVERADDANSYNRIRG (SEGGCPRGSPYRGQAVELHVLTGSGCARATOABLYTCSSYL (KLIATHHRVELHSIDIKYGSGGQCGVELTUPENDATSYNELSY) GSGCGSSPIRGGGGGRERGARARQAQLRNLEAYAANPHSFVFT GGCGSSPIRGGGGGRERGARARQAQLRNLEAYAANPHSFVFT RCCGRNIRGISLDVRRVMEPLTASRLQVRKENSLKDCVAVAGG LGVTHPLILSKTEINTVYFLINKLEGGTIKTGVRXSVLVDVVS SLRRHMHRGQFAHPFLIVINSFGFHGMHVKLMATMFGNLFFBI RCCGRNIRGISLDVRRVMEPLTASRLQVRKENSLKDCVAVAGG LGVTHPLILSKTEINTVYFLINKLEGGTIKTGVRXSVLVDVVS SLRRHMHRGQFAHPFLIVINSFGFHGMHVKLMATMFGNLFFBI RVHLVMLHTIKKCLLUTVPDSGCELDFWFISIKTVVVYGASRGMK KLLQEKFPNNSELQDISELLATGAGLSESEARPGGANVGKKGGRRRH RKSLGGMKRAVGGARARGFGAARGAGAQAQANVGKKGGRRHH RKSLGGMKRAVGGARARGFGAARGAGGAGAANVGKKGGRRHA RKSLGGMKRAVGGARARGFGAARGAGGAGAANVGKKGGRRHA RKSLGGMKGAVGGGRREGGGGGGGGGGGGGGGGGAGGAGGAGGAGGAGGAGGAGGA	1		A	
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SEGGCPRGSPVRCGGAVRITHVLTGKNLHTHIFPSPLSNNOGUS SAFGEDGGGDLDLATVRCGGGHURERANVERDEVSTURSYT GSQTGSPTRGGHEVHGMPSANTHNTWKAMEGIFIKPSVEPSAGH DEL  5546  1592  146  FVPRGGGSSMGGGRSHRGGRARAGAGLANLERYAANHBEFYEN GCGRNTRGGLEGUDVRRMPENTASHLQUPKRSHLKDCVAVAGE LGVTHELLISKTETRVYFKIMELGGGPTLTFQVRKYSLVEDVVS SLRRHMHEGOPHPHPLILVINSFOPMGHWISTLKDCVAVAGE LLGVTHELLISKTETRVYFKIMELGGGPTLTFQVRKYSLVEDVVS SLRRHMHEGOPHPHPLILVINSFOPMGHWISTLKAUCKAVAGE NHAVHASTITIKCLLIDVRDSGELDPRHYSIKVVPVGASRCK KLLGKFPRMSHLGOISELLARGAGLSSERSENDGLNFTELD AVAGRGNMRAGGSAVRLTETGPRHTGLLKVGGSVGECKVMPHS FVSKTEEBLGALLERKEKLRLKANGROAGAGAGNVGEGGRBH RKKSLIGWKKARVGGSDBSAGIFSPTRALELGEDDBSGDDDI EYFCQAVGGAPSEDLFPBAAGKGRLASSPGRENDGGGRGRHGKEVA AVAGRGNMRAGGGSSRRHGERARGAGAGLANTSSVLTBVS FVSKTEEBLGALLERKEKLRLKANGROAGAGAGNVGEGGRBH RKKSLIGWKARVGGSDBSAGGTSHTASLLLGEDDBSGDDDI EYFCQAVGGAPSEDLFPBAAGKGRLASSPGATHSFSVPT RCCGGSTRTRGLISLDVRRVWSPLTTSSLLQVRKNSKLKOCVAVAGE LGVYHFLLLSKTSTVVFKIMELGAGPTLTSVVGARRGKW KLLGEKFPRMSHLGDISBLLATGAGLSSBSRAPEDGGHRTGGREPCKEVA  SLRHHMHEGQFAHPPLLIVANS FCPHGMHVKLMATWFQNLFPBI INHEVENIATIKGGLDPRHYSIKVVGARRGKW KLLGEKFPRMSHLGDISBLLATGAGLSSBSRAPEDGGHRTGERCHWFHS PVSKTEBELGATLERAKSKLRLKAGGGAAGAGAGRORGEKTWFHS FVSKTEBELGATLERAKSKLRLKAGGGAAGAGAGRORGEKTWFHS FVSKTEBELGATLERAKSKLRLKAGGGAAGAGAGRORGEKTWFHS FVSKTEBELGATLERAKSKLRLKAGGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	3343	802	134	1
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RCCTGRININGLSLDVERYMEPLICASRLOVEKKISCKUCVAVAGE LEVYHELLIS KETENTVYEKMELPGEPTLICYKYSLSVEDVVE SLREHRHEGOPAHPPLIVIASFORMCHVKIMATMPONLFPSI RVHKVNINT I KRCLLID INPDSQELDFHYS I KVVPVQASRCMK KLIQEKFPRMSRLQIS SLLATGAGLESSEAPDODINI TIELPO AVAGRAMBAQQSAVRLETGPERTICLIKVQEGVGEKKWHIS FVSKTEBELQAILEAKEKKIRKAGROAQQAGVVGKRQRGREH RKKELEGMKRARVGGSDEBASGI PERTASLELGEDDDEDDDDI EYFCQAVGER SEDLEPPERKQRLAKSPGRKKRWENDRORGRI CDGFPKTKDKSQGAQARRGPRGASRDGGRGRGRGRVAVA FORGHISSMAGSGSRSRNGKARAAQAQLKRIKKSKUKVANDRORGREH CDGFPKTKDKSQGAQARRGPRGASRDGGRGRGRGRVAVA FORGHISSMAGSGSRSRNGKARAAQAQLKRIKKSKUKVAVAGP LOVYHPLILSKTETNVYPKIMAPLOGPTLIPGENYAMPISFYTY RCCTGRINIQLISLDVERWEPLTASRLQVEKKISLKDCVAVAGP LOVYHPLILSKTETNVYPKIMAPLOGPTLIPGENYAMPISFYTY RCCTGRINIQLISLDVERWEPLTASRLQVEKKISLKDCVAVAGP LOVYHPLILSKTETNVYPKIMAPLOGPTLIPGKYSLVEDVVS SLREHRHEQQFAHPPLIVANSGGPHGHVKKMARMGONFPSI NNHVNIANTIRCLLIDVINPSGEDPHHVIALIKUKYSLVEDVVS SLREHRHEQQFAHPPLIVANSGGPHGHVKKMARMGONFPSI NNHVNIANTIRCLLIDVINPSGEDPHHVIALIKUKYSLVEDVVS SLREHRHEQQFAHPPLIVANSGGPHGHVKKMARMGONGRC KILDEKFPNMSRLQDISELLANGLGSBRAPDGDINITELPQ AVAGRGNMBAQGSAVELTET GPRMTIQLI LVOYPQASRGMK KILDEKFPNMSRLQDISELLANGLGSBRAPDGDDINITELPQ AVAGRGNMBAQGSAVELTET GPRMTIQLI LVOYPQASRGMK KILDEKFPNMSRLQDISELLANGLGSBRAPDGRORGRGRGRGRKVAV DOYPGFTARTFPRSTTMELFLEFLLLLVGFSELDEDDINITELPQ AVAGRGNMBAQGSAVELTET GPRMTIQLI LVOYPGASRGMK RKKSLEGMKKARVOGSDEBASGI PSRTASLELGEDDINITELPQ AVAGRGNBARDAGSAVLTET GPRMTIQLI LVOYPGASRGMKVAV DOYSTPSTATATTTSGPPDFGASGPLAAGLGKRKKRMEMBRORGRE FYSTTEBELQALLEARAKKARMEMBRORGRAF RKKSLEGMKKARVOGSDEBASGI PSRTASLELGGDEDDINITELPQ AVAGRGNBARDAGSAVLTET GPRMTIQLILANGLGKVAVA DENDITYTTTGGPPDFGASGPLALAKELGKAVAV  SONSTTTTTGGPPDFGASGPLALAKELGARGGGTGGGRGRGRGRGRARGARGA  SS48  1 2153 DQTGPPSTLATFPRSTTMELFLOFLLLVGASGGGTGVAVA  FYSTERSELQALLANGLASSEGGRAVAVATGERGCONATAGRAVAVA  ERGKRAVATISTDENGAVATAGAGGGTGGGRGRGRGRGRAVAVA  FYSTERDHAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG		1500		
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KILOBKFPMSRLODISELLATGGILSESAAPDGGINTTELDG ANAGRGMRAGOGAVAITIGPRITUGLVGGGVGGKWMHS FVSKTEEBLQAILEAKEKKIAIKAQRGAQAQAGNVGRKQBQRRAH RKKSLEGMKRAPVGGSDEBAGJTSFRTALEGEDDDDGDDDD EYFCQAVGBAPSEDLPPEAKQRLAKSPGRKEKWEMDRGRGRL CDQKFPKTKDKSQGAQARRGPRGASKDGGRGRGRGRGRGRUX  5547  1592  146  FVPRGGHISRMGSGRGREHGKARRAQQAGKHENDEATANDPHSFVFT RCTGRNIRGUSLDVRRVMEPLTASKLQVRKKNSLKDCVAVAGP LGVTHFILISKTETNVYFUKRSGGGTFLVKKYSLVRDVVS SLRRHMHEQGFAHPELLVLANSFGDHGMHVKLMATMGQLFPSI NVHKVNIAITIKRCLLIDVHPDSGGLDFRHYKKYSLVRDVVS SLRRHMHEQGFAHPELLATGGGLSSESABPDGDGNITTELPG AVAGRGMRAQQSAVRITIGGFRTTLQLISKVPVGASRGMK KLLQBKFPMSRLQDISELLATGGLSSESABPDGDGNITTELPG AVAGRGMRAQQSAVRITIGGFRTTLQLIGGGBGKWPHS FVSKTEBELQAILEAKEKKLRLKARGRAQQAQANVQRKGGRBAH RKKSLEGMKARVGGSDESAGSIPSKTAGLEGDDDGEDDDI EYFCQAVGBAPSEDLFPEAKQKRLAKSPGRKRKRMENBRGRGRL CDQKFPFTKDKSQGAQARAGGPGASSTGGRGRGRGKVX  5548  1 2153  DQTGFPFTTAFTFPRSTMEPLCFLLLVGFSLPLARALRGNETA BNSTTTTSGPPPDGASQPLLAWHLIPFILLLULVLLLAAYFFRA RKGRKAVVSTSDKGMANTLEBEDQGQVAVLSSBFSGAKKYFPT PVBHLEBEIRIRSADDCKQFREFFNSLPSGFHQGTFLANKESE REKMRYPNILBVDHSKVILBGLGDIGSVJXIAASYIDGYKKKNK FIRAQGPKGBTVNDFVRMWRQKSATTVULINLIKEREKCHQV WPDQGCWTYGRIRVCVDECVVLUDYTIRKFCQLQDLDGCKAPR LUSQLHFTSWDDFGVVFTUNDFTLKFCQLQDLDGCKAPR LUSQLHFTSWDDFGVVFTUNDFTLKFCQLQDLDGCKAPR LUSQLHFTSWDDFGVVFTUNDFTLKRCRVQTVIRDFTHRFCLQCDLDGCKAPR VILSMKRGGEYTDY INASSIDGKRQKVYFIATOGPLAFTHDK GGBETFRILTVINTEINKBMRTGNLDANMRARVGVTGLGBGTTTTHDK TJAGKKGGTTYTVIAAKAMMILAGCKUVVFSYSIRNGRPGWTFTHDK KGLEEFFRICTIVUTATIKGRREKCHQVV UPDGCWTFTSVILARAGRACHQTHFTTHDK LGLEEFFRICTIVUTATIKGRREKCHQVV UPDGCWTFTSVILARAGRACHATHTHRFTHDK RNDHLSEATSIRDFLUTINQPQARGEQVVVVRQFHHHWPTIG IPAGGKGMTUNDLAFTVANGAKGRACHTORFTTHAK NOTLSEATSIRDFLUTINQPQARGEQVVVVRQFHHHWPTIG IPAGGKGMTUNDLAFTVANGAGAGRTCTPLAL SNILERVKAEGLLDVPQAVISLRLQRPHWVQTLEQUEFCYKVVQ DFIDISDYAFK  S549  915  256  FRATGKKRAPUTATING HKREMMRTGNLDANMERVFSIGARGRTGTFTHAK KRILDHAGGVTYTERFRITINHAGAGAGAGRTCTPTLAL SNILERVKAEGLAVRKTISUVELDAFFKVESSVETSASGGTV VTUSEHMPROGOVTTELDLTERTLTRPPMSRARREVINGAF RKLDKTGRUNTATAGAGAGTARTHRKIL SNILERVKAEGLAVRARHHHKYCYNGEWSBEQUFRKLI  5550  2364  1210	ļ			
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FVSKTEEELQALLEAKEKLIRLKAOROAQAQONVORKORGEREA RIKKELEGMKKARVGOSDERAGI FERTASLELGEDDDEQEDDDI EYFCQAVGER9EDLFPEAKQKRLAKSPERREKKEMENDEGERL CDCKFPKTKOKSQAQARGPRGASRAGGRGGRGRGRGRGRCR  FVPRGGHSEMGGGGSEKRÜKRARAGAQLRINEAYAANPHISFVFT RCCTGRINIRGLELDVRRVMEPLTASRLQVRKWISLKUCVAVAGP LOVTHFLILSKTETINVYKIKMELGEPTILTVQVKKYSLVRDVVS SLRHRMHEQQFAHPPLLVLINSFGPHGHHVUKIMATMFQALFPSI NYHKVNILTIKRCELIDVYKKIMELGEPTILTVQVKKYSLVRDVVS SLRHRMHEQQFAHPPLLVLINSFGPHGHHVUKIMATMFQALFPSI NYHKVNILTIKRCELIDVYFKIMELGEPTILTVQVKKYSLVRDVVS SLRHRMHEQQFAHPPLLVLINSFGPHGHHVUKIMATMFQALFPSI NYHKVNILTIKRCELIDVYFLTGPRMICLIKVGSGVGEGKGWHS KILLQEKFPNNSRLQDISELLATGAGLSESRAEPDGOHNTTELPQ AVAGRGMRAQGSAVNTETTGPRMICLIKVGSGVGEGKWHS FVSKTEEELQAILEAKEKKLRLKAQRQAQQAVQVQRKQEQREAH RKKSLEGMKRARVGGSDEEASGIFSRTASLELGEDDBGQEDDDI SYFCQAVGEAPSEDLIFPEAKQRILAKSGGRRRRWENDRGRGRL CDGFFPKTDINSQGAQARRGPRGASRDGGRGRGRGFGKVA  DONSPTTATSGPPDGASGPLLAMLLIPLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLL	1			1 -
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STYCOAVGEAPSEDLEPPEAKORALAKSPIGRRRKWENDERGRAN   S547   1592   146   FVPRGHISSMGQSGRSHQKRARAQAQLRNLEAYAANPHSFUFT   RGCTGRNIRQLSLDVRRVMEPLTASRLQVRKKUSLKOCVAVAGG   LOVIPHILIDSKTETINVYKIMELPGGPTJLTFQVKKYSLVRDVS   SLRHRMHEQGPAHPPILVLNISTGPHGHHVLKLMATMFQALPFSI   NYHKVNILTIKRCLIDVYKKMELPGGPTJLTFQVKKYSLVRDVS   SLRHRMHEQGPAHPPILVLNISTGPHGHHVLKLMATMFQALPFSI   NYHKVNILTIKRCLIDVYKKMELPGPFHYSIKVVPVQASRGMK   KILGEKPPMNSRLQDISELLATGAGLSSEAEPDGOHNITELPG   AVAGRGMRAQGSAVRTETGFRMTLIKVGEVGASRGMK   KILGEKPPMNSRLQDISELLATGAGLSSEAEPDGOHNITELPG   AVAGRGMRAQGSAVARTETGFRMTLIKVGEVGASRGMK   KILGEKPPMNSRLQDISELLATGAGLSSEAEPDGOHNTTELPG   AVAGRGMRAQGSAVARTETGFRMTLIKVGEVGAGRGREGKVMHA   FVSTTEEELQALLEAKSKLRUKAQRQAQANVORKORDRAH   RKKSLEGMKKARVGGSDEASGIPSRTASLELGEDDDEQEDDD   EYFCQAVGEAPSEDLFPERAQKRLAKSPGKRRRWENDRIRGRR.L   CDQFFPKTRUKSQGAQARRGPRASPGRGRGRGRGKRVA   DSNSTTTTSGPPDPGASQPLLAMILLFLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLL	1			
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146   FPERGISSINGGSGRSREUGVERARAQAGLIRILERYANDPISFUFT   RCTGRINGLSLDVRRUMEPLTARRLYGRKINSLKDCVAVAGE   LGVTHFILISKTETNVYRKLMILEGGFTLIFGVKKISLVRDVVS   SIRRHRHEQGFHIPPLIJSKTETNVYRKLMILEGGFTLIFGVKKISLVRDVVS   SIRRHRHEQGFHIPPLIJSKTETNVYRKLMILEGGFTLIFGVKKISLVRDVVS   SIRRHRHEQGFHIPPLIJSKTETNVYRKLMILEGGFTLIFGVKKISLVRDVVS   SIRRHRHEQGFHIPPLIJSKTETNIFVRUKMATMFGNLIPSI   NYHKVILLITURRILLIDVIPPSSGEPHIYSIKUVVGASRGMK   KILGEKPPINNSRILDISELLATGRGLSESEAPPDGDHNITELPO   AVAGRGMRAQGAVALTETIGFATLLI IRVOGSUGEKVMEHIS   FVSKTEBELQATLEAKEKKLRLKAQRQAQAQNVQRKQEQREAH   RKKSLEGMKKARVGSDEBASGIPSRTASILGEDDISEGDDDI   EYFCQAVGEAPSELDFPERAVKRILAKSPGGKKRRMBRGRGRI, CDQKFPKTKNKSQGAQARRGRGRAGRGRGRGRGRCRCRPCKRVA   DOTGFPETTHFTFFRSTMEPLICHJUFSFLPLAKEGNETAR   RKGKKAVSTSDKNSMOGLIBEDGEQGRVMLLEDSPERGKRKTPI   DONETTTTSGPPDPGASQPLLAWLLLPLLLLVLLLAAYFFF   RKGKKAVSTSDKNSMOGLIBEDGEQGRVMLLERSPSGFKKTFFI   PVEHLBEETRISADDCKOPREETRITAMITNIK KREKEKCHQV   WEDGGCMTYGNTRVCUEDCUVLUDYTTRKECJOPQLPDGCKAPR   LVSQLHFTSWPDFGVPFTPIGMLKFIKKVKTLNPVHAGPIVVHC   SAGVGRTGTFIVIDAMMAMHIAGCKVDVFEFYST RNGREGMVQ   TDMYTFI VQALLEVYLVGDTELDVSSLEHKHQTHHGTTTHFDK   GILBEFRKLTAVRI MENNEMTGINALVHGENTIEL   KNDTLSEAISIRDFLUVTLNOPGARGEQVVVVQPHFGSVTHGETTIEL   KNDTLSEAISIRDFLUVTLNOPGARGEQVVVVQPHFHGSVTHGETTIEL   KNDTLSEAISIRDFLUVTLNOPGARGEGQRVVVRQPHFHGWPLIC   IPAEGKGMILDLAAVQKQQQTGNHPITTHGESTIADHGEL   KNDTLSEAISIRDFLUVTLNOPGARGEGQPKCVVRQPHFHGWPLIC   IPAEGKGMILDLAAVQKQQQTGNHPITTHGETTIELDC   CLARGSAGIKGIGRVPRIMODDNNRTLDFKEFMKGLNDYAVVME   KEEVEBLFQRFORDONSTITDNEFLLUTLREPMSRARKEVIMQAP   KRLJKTGOVITIEDLREVVNACHHHKYYONGEWSEGVFFKFLD   NFDSPYDKGGLUTPEEPMNYYAGVSASILDAFFKYPESYVETSASGGTV   SLIAFTTMALLTIMEFSVYQDTMMKYEYEVDKDFSSKLRINIDI   TVAKKCQIVGADVLDJAFTMVASADGLVVFFTSASGGTV   SLIAFTTMALLTIMEFSVYQDTMMKYEYEVDKDFSSKLRINIDI   TVAKKCQIVGADVLDJAFTMVASADGLVVFTSASGGTV   SKALKTGOSVITIEDLREVVNACHHHKYYONGEWSEGDFSPGSGGRGGRAGGRAGGRENG   RKGLKTKTISJVVELDAFFKYTESTASGFTV   PSHIBDJSSQCKMQ   RKGLKTKTISJVELGLDAFFKYTESTAGLHGVSTTYFDISPQCKEMG   RKGLKTKTISJVELGLDAFFKYTESTAGLPFVFDISPQCKEMG   RKGLKTKTISJVELGLDAFFKYTESTAGLPFTYFDISPQC	1	j		
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DFIDIFSDYANFK  5549 915 256 FEATGGKRLAFKMAGTARHDREMAIQAKKKLTTATDPIERLRLQ CLARGSAGIKGLGRVFRIMDDDNNRTLDFKEFMKGLNDYAVVME KEEVEBLFQRFDKDGNGTIDFNEFLLTLRPPMSRARKEVIMQAF RKLDKTGDGVITIEDLREVYNAKHHPKYQNGEWSEGQVFRKFLD NFDSPYDKDGLVTPEEFMNYYAGVSASIDTDVYFIIMMRTAWKL  5550 2364 1210 RKRKVFLKMRRLNRKKTLSLVKELDAFFKVPESYVETSASGGTV SLIAFTTMALLTIMEFSVYQDTWMKYEYEVDKDFSSKLRINIDI TVAMKCQYVGADVLDLAETMVASADGLVYEPTVFDLSPQQKEWQ RMLQLIQSRLQBEHSLQDVIFKSAFKSTSTALPPREDDSSQSPN ACRIHGHLYVNKVAGNFHITVGKAIPHPRGHAHLAALVNHESYN FSHRIDHLSFGBLVPAIINPLDGTEKIAIDHNQMFQYFITVVPT KLHTYKISADTHQFSVTERRRIINHAAGSHGVSGIFMKVDLSSL MVTVTEEHMPFWQFFVRLCGIVGGIFSTTGMLHGIGKFIVEIIC CRFRLGSYKPVNSVPFEDGHTDNHLPLLENNTH				
5549 915 256 FEATGGKRLAFKMAGTARHDREMAIQAKKKITTATDPIERIRLQ CLARGSAGIKGLGRVFRIMDDDNNRTLDFKEFMKGLNDYAVVME KEEVELFQRFDKDGNGTIDFNEFLLTLRPPMSRARKEVIMQAF RKLDKTGDGVITIEDLREVYNAKHHPKYQNGEWSEGQVFRKFLD NFDSPYDKDGLVTPEEFMNYYAGVSASIDTDVYFIIMMRTAWKL RKRKVFLKMRRLNRKKTLSLVKELDAFPKVPESYVETSASGGTV SLIAFTTMALLTIMEFSVYQDTWMKYEYEVDKDFSSKLRINIDI TVAMKCQYVGADVLDLAETMVASADGLVYEPTVFDLSPQQKEWQ RMLQLIQSRLQBEHSLQDVIFKSAFKSTSTALPPREDDSSQSPN ACRIHGHLYVMKVAGNFHITVGKAIPHPRGHAHLAALVMHESYN FSHRIDHLSFGBLVPAIINPLDGTEKIAIDHNQMFQYFITVPT KLHTYKISADTHQFSVTERBRIINHAAGSHGVSGIFMKVDLSSL MVTVTEEHMPFWQFFVRLCGIVGGIFSTTGMLHGIGKFIVEIIC CRFRLGSYKPVNSVPFEDGHTDNHLPLLENNTH	<b>)</b>			<del>-</del> <del>-</del>
CLARGSAGIKGLGRVFRIMDDDNNRTLDFKEFMKGLNDYAVVME KEEVEBLFQRFDKDGNGTIDFNEFLLTLRPPMSRARKEVIMQAF RKLDKTGDGVITIEDLREVYNAKHHPKYQNGEWSEGQVFRKFLD NFDSPYDKDGLVTPEEFMNYYAGVSASIDTDVYFIIMTAWKL SELAFTTMALLTIMEFSVYQDTWMKYEYEVDKDFSSKLRINIDI TVAMKCQYVGADVLDLAETMVASADGLVYEPTVFDLSPQQKEWQ RMLQLIQSRLQBEHSLQDVIFKSAFKSTSTALPPREDDSSQSPN ACRIHGHLYVNKVAGNFHITVGKAIPHPRGHAHLAALVNHESYN FSHRIDHLSFGBLVPAIINPLDGTEKIAIDHNQMFQYFTVVPT KLHTYKISADTHQFSVTERERIINHAAGSHGVSGIFMKYDLSSL MVTVTEEHMPFWQFFVRLCGIVGGIFSTTGMLHGIGKFIVEIIC CRFRLGSYKPVNSVPFEDGHTDNHLPLLENNTH	5540	915	255	
KEEVEELFQRFDKDGNGTIDFNEFLLTLRPPMSRARKEVIMQAF RKLDKTGDGVITIEDLREVYNAKHHPKYQNGEWSEEQVFRKFLD NFDSFYDKDGLVTPEEFMNYYAGVSASIDTDVYFIIMMTAWKL  5550 2364 1210 RKRKVFLKMRRLNRKKTLSLVKELDAFPKVPESYVETSASGGTV SLIAFTTMALLTIMEFSVYQDTWMKYEYEVDKDFSSKLRINIDI TVAMKCQYVGADVLDLAETMVASADGLVVEPTVFDI.SPQCKEWQ RMLQLIQSRLQBEHSLQDVIFKSAFKSTSTALPPREDDSSQSPN ACRIHGHLYVNKVAGNFHITVGKAIPHPRGHAHLAALVAHESYN FSHRIDHLSFGELVPAIINPLDGTEKIAIDHNQMFQYFITVVPT KLHTYKISADTHQFSVTERERIINHAAGSHGVSGIFMKYDLSSL MVTVTEEHMPFWQFFVRLCGIVGGIFSTTGMLHGIGKFIVEIIC CRFRLGSYKPVNSVPFEDGHTDNHLPLLENNTH	3349		230	
RKLDKTGDGVITIEDLREVYNAKHHPKYQNGEWSEEQVFRKFLD NFDSPYDKDGLVTPEEFMNYYAGVSASIDTDVYFIIMMRTAWKL  5550 2364 1210 RKRKVFLKMRRINRKKTLSLVKELDAFFKVPESYVETSASGGTV SLIAFTTMALLTIMEFSVYQDTWMKYEYEVDKDFSSKLRINIDI TVAMKCQYVGADVLDLAETMVASADGLVYEPTVFDI.SPQQKEWQ RMLQLIQSRLQBEHSLQDVIFKSAFKSTSTALPPREDDSSQSPN ACRIHGHLYVNKVAGNFHITVGKAIPHPRCHAHLAALVAHESYN FSHRIDHLSFGELVPAIINPLDGTEKIAIDHNQMFQYFITVVPT KLHTYKISADTHQFSVTERERIINHAAGSHGVSGIFMKYDLSSL MVTVTEEHMPFWQFFVRLCGIVGGIFSTTGMLHGIGKFIVEIIC CRFRLGSYKPVNSVPFEDGHTDNHLPLLENNTH	1			
NFDSPYDKDGLVTPEEFMNYYAGVSASIDTDVYFIIMMRTAWKL  5550 2364 1210 RKRKVFLKMRRLNRKKTLSLVKELDAFPKVPESYVETSASGGTV SLIAFTTMALLTIMEFSVYQDTWMKYEYEVDKDFSSKLRINIDI TVAMKCQYVGADVLDLAETMVASADGLVYEPTVFDI.SPQQKEWQ RMLQLIQSRLQBEHSLQDVIFKSAFKSTSTALPPREDDSSQSPN ACRIHGHLYVNKVAGNFHITVGKAIPHPRGHAHLAALVNHESYN FSHRIDHLSFGBLVPAIINPLDGTEKIAIDHNQMFQYFITVVPT KLHTYKISADTMQFSVTERBRIINHAAGSHGVSGIFMKVDLSSL MVTVTEEHMPFWQFFVRLCGIVGGIFSTTGMLHGIGKFIVEIIC CRFRLGSYKPVNSVPFEDGHTDNHLPLLENNTH	[			i — — — — — — — — — — — — — — — — — — —
5550 2364 1210 RKRKVFLKMRRLNRKKTLSLVKELDAFPKVPESYVETSASGGTV SLIAFTTMALLTIMEFSVYQDTWMKYEYEVDKDFSSKLRINIDI TVAMKCQYVGADVLDLAFTMVASADGLVYEPTVFDLSPQQKENQ RMLQLIQSRLQBEHSLQDVIFKSAFKSTSTALPPREDDSSQSPN ACRIHGHLYVNKVAGNFHITVGKAIPHPRGHAHLAALVNHESYN FSHRIDHLSFGELVPAIINPLDGTEKIAIDHNQMFQYFITVVPT KLHTYKISADTMQFSVTERBRIINHAAGSHGVSGIFMKYDLSSL MVTVTEEHMPFWQFFVRLCGIVGGIFSTTGMLHGIGKFIVEIIC CRFRLGSYKPVNSVPFEDGHTDNHLPLLENNTH	1	•		· · · · · · · · · · · · · · · · · · ·
SLIAFTTMALLTIMEFSVYQDTWMKYEYEVDKDFSSKLRINIDI TVAMKCQYVGADVLDLAETMVASADGLVYEPTVFDLSPQQKENQ RMLQLIQSRLQBEHSLQDVIFKSAFKSTSTALPPREDDSSQSPN ACRIHGHLYVNKVAGNFHITVGKAIPHPRGHAHLAALVNHESYN FSHRIDHLSFGBLVPAIINPLDGTEKIAIDHNQMFQYFITVVPT KLHTYKISADTHQFSVTERERIINHAAGSHGVSGIFMKYDLSSL MVTVTEEHMPFWQFFVRLCGIVGGIFSTTGMLHGIGKFIVEIIC CRFRLGSYKPVNSVPFEDGHTDNHLPLLENNTH	SEE A	2254	1310	
TVAMKCQYVGADVLDLAFTMVASADGLVYEPTVFDLSPQQKENQ RMLQLIQSRLQBEHSLQDVIFKSAFKSTSTALPPREDDSSQSPN ACRIHGHLYVNKVAGNFHITVGKAIPHPRGHAHLAALVAHESYN FSHRIDHLSFGBLVPAIINPLDGTEKIAIDHNQMFQYFITVVPT KLHTYKISADTHQFSVTERERIINHAAGSHGVSGIFMKYDLSSL MVTVTEEHMPFWQFFVRLCGIVGGIFSTTGMLHGIGKFIVEIIC CRFRLGSYKPVNSVPFEDGHTDNHLPLLENNTH	3350	2304	1410	
RMLQLIQSRLQBEHSLQDVIFKSAFKSTSTALPPREDDSSQSPN ACRIHGHLYVNKVAGNFHITVGKAIPHPRCHAHLAALVAHESYN FSHRIDHLSFGELVPAIINPLDGTEKIAIDHAQFQYFITVVPT KLHTYKISADTHQFSVTERERIINHAAGSHGVSGIFMKYDLSSL MVTVTEEHMPFMQFFVRLCGIVGGIFSTTGMLHGIGKFIVEIIC CRFRLGSYKPVNSVPFEDGHTDNHLPLLENNTH				
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FSHRIDHLSFGBLVPAIINPLDGTEKIAIDHNQMFQYFITVVPT KLHTYKISADTHQFSVTERERIINHAAGSHGVSGIFMKYDLSSL MVTVTEEHMPFWQFFVRLCGIVGGIFSTTGMLHGIGKFIVEIIC CRFRLGSYKPVNSVPFEDGHTDNHLPLLENNTH	j l			
KLHTYKISADTHQFSVTERERIINHAAGSHGVSGIFMKYDLSSL MVTVTEEHMPFWQFFVRLCGIVGGIFSTTGMLHGIGKFIVEIIC CRFRLGSYKPVNSVPFEDGHTDNHLPLLENNTH	1			
MVTVTEEHMPFWQFFVRLCGIVGGIFSTTGMLHGIGKFIVEIIC CRFRLGSYKPVNSVPFEDGHTDNHLPLLENNTH	į			, , , , , , , , , , , , , , , , , , ,
CRFRLGSYKPVNSVPFEDGHTDNHLPLLENNTH	[	1	;	
<del></del>	] ]	1		· · · · · · · · · · · · · · · · · · ·
COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN				
		Z11 ]	1700	MORDHIMDYKESCPSVSIPSSDEHREKKKRFTVYKVLVSVGRSE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid residue of	residue of	S=Serine, T=Threonine, V=Valine,
1	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
	sequence	<del> </del>	\=possible nucleotide insertion)
<b>!</b>	1		WFVFRRYAEFDKLYNTLKKQFPAMALKIPAKRIFGDNFDPDFIK
1	1	1	QRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSDPSEDE
1		ł .	DERSSQKLHSTSQNINLGPSGNPHAKPTDFDFLKVIGKGSFGKV
			LLAKRKLDGKFYAVKVLQKKIVLNRKEQKHIMAERNVLLKNVKH PFLVGLHYSFQTTEKLYFVLDFVNGGELFFHLQRERSFPEHRAR
l	[		FYAAEIASALGYLHSIKIVYRDLKPENILLDSVGHVVLTDFGLC
1	ĺ		KEGIAISDTTTTFCGTPEYLAPEVIRKQPYDNTVDWWCLGAVLY
	ļ		EMLYGLPPFYCRDVAEMYDNILHKPLSLRPGVSLTAWSILEELL
1			EKDRONRLGAKEDFLEIONHPFFESLSWADLVOKKIPPPFNPNV
			AGPDDIRNFDTAFTEETVPYSVCVSSDYSIVNASVLEADDAFVG
			FSYAPPSEDLFL
5552	2748	930	LGPAAGAAMGKKHKKHKAEWRSSYEDYADKPLEKPLKLVLKVGG
			SEVTELSGSGHDSSYYDDRSDHERERHKEKKKKKKKKKSEKEKHL
}	}		DDEERRKRKEEKKRKREREHCDTEGEADDFDPGKKVEVEPPPDR
			PVRACRTQPAENESTPIQQLLEHFLRQLQRKOPHGFFAFPVTDA
}			IAPGYSMIIKHPMDFGTMKDKIVANEYKSVTEFKADFKLMCDNA
ļ			MTYNRPDTVYYKLAKKILHAGFKMMSKQAALLGNBDTAVEEPVP
1			EVVPVQVETAKKSKKPSREVISCMFEPEGNACSLTDSTAEEHVL
			ALVEHAADEARDRINRFLPGGKMGYLKRNGDGSLLYSVVNTAEP
1 1			DADEEETHPVDLSSLSSKLLPGFTTLGFKDERRNKVTFLSSATT
i			ALSMONNSVFGDLKSDEMELLYSAYGDETGVQCALSLQEFVKDA
1 1	!		GSYSKKVVDDLLDQITGGDHSRTLFQLKQRRNVPMKPPDEAKVG
1 1		İ	DTLGDSSSSVLEFMSMKSYPDVSVDISMLSSLGKVKKELDPDDS HLNLDETTKLLQDLHEAQAERGGSRPSSNLSSLSNASERDOHHL
1 1			GSPSRLSVGEQPDVTHDPYEFLQSPEPAASAKT
5553	74	1095	LGREAVYLVSRMDGPVAEHAKQEPFHVVTPLLESWALSQVAGMP
1 . 1			VFLKCENVQPSGSFKIRGIGHFCQEMAKKGCRHLVCSSGGNAGI
] ]	j		AAAYAARKLGIPATIVLPESTSLQVVQRLQGEGAEVQLTGKVWD
1 1			EANLRAQELAKROGWENVPPFDHPLIWKGHASLVQELKAVLRTP
1 1			PGALVLAVGGGGLLAGVVAGLLEVGWQHVPIIAMETHGAHCFNA
	•		AITAGKLVTLPDITSVAKSLGAKTVAARALECMQVCKIHSEVVE
}			DTEAVSAVQQLLDDERMLVEPACGAALAAIYSGLLRRLQAEGCL
5554	166	3330	PPSLTSVVVIVCGGNNINSRELQALKTHLGQV
3354	100	2318	CSGRTGGRGSLRPAENVCLTCKLSGAETRGLLCPALRTWIMKVL
1			GRSFFWVLFPVLPWAVQAVEHEEVAQRVIKLHRGRGVAAMQSRQ
f (	1		WVRDSCRKLSGLLRQKNAVLNKLKTAIGAVEKDVGLSDEEKLFQ
]	ļ		VHTFEIFQKELNESENSVFQAVYGLQRALQGDYKDVVNMKESSR QRLEALREAAIKEETEYMELLAABKHQVEALKNMQHQNQSLSML
	. 1		DBILEDVRKAADRLEEBIEEHAFDDNKSVKGVNFEAVLRVEEEE
1 1			ANSKQNITKREVEDDLGLSMLIDSQNNQYILTKPRDSTIPRADH
(			HFIKDIVTIGMLSLPCGWLCTAIGLPTMFGYIICGVLLGPSGLM
, 1			SIKSİVQVETLGEFGVFFTLFLVGLEFSPEKLRKVWKISLQGPC
	ĺ	ĺ	YMTLLMIAFGLLWGHLLRIKPTQSVFISTCLSLSSTPLVSRFLM
ļ		)	GSARGDKEGDIDYSTVLLGMLVTQDVQLGLFMAVMPTLIQAGAS
] [			ASSSIVVEVLRILVLIGQILFSLAAVFLLCLVIKKYLIGPYYRK
] ]		}	LHMESKGNKEILILGISAFIFLMLTVTELLDVSMELGCFLAGAL
1		į	VSSCGPVVTEEIATSIEPIRDFLAIVFFASIGLHVFPTFVAYEL
1 1			TVLVFLTLSVVVMKFLLAALVLSLILPRSSQYIKWIVSAGLAQV
			SEFSFVLGSRARRAGVISREVYLLILSVTTLSLLLAPVLWRAAI
<u></u>			TRCVPRPERRSSL
5555	212	1425	LSLRTRETPAPPRCEAASQGRVGWRADAAAEEAVRSVWNRTRDR
1	1		GTMAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIK
		[	KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY
	1	1	DTYGEEGLKDGHQSSHGDIFSHFFGDFGFMFGGTPRQQDRNIPR
			GSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQE
ĺ		[	MRTTQLGPGRFQMTQEVGCDECPNVKLVNEERTLEVEIEPGVRD
	j	Í	GMEYPFIGEGEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNV TISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGL
	{	ĺ	PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK
	. ]	}	ANACPÓGX SANDAMA LYGRIT LIADADE É KEÓPLE EWEGTVÓRPVÓGRÁ ÓK
5556	5835	3346	RTRGMSKNCVPMEFEEYLLRMFQGTFYLLQKITKDNNAHTVKSR
			AND ANT DESCRIPTION OF THE PARTY AND

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cvsteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Ì	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ì	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
<b> </b>	sequence		\=possible nucleotide insertion) LEELDESYIEKFTDFLRLFVSVHLRRIESYSOFPVVEFLTLLFK
	İ	ł	YTFHQPTHEGYFSCLDIWTLFLDYLTSKIKSRLGDKEAVLNRYE
1			DALVLLTEVLNRIOFRYNOAOLEELDDETLDDDOOTEWORYLR
Į	Į.	ļ	QSLEVVAKVMELLPTHAFSTLFPVLQDNLEVYLGLQQFIVTSGS
j	1		GHRLNITAENDCRRLHCSLRDLSSLLQAVGRLAEYFIGDVFAAR
	1		FNDALTVVERLVKVTLYGSQIKLYNIETAVPSVLKPDLIDVHAQ
1		1	SLAALQAYSHWLAQYCSEVHRQNTQQFVTLISTTMDAITPLIST
1	}	}	KVQDKLLLSACHLLVSLATTVRPVFLISIPAVQKVFNRITDASA
	j		LRLVDKAQVLVCRALSNILLLPWPNLPENEQQWPVRSINHASLI
			SALSRDYRNLKPSAVAPQRKMPLDDTKLIIHQTLSVLEDIVENI
1			SGESTKSRQICYQSLQESVQVSLALFPAFIHQSDVTDEMLSFFL
		ļ	TLFRGLRVQMGVPFTEQIIQTFLNMFTREQLAESILHEGSTGCR VVEKFLKILQVVVQEPGQVFKPFLPSIIALCMEQVYPIIAERPS
1	1	1	PDVKAELFELLFRTLHHNWRYFFKSTVLASVQRGIAEEQMENEP
1			QFSAIMQAFGQSFLQPDIHLFKQNLFYLETLNTKQKLYHKKIFR
1		1	TAMLFQFVNVLLQVLVHKSHDLLQEEIGIAIYNMASVDFDGFFA
}	1		AFLPEFLTSCDGVDANQKSVLGRNFKMDRVRRERGRAKRRAEWA
L			RKPGTCAARRGHIEASGRGLCPPCSLAAAHEMPADLVL
5557	1712	491	VILGAGLRDKDMWIPVVGLPRRLRLSALAGAGRFCILGSEAATR
1	1		KHLPARNHCGLSDSSPQLWPEPDFRNPPRKASKASLDFKRYVTD
1	)		RRLAETLAQIYLGKPSRPPHLLLECNPGPGILTQALLEAGAKVV ALESDKTFIPHLESLGKNLDGKLRVIHCDFFKLDPRSGGVIKPP
			AMSSRGLFKNLGIEAVPWTADIPLKVVGMFPSRGEKRALWKLAY
1	1		DLYSCTSIYKFGRIEVNMFIGEKEFOKLMADPGNPDLYHVLSVI
1			WQLACEIKVLHMEPWSSFDIYTRKGPLENPKRRELLDQLQQKLY
1			LIQMIPRONLFTKNLTPMNYNIFFHLLKHCFGRRSATVIDHLRS
1			LTPLDARDILMQIGKQEDEKVVNMHPQDFKTLFETIERSKDCAY
			KWLYDETLEDR
5558	1509	96	RAGCTHPQVPADLGAPAEPRRPQKTCVCLLQPQPGGQRGPTTMI
1			TGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRS
1			LLKLKMVQVVFRHGARSPLKPLPLEEQVEWNPQLLEVPPQTQFD
ſ	[		YTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQLTKVGMQQMFA
1			LGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLA GLFQCQKEGPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTA
}			SLOPGISEDLKKVKDRMGIDSSDKVDFFILLDNVAAEQAHNLPS
}			CPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFLHILES
i	ļ i		NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPP
		1	FAVDLTMELYQHLESKEWFVQLYYHGKEQVPRGCPDGLCPLDMF
			LNAMSVYTLSPEKYHALCSQTQVMEVGNEE
5559	150	1983	PLAATAHFAKMSRVAKYRRQVSEDPDIDSLLETLSPEEMEELEK
1	į į		ELDVVDPDGSVPVGLRQRNQTEKQSTGVYNREAMLNFCEKETKK
1			LMQREMSMDESKQVETKTDAKNGEERGRDASKKALGPRRDSDLG
1			KEPKRGGLKKSFSRDRDEAGGKSGEKPKEEKIIRGIDKGRVRAA  VDKKEAGKDGRGEERAVATKKEEEKKGSDRNTGLSRDKDKKREE
			MKEVAKKEDDEKVKGERRNTDTRKEGEKMKRAGGNTDMKKEDEK
1	<b>[</b>		VKRGTGNTDTKKDDEKVKKNEPLHEKEAKDDSKTKTPEKQTPSG
(			PTKPSEGPAKVEEEAAPSIFDEPLERVKNNDPEMTEVNVNNSDC
1	<b>,</b>		ITNEILVRFTEALEFNTVVKLFALANTRADDHVAFAIAIMLKAN
1			KTITSLNLDSNHITGKGILAIFRALLQNNTLTELRFHNQRHICG
[			GKTEMEIAKLLKENTTLLKLGYHFELAGPRMTVTNLLSRNMDKQ
			ROKRLOEORQAQEAKGEKKOLLEVPKAGAVAKGSPKPSPQPSPK
			PSPKNSPKKGGAPAAPPPPPPPPLAPPLIMENLKNSLSPATQRKM
5560		021	GDKVLPAQEKNSRDQLLAAIRSSNLKQLKKVEVPKLLQ
3360	9	921	SSVVEFSALSVSMACLSPSQLQKFQQDGFLVLEGFLSAEECVAM
}			QQRIGEIVAEMDVPLHCRTEFSTQEEEQLRAQGSTDYFLSSGDK IRFFFEKGVFDEKGNFLVPPEKSINKIGHALHAHDPVFKSITHS
			FKVQTLARSLGLQMPVVVQSMYIFKQPHFGGEVSPHQDASFLYT
			EPLGRVLGVWIAVEDATLENGCLWFIPGSHTSGVSRRMVRAPVG
			SAPGTSFLGSEPARDNSLFVPTPVQRGALVLIHGEVVHKSKQNL
			SDRSRQAYTFHLMEASGTTWSPENWLQPTAELPFPQLYT
5561	2175	1775	CYFIFQFFSSPYPGLHPHQTPAPLPNPGLYPPPVSMSPGQPPPQ

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
dī	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
No:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
- {	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion}
			QLLAPTYFSAPGVMNFGNPSYPYAPGALPPPPPPHLYPNTQAPS
}		J	QVYGGVTYYNPAQQQVQPKPSPPRRTPQPVTIKPPPPEVVSRGS
			S
5562	342	1385	SSGKNDMAAAGAAGLVRGLKAGVLSQADYLNLVQCETLEDLKLH
1			LQSTDYGNFLANEASPLTVSVIDDRLKEKMVVEFRHMRNHAYEP
{			LASFLDFITYSYMIDNVILLITGTLHQRSIAELVPKCHPLGSFE
ł	ĺ	}	QMEAVNIAQTPAELYNAILVDTPLAAFFQDCISEQDLDEMNIEI
		1	IRNTLYKAYLESFYKFCTLLGGTTADAMCPILEFEADRRAFIIT
[	ĺ	i	INSFGTELSKEDRAKLFPHCGRLYPEGLAQLARADDYEQVKNVA
1 .	}		DYYPEYKLLFEGAGSNPGDKTLEDRFFEHEVKLNKLAPLNQFHF
			GVFYAFVKLKEQECRNIVWIAECIAQRHRAKIDNYIPIF
5563	342	1385	SSGKNDMAAAGAAGLVRGLKAGVLSQADYLNLVQCETLEDLKLH
1			LQSTDYGNPLANEASPLTVSVIDDRLKEKMVVEFRHMRNHAYEP
1			LASFLDFITYSYMIDNVILLITGTLHORSIABLVPKCHPLGSFE
] .			QMEAVNIAQTPAELYNAILVDTPLAAFFODCISEODLDEMNIEI
1			IRNTLYKAYLESFYKFCTLLGGTTADAMCPILEFEADRRAFIIT
1 1			INSFGTELSKEDRAKLFPHCGRLYPEGLAQLARADDYEOVKNVA
}			DYYPEYKLLFEGAGSNPGDKTLEDRFFEHEVKLNKLAFLNOFHF
		:	GVFYAFVKLKEQECRNIVWIAECIAQRHRAKIDNYIPIF
5564	3	914	RVRRDKRAVWTARGRRRCGDSMSGGWMAOVGAWRTGALGLALLI.
			LLGLGLGLEAAASPLSTPTSAOAAGPSSGSCPPTKFOCRTSGLC
1 1		l	VPLTWRCDRDLDCSDGSDEEECRIEPCTOKGOCPPPPGLPCPCT
	j		GVSDCSGGTDKKLRNCSRLACLAGELRCTLSDDCIPLTWRCDGH
1 1			PDCPDSSDELGCGTNEILPEGDATTMGPPVTLESVTSLRNATTM
1 1			GPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAAVLSASLV
<del>  </del>			TATLLLSWLRAQERLRPLGLLVAMKESLLLSEOKTSLP
5565	993	138	RWNSPNPARAGSISRPORAPGSVSAVAMTAAVFFGCAFIAFGPA
1 1			LALYVFTIATEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIID
1			NKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSIN
1 1			PGETAPSMRLLAYVSGLGFGIMSGVFSFVNTLSDSLGPGTVGIH
) )	ļ		GDSPQFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKWGILLIVL
1	İ		LTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRS
5566	2043	1020	LKLCLLCQDKNFLLYNQRSR
3300	2043	1232	SHIQHHGRGAQAPVKMVSWMISRAVVLVFGMLYPAYYSYKAVKT
1		1	KNVKEYVRWMMYWIVFALYTVIETVADQTVAWFPLYYELKIAFV
1			IWLLSPYTKGASLIYRKFLHPLLSSKEREIDDYIVQAKERGYET
]			MVNFGRQGLNLAATAAVTAAVKSQGAITERLRSFSMHDLTTIQG
1 1	[		DEPVGQRPYQPLPEAKKKSKPAPSESAGYGIPLKDGDEKTDEEA
1	1		EGPYSDNEMLTHKG?RRSQSMKSVKTTKGRKEVRYGSLKYKVKK RPQVYF
5567	1554	233	
1	-554	دده	EFLGSGVSPDLANEDGLTALHQCCIDDFREMVQQLLEAGANINA
] ]			CDSECWTPLHAAATCGHLHLVELLIASGANLLAVNTDGNMPYDL
	ļ	[	CDDEQTLDCLETAMADRGITQDSIEAARAVPELRMLDDIRSRLQ AGADLHAPLDHGATLLHVAAANGFSEAAALLLEHRASLSAKDOD
1	1	ł	CNEDI WA A VICCOURT MET I WAYOU THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO THE TANKS TO
1		i	GNEPLHAAAYWGQVPLVELLVAHGADLNAKSLMDETPLDVCGDE EVRAKLLELKHKHDALLRAQSRQRSLLRRRTSSAGSRGKVVRRV
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1		Į.	SLTQRTDLYRKQHAQEAIVWQQPPPTSPEPPEDNDDRQTGAELR
1		İ	PPPPEEDNPEVVRPHNGRVGGSPVRHLYSKRLDRSVSYQLSPLD
1 1	1	1	STTPHTLVHDKAHHTLADLKRQRAAAKLQRPPPEGPESPETAEP
5568	1731	587	GLPGDTVTPQPDCGFRAGGDPPLLKLTAPAVEAPVERRPCCLLM
1 1		307	AEDROPASRRGAGTTAAMAASGPGCRSWCLCPEVPSATFFTALL
ļ ,		ļ	SLLVSGPRLFLLQQPLAPSGLTLKSEALRNWQVYRLVTYIFVYE
1			NPISLLCGALIIWRFAGNFERTVGTVRHCFFTVIFAIFSAIIFL
1	-		SFEAVSSLSKLGEVEDARGFTPVAFAMLGVTTVRSRMRRALVFG
]			MVVPSVLVPWLLLGASWLIPQTSFLSNVCGLSIGLAYGLTYCYS
]	İ		IDLSERVALKLDQTFPFSLMRRISVFKYVSGSSAERRAAQSRKL
!!			NPVPGSYPTQSCHPHLSPSHPVSQTQHASGQKLASWPSCTPGHM
1	1	ľ	PTLPPYQPASGLCYVQNHFGPNPTSSSVYPASAGTSLGIQPPTP
5569	2		VNSPGTVYSGALGTPGAAGSKESSRVPMP QTPCPLAWERGSRSEDISVPGQKPPTCSSFSGMDVGPSSLPHLG

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
i	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
{	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	•	\=possible nucleotide insertion)
	<del></del>		LKLLLLLLLPLRGQANTGCYGIPGMPGLPGAPGKDGYDGLPGP
	1	1	KGEPGIPAIPGIRGPKGOKGEPGLPGHPGKNGPMGPPGMPGVPG
			PMGIPGEPGEEGRYKQKFQSVFTVTRQTHQPPAPNSLIRFNAVL
		1	TNPQGDYDTSTGKFTCKVPGLYYFVYHASHTANLCVLLYRSGVK
	1		VVTFCGHTSKTNQVNSGGVLLRLQVGEEVWLAVNDYYDMVGIOG
i	l·		SDSVFSGFLLFPD
5570	264	946	RDRRDRGGVATSTEEPARPRAPOSRGPGPVSOTGRGRERGGGDT
]	}	}	MSSPSPGKRRMDTDVVKLIESKHEVTILGGLNEFVVKFYGPOGT
	[	1	PYEGGVWKVRVDLPDKYPFKSPSIGFMNKIFHPNIDEASGTVCL
		}	DVINGTNTALYDLTNIFESFLPQLLAYPNPIDPLNGDAAAMYLH
			RPEBYKQKIKBYIQKYATEBALKEQEEGTGDSSSESSMSDFSED
1		1	EAODMEL
5571	264	946	RDRRDRGGVATSTEEPARPRAPOSRGPGPVSOTGRGRERGGGDT
			MSSPSPGKRRMDTDVVKLIESKHEVTILGGLNEFVVKFYGPOGT
		1	PYEGGVWKVRVDLPDKYPFKSPSIGFMNKIFHPNIDEASGTVCL
	]	j	DVINOTWTALYDLTNIFESFLPOLLAYPNPIDPLNGDAAAMYLH
1	1		RPEBYKQKIKEYIQKYATEEALKEQEEGTGDSSSESSMSDFSED
	1	1	EAODMEL
5572	2802	2085	RTDYRTGIPGRRFRVMAAGDGDVKLGTLGSGSESSNDGGSESPG
			DAGAAAEGGGWAAAALALLTGGGEMLLNVALVALVLLGAYRLWV
1	Į	•	RWGRRGLGAGAGAGEESPATSLPRMKKRDFSLEQLRQYDGSRNP
1			RILLAVNGKVFDVTKGSKFYGPAGPYGIFAGRDASRGLATFCLD
1 :	<b>!</b>		KDALRDEYDDLSDLNAVQMESVREWEMQFKEKYDYVGRLLKPGE
	[		EPSEYTDEEDTKDHNKQD
5573	2562	219	VPARTPNAEDOGPEARAATATPCOSGGRERAGEAAEDGVKMAAF
			SEMGVMPEIAQAVEEMDWLLPTDIQAESIPLILGGGDVLMAAET
	ļ		GSGKTGAFSIPVIQIVYETLKDQQEGKKGKTTIKTGASVLNKWO
			MNPYDRGSAFAIGSDGLCCQSREVKEWHGCRATKGLMKGKHYYE
	}		VSCHDQGLCRVGWSTMQASLDLGTDKFGFGFGGTGKKSHNKQFD
			NYGEEFTMHDTIGCYLDIDXGHVKFSKNGKDLGLAFEIPPHMKN
		i	QALFPACVLKNAELKFNFGEEEFKFPPKDGFVALSKAPDGYIVK
	j	ļ	SOHSGNAOVTOTKFLPNAPKALIVEPSRELAEOTLNNIKOFKKY
1 1			IDNPKLRELLIIGGVAARDQLSVLENGVDIVVGTPGRLDDLVST
1 1			GKLNLSQVRFLVLDEADGLLSQGYSDFINRMHNQIPQVTSDGKR
1 1	ĺ		LQVIVCSATLHSFDVKKLSEKIMHFPTWVDLKGEDSVPDTVHHV
!!!			VVPVNPKTDRLWERLGKSHIRTDDVHAKDNTRPGANSPEMWSEA
1 1			IKILKGEYAVRAIKEHKMDQAIIFCRTKIDCDNLEQYFIQQGGG
1 1			PDKKGHQFSCVCLHGDRKPHERKQNLERFKKGDVRFLICTDVAA
(			RGIDIHGVPYVINVTLPDEKQNYVHRIGRVGRAERMGLAISLVA
į J	·		TEKEKVWYHVCSSRGKGCYNTRLKEDGGCTIWYNEMQLLSEIEE
			HLNCTISQVEPDIKVPVDEFDGKVTYGQKRAAGGGSYKGHVDIL
1			APTVQELAALEKEAQTSFLHLGYLPNQLFRTF
5574	1731	952	NEGLEVFKEQELQPEDKGAVPEDASTERSAMASLGLQLVGYILG
] [			LLGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHS
1 1			TGITQCDIYSTLLGLPADIQAAQAMMVTSSAISSLACIISVVGM
			RCTVFCQESRAKDRVAVAGGVFFILGGLLGFIPVAWNLHGILRD
í í	İ		FYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCSCQRN
j .			RSNYYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV
5575	456	766	LLWALPCPPPTAAAVLLSSTGLMELLEKMLALTLAKADSPRTAL
1			LCSAWLLTASFSAQQHKGSLQKDPLLSQACVGCLEALLDYLDAR
j f			SPDIGRNSPHYLMFP
5576	249	2146	RSWGAPWFWRMRLLRRRHMPLRLAMVGCAFVLFLFLLHRDVSSR
{ }			EEATEKPWLKSLVSRKDHVLDLMLEAMNNLRDSMPKLQIRAPEA
			QQTLFSINQSCLPGFYTPAELKPFWERPPQDPNAPGADGKAFQK
[ [			SKWTPLETQEKEEGYKKHCFNAFASDRISLQRSLGPDTRPPECV
1 1			DOKFRECPPLATTSVIIVFHNEAWSTLLRTVYSVLHTTPAILLK
1	1		
. 1			EIILVDDASTEBHLKEKLEQYVKOLOVVRVVROEERKGLTTARL
.			EIILVDDASTEBHLKEKLEQYVKQLQVVRVVRQEERKGLITARL LGASVAQAEVLTFLDAHCECFHGWLEPLLARIAEDKTVVVSPDI
.			EIILVDDASTEBHLKEKLBOYVKOLOVVRVVRQEERKGLITARL LGASVAQAEVLTFLDAHCECFHGWLEPLLARIAEDKTVVVSPDI VTIDLNTFEFAKPVQRGRVHSRGNFDWSLTFGWBTLPPHEKORR
			LGASVAQAEVLTFLDAHCECFHGWLEPLLARIAEDKTVVVSPDI

Desinning   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location	SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
Moclection   Corresponding to first amino acid Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Securi	1 -		1	
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corresponding to first amino acid residue of amino acid residue of amino acid sequence and control of the state of amino acid sequence and control of the state of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence	1		1	
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S578   3   AVERMASFGAGRAPFELERNCGYREVEYNDORYGGADSAPYD	}	1		EKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEATYMTMEPV
WFGDPSSFRALLEPELRPEDRILVLGCGNSALSYELFIGGFRW TSVDYSSVVVAMQARYAHVPQLEWETMDVRKLDFFSASFDVVL EKGTLDALLAGERUDVTVSSEGVETMDVRLDFFSASFDVVL EKGTLDALLAGERUDVTVSSEGVETMDVRLDFFSASFDVVL SMTSAAPHFRIRNYAQAYYGHSLHANYGSGSPHFHLYIMHRGGK LSVAQLALGAQILSPPRPTSPCTLQDSBEDPLSAIQL  5579 3 1540 RNSGLARGASLAGRIGGGLAGGVCHDCCACASRCQGVMEGILTR CRALPALATCSRQLSGYVPCRFHHCAPRRGRALLSRVFQPQNL REDRVLSLQDKSDDLTCKSQRLMUQVSLTYPASPGCYTHLLPTYV RAMKKLVRVIDQEMQALGGGKVMMPSLSPAELMQATNRWDLMGK ELLKLRRNHKSSYCLGPTHEART LASGKKLSKVGLPFLLYQ VTRKFRDERPERFGLLRGREFYMKDMYTFDSSPEAAQOTYSLVC DAYGSLFNKLGJPFVKVQADUGT LASGKKLSKVGLPFLLYQ VTRKFRDERPERFGLLRGREFYMKDMYTFDSSPEAAQOTYSLVC DAYGSLFNKLGJPFVKVQADUGT LASGKKLSKVGLPFLLYQ VTRKFRDERPERFGLLRGREFYMKDMYTFDSSPEAAQOTYSLVC DAYGSLFNKLGJPFVKVQADUGT LASGKKLSKVGLPFLLYQ VTRKFRDERPERFGLLRGREFYMKDMYTFDSSPEAAQOTYSLVC DAYGSLFNKLGJPFVKVQADUGT LASGKKLSKVGLPFLYG KYSSIRNAGPTRVCGKPTLABMGCYGLGVTRE*LAAATISVLSTEB CVCRMPSLLAPYQACLIPFKKGSKGAASELIGGLVGHTFYLGT KYSSIRNAGPTRVCGKPTLABMGCYGLGVTRE*LAAATISVLSTEB CVCRMPSLLAPYQACLIPFKKGSKGAASELIGGLVGHTTEAPA EVKCQNIGSVAFLTKGGMDLATFGVTVTV  5580 1681 450 ADAGTRCTPGFVVPSGAGYSAPAQGGRRSSGEMRAAAPGLTAP NRLLQCCELBAGELGMAVPAAAMGFSALGQSGGSGMAPMCSVSS GPSKYVLGWQBLFRGHSKTREFLAHSAKVHSVAWCCDGRRLASG SFDKTASVFLLBKDRLWKENNYRGHGDSVOQCKWHESMPDLFVT ASGKKTTR LWDVTRTKCLATVNTKGENINICKSPDGGYTAVGMK DDVVTFIDAKTRRSKAEBGFKFEVNEISMNNNMFFLTNINGG INLLSYPELKPVOSINAHPSNCIC LYDPMGKYFRATGADALVS LWDVDELVCVRCFSRLDWPVTTLSFSHDGKMLASASEDHFIDLA EVETGDKLMEVQCESPTFTVAWHFRRPLLAFACDKDGKKNDSC CSPPOGSSTMNEVVSPVDYQGAQPYGNKNANTGTGYPTAPAAAPA YNPSLYPTNSPSYAPEVQFLHSAYATLLMKQAWPONSSCGTZG TFHLPVDTGTERRTYQASSAAFRYTAGTFYKPPTQANAPHTAA CSPPOGSSTMNEVVSPVDYQGAQPYGNKNANTGTGYPTAPAAAPA YNPSLYPTNSPSAYPPGAAYATLLMKQAWPONSSCGTZG TFHLPVDTGTERRTYQASSAAFRYTAGTFYKVPPTQSNTAPPYP SSEPNIFYCTAMPTFIRSYPQOMLYAAGGEDKTAGWFTHMASAGTLL TTOHTALGAHPVSMPTYTAQGTPSYVPPTW TTVQVNSIFSAIYPPTVAAMPTNAGATATLPFKRARANELSFTMSCKTFTMLSK SSEPNIFYCTAMPTFIRSYPQOMLYAAGGEDKLGCLLHVNRAACYFTMGLY EKALEDSEKALGLBSSIRALFRKARALELGRHLCSRKCYFTMGLY EKALEDSEKALGLBSSIRALFRKARANELSRKLETSSLLSN TAGGVADQGTSNGGSIDDIETDCYVDPRGSPALLPS			1	
TSVDYSSVVVAMQARYAHUPOLEMETMDVRKLDFPSASETUVIL EKGTLDALLAGERDPWTVSSEGVHTUDQULSEVSRVLVPGGRF1 SWTSAAPHFRTRHYAQAYYGWSLRHATYGSGYHFLLYLMHRGGG LSVAQLALGAQILSPPRPTTSPCTLQDSDBERDFLSAIQL TSVAQLALGAQILSPPRPTTSPCTLQDSDBERDFLSAIQL RRSGLAGRASALARHGGGLAGGVCOMDCGACASRCGOVMEGLLTR CRALPALATCSQLSGYVPCFFHHCAPRGRRLLLSRVFQPQNL REBEVLSLQDKSDDLTCKSQRLMGVLJTYPASPGCYBLLPTYV RAMEKLURVIDQEMQAIGGGVUNMPSLSPAELWQATNRHDLMGK BLLRLRDRHGKESYCLGPTHEEAITALIAGKLSYKQLPFLLYQ VTRKFRDEBFRPRFGLLRGREFYWCQADUGTIGGTVSHERGFLYDUTGEBRIA ICPRCSFSANMETLDLSQMNCPACQGFLTKTKGISVGHTFYLGT KYSSINAGPTHVCGKPTLABMGCYGLGVTR-LIAPAIEVLSTED CVRMPSLLAPYQACLTPFKKOGRADELIGGLVDHTTEAVPQ LHGSVLLDDRTHLTGNRLKOANKFGYPFVITAGKRALEDPAHF EVWCQNTGSVAFLTKOGWMDLLTPVCTV LHGSVLLDDRTHLTGNRLKOANKFGYPFVITAGKRALEDPAHF EVWCQNTGSVAFLTKOGWMDLLTPVCTV AGAKTRI HEVRTKELATVATNGAKHISVUNGTORTLASG GFSRYVLGMOELFRGHISKTEFLJAKHISVUNGTORTLASG GFSRYVLGMOELFRGHISKTEFLJAKHISVUNGTORTLASG GFSRYVLGMOELFRGHISKTEFLJAKHISVUNGTORTLASG GFSRYVLGMOELFRGHISKTEFLJAKHINLCSSPGOGTAAVGHK AGAKTRI HEVORTKICLATVATNGAKHISVUNGTORTLASG GFSRYVLGMOELFRGHISKTEFLJAKHINLCSSPGOGTAAVGHK DDVVTPIDAKTHRSKABEQFKFEVNEISMNDNNMFFLTNGNGC INILISTPELKSVQSINAHPSNCICIFFDRGKYFATGSADALVS LWDVDBLVCVRCFSRLDWPVTLTSFHDCKMLASASEDHFIDLA EVETGBKLMEVQCSSPTFTVAMHFKRPLLAFACDKKOKYNSSG SATVLKJELDBDS  5581 54 947 GGGGGPRADSATLLDTGESVAAVASGEDKGTAASAAAAAVFACS CSPDPQSSTMNPVSPVQPGAPYGNPKNMAYTGYPTAYPAAARA YNSELYTINSPSYAPEZGJHASYAYDLLMKQAWPONSSCGTZG TFHLPVDTGTERRTYQASSAAFRYTAGTFYKVPTQSNTAPPYP SPSPNPYQTAMPTIRSAYPQOKLAYVYPPW SPSPNPYTQAMPTIRSAYPQOKLAYVYPPW SPSPNPYTQAMPTIRSAYPQOKLAYVYPPW SPSPNPYTQAMPTIRSAYPQOKLAYVYPPW TTVOVNSTPSAITPBAVDAARGRUNGTTMAMSAGTLL TTPQHTALGAHPUSMPYTRAQGTBAYYTPDVAAQPWINH TTVVONSTPSAITPBAVDAARGRUNGATHGKAYPCSSKC SLEDESKALGEDSSIRALPKKARANMELGRIKKERYECSSKC SLEDESKALGEDSSIRALPKKARANMELGRIKKERYECSSKC SLEDESVALGEBSVASSLEPGLLOKLHUNRAACYFTMGLY EKALEDSSKALGEBSSTRALPKKARANMELGRIKERYECSSKC SLEDESSVASSLEPGLLOKLHUNGARVYPPBLFTSLLSNG TAGVADQGTSNGLGSIDDIETDCVVDPRGSPALLPSLLSSLEP PHVIDLLAPLDSSRTLESSTDIDDEPEDDVORGPBLDTLLDSLSLE	5578	3	783	AVESMASPGACRAPPELPERNCGYREVEYWDQRYQGAADSAPYD
BEGTLDALLAGEEDPHTVSSEGVHTVCQVLSEVSRVLVPGGRFT SMTSAAPHFRTRYAQAYYGWSLRHATYGSGFHFHLYLMHKGGK LSVAQLALGAQILSPPRPTBSCFLQDSDHEDPLSATQL TRANSCLARGASALARHGGGLAGGVGWDCGACASGCGVWGGLTT RNSGLARGASALARHGGGLAGGVGWDCGACASGCGGVWGGLTT RNSGLARGASALARHGGGLAGGVGWDCGACASGCCGVWGGLTT RAMEKURVIDQEWQALGGGVWDPLGCACASGCCGVWGGLTT RAMEKURVIDQEWQALGGGVWDPLGCACASGCCGVWGGLTT RAMEKURVIDQEWQALGGGVWDPLGCACASGCCGVWGGLTT RAMEKURVIDQEWQALGGGVGWDCACAGCHLWFYV VTRFRDEPRFRFGLLRGEFYMKDWTYDSSPEAQQTYSLVC DAYCSLENKLGJEPFVKVQADVGGTGYWFTELAATEVLSTBT CYCRFSLARMETLDLSQNNCDACGGPLTKTKGTEVGHFTYLGT KYSSIFNAQFTNVCKPTLAKGGTGGTWHTFQLPUDIGEDRIA ICPRCSFSAMMETLDLSQNNCDACGGPLTKTKGTEVGHFTYLGT KYSSIFNAQFTNVCKCKPTLAKGGVGLGVTTLLAATEVLSTBT CVRRPSLLAPYQACLIPPKKGGKEQASGLIGQVTCHAATEVLSTBT CVRRPSLLAPYQACLIPPKKGGKEQASGLIGQUTYDHITEAVPQ LINGVLLADPYACLIPPKKGGKEQASGLIGQUTYDHITEAVPQ LINGVLLADPYACLIPPKKGGKEQASGLIGQUTYDHITEAVPQ LINGVLLADPYACLIPPKKGGKEQASGLIGQLYDHITEAVPQ LINGVLLAPYQACLIPPKKGGKEQASGLIGQLYDHITEAVPQ LINGVLLAPYQACLIPPKKGGKEQASGLIGQLYDHITEAVPQ SPDKTASVFLLEKDRIVKGWAGAGGRESSGCMRAAAAAGLTAG GFSFYVLGMQELFFGHSKTREFLAHSAVHSVANGCCGRRLAGG SPDKTASVFLLEKDRLVKENNYRGHDSVVQLCWHPENPDLFVT ASGKTTRHDVKTTKCLATVNTKGENINICWSPDGGTLAVGKK DDVVTFIDAKTHRSKAEBCFKFEVNEI SHNDNNMFFLITKGNGC INILSYFELKPVQSINAHPSKICLIKFPDMKKYRAGSASEDHFIDLA EVETGDKHWEVQCESFTFTVAWHPKRPLLAFACDKDKDGKVDSS CSPDFYGXLMEVQCESFTFTVAWHPKRPLLAFACDKDKDGKVDSS EAGTTVKLPGLPBDS  5581 54 947 GGGSGFRAPSATLLDTGESVANVASGEDKGIASAAAAVFACS CSPDFQGSTMNPVYSPVQGAGPYNDRMMAYTGYPTAYPAAAPA YNPSLYPTNSPSYAPFCPCHSAVATLLMKQAWPONSSCCTZG TFHLPVDTGTENTYQASSAAFRYTAGTPYKVPPTWAPPAAPA YNPSLYPTNSPSYAPFCPCHSAVATLLMKQAWPONSSCCTZG TFHLPVDTGTENTYQASSAAFRYTAGTPYKVPPTWAPPAAPA YNPSLYPTNSPSYAPFLAGATYTAGTPYKVPPTWAPPAAPA TTVQDNSTPSAIYPAPPAAPRTNCVAMMWAGTTMMASGTLL TTOQTATAGAHPVYSPDYTAGAGTYSVVPPHW  5582 5775 2739 IITMNNVIIPLVIAYHLSGSAQARGERSPARRIMERQKKKAMI EKALGPIGSTGLIGGEAGALALDFRIDLKVNKYKPQCELTFSLLSKG YAQUADGGTNGLIGGEAGALALDFRIDLKVNKYKYPCPCLETFSLLSKG SLALPIPGSVTOLOGGLAKALDFRIDLKVNKYKPCPCLETFSLLSKG YAQUADGTSNGLIGGEAGALALPRINCYKRYKPCPCLETFSLLSKG YAQUADGTSNGLIGGEAGALALPRINCYKAVKYCPC	1			WFGDFSSFRALLEPELRPEDRILVLGCGNSALSYELFLGGFPNV
SMTSAAPHFRTRHYAGAYYGMSLRHATYGSGFHFHLIMHKGGK LSVAQLALGAQILSPPRPPTSPCFLQDSDHEDFLSAIQL  5579  3 1540 RNSGLARGASALARHGGGLAGCGWDCCACASRCCGWMEGLITR CRALPALATCSRQLSGYVPCRFHHCAPRRGRRLLLSRVFQFQNL REDRUSLQDASDLTCKSGQTMUGGLITYASPGCYHLLEYTY RAMKKLURVIDQBMQALGGGKVNMPSLSPAGLWGATNRWDLMGK BLLRLRDRHGKSYCLGPTHEAITALIASQGKLSYKQLFFLLYQ UTRKFRDERPFRFGLLRGREYMKDMYTPDSSPERAQQTYSLVC DAYCSLFNKLGLFFVKVQADVGTIGGTVSHEFQLPVDLIGEDRLA ICPRCSFSAMMETLDLSQMNCAGPHTKYRG EVGHTFYLG  CVRWPSLLAPYQACLIPPKKGSKCQASPLIGQLYDHITEAVPG CVRWPSLLAPYQACLIPPKKGSKCQASPLIGQLYDHITEAVPG CVRWPSLLAPYQACLIPPKKGSKCQASPLIGQLYDHITEAVPG CVRWPSLLAPYQACLIPPKKGSKCQASPLIGQLYDHITEAVPG CVRWPSLLAPYQACLIPPKKGSKCQASPLIGQLYDHITEAVPG CVRWPSLLAPYQACLIPPKKGSKCQASPLIGQLYDHITEAVPG CVRWPSLLAPYQACLIPPKKGSKCQASPLIGQLYDHITEAVPG CVRWPSLAPYYGSAGYSAPQKGRRSSGGMRAARAPGLTAP WRLLQCCELEAGELGMAVPAAMGPSALGQSGPGMAPWCSVSS GPSRYVLGMQELFRGHSKTREFLHISAKVHSVMSCCGRRLASG SFDKTASVFLLECDRLVKENNYRGHGDSVQLCWHSNPDLFVT ASGKTIRHDVRTTKCLATVNTKGENINICMSPDGGTLAVGNK DDVVTFLDAKTHRSKABEQFKRWLISHMINDMFFLTMGNGC INILSYPELKPVQSINAHPSNCICIKFDPMGKYPATGSADALVS LWDUDELVCVRCFSRLDMPVRTLSFSHBGKMLASASBDHFDLA EVETGRKLMEVQCESPSTTVAMHPKRPLLAPACDDKDGKVDSSS EAGTVKLFGLPNDS  5581  54  947  GGGSGPAPSATLLDTGESVAAVASGEDKGTAASAAAAAVPACS CSEPPGSSTMNVYSPVQPGAPYCMPKMMATGYPTAYPAAAPA YNBSLYFTNSPSYAPEFGPLHSAYATLLMKQAWPONSSGGTZG TFHLFVDTGTERRTYQASSAAFTYSGTPYKVPPTUSNTAPPY SPSPNPYQTAMYPIRSAYPQONLYAQGAYTQPVYAAQPHVIHH TTVQHTAIGAHVSMPTTRAGATSYVPPHW SPSPNPYQTAMYPIRSAYPQANLYAQGAYTQPVYAAQPHVIHH TTVQHTAIGAHVSMPTTRAGATSYVPPHW EKGLQFIQSTLPIKQEEYBAFLLKLVONLFABGNDLFREKDYKQ ALVQYMEGLNVADYAASDQVALPRELLCKHVNRAACYFTMGLY EKALDESBKALGLDSBSTRALFRRARALNELGSRKCATEGSSKC SLALPHDESVTOLGGLACKLGLGALARKATYRCSSRC SLALPHDESVTOLGGLACKLGLGARKAATICLSKNOCK SLALPHDESVTOLGGLACKLGLRKKAYTGCGSPALLPSTPMPLP PHVIDLLAPLDSSRTLPSTDSLDDPSDDVFGPELDTLLDSLSL	1	<b>f</b>		TSVDYSSVVVAAMQARYAHVPQLRWETMDVRKLDFPSASFDVVL
LSVAQLALGAQILSPRPPTSCFLQDSDHEDFLSATQL  S579  3 1540  RNSGLARGASALARHGGGLAGGVONDCGACASRCQGVMEGLTR CRALPALATCSRQLSGYVDCRHHCAPRRGRLLLSRVFQPQNL REDRVLSLQDKSDDLTCKSQRLMLQVGLIYPASPGCYHLLBYTY RAMMEKUNVIDGENQAIGGGVVNMPSLGPABLWGATKRWDLMGK RELRLRDRHGKSYCLGPTHEEAITALIASQKKLSYKQLPFLLYQ VTRFRDEPRFRRGLLRGRENYMKDMYTPDSSPBAAQQTYSLVC DAYCSLPNKLGJEPFVKVQADVCTIGGTVSHEFQLPUDIGEBRLA ICPRCSFSAMMETLDLSQNNCDACQGPLTKTKGTEVCHTFYLGT KYSSIPAQPTMVCQKPTLABKGCYGLGVTRILAAAIEVLSTED CVRWPSLLAPYQACLIPPKKGSKRQAASELIGQLYDHITERVPQ LHGSVLLDDRTHLTIGNRLKDANKFGYFFVIIAKRALEDPAHF EVWCQNTGSWPAITKTBGWMDLLTFVQTV  S580  1681  450  ADAGTRCIPGFVVPSGAGYSAPAQRGRRSSGRMRAAAAPGLTAP WRLLQCCEBLEGELGMAVPAAAMGPSALGGSGPGSMAPMCSVSS GPSRYVLGMGEJFFCHSKTTRETLAHSAKVHSVAWSCCORRLASG SFDKTASVFLLEKDRIJVKENNYRGHGDSVDQLCHHPSNPDLFVT ASGKTTRIMDVRTTKCIATVNTKGENINICMSPDQGTIAVGNK SFDKTASVFLLEKDRIJVKENNYRGHGDSVDQLCHHPSNPDLFVT ASGKTTRIMDVRTTKCIATVNTKGENINICMSPDGGTIAVGNK LWDVDELUCVCRGFSRLDMPVRTSHDGKVTRASABADALVS LWDVDELUCVCRGFSRLDMPVRTSHDGKVTRASABADALVS LWDVDELUCVCRGFSRLDMPVRTSHDGKVTRASABADALVS EVETGOKLMSVQCESPTFTVAWHPKRPLLAFACDDKDGKYDSSR EAGTVKLIPGLBNDS  5581  54  947  GGGSGFRAPSATLDTGESVAAVASGEDKGTAASAAAAAVFACS CSPPDGOSTMNPVYSPVQDGAPYGNPKMAATGYPTAYPAAAPA YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWPONSSSCGTEG TFHLPVDTGTERNTYQASSAAFRTTAGTPYKVPPTGSNTAPPPY SPSNPYGTAMYPIRSAYPQONLYAQGAYYTQPVYAAQPRVIHH TTVVQDNSIPSAITYPPAVAAPTALLMKQAWFONSSCGTEG TFHLPVDTGTERNTYQASSAFRTTAGTPYKVPPTGSNTAPPPY SPSNPYGTAMYPIRSAYPQONLYAQGAYTYQPVYAAQPRVIHH TTVVQDNSIPSAITYPPAVAAPTAVAMGMVAGTTMMASGTLL TTQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW  5582  5775  2739  IIMNNNVIJFLVIAYHLSGSAQARGERSPAERLMERQKKKADI EKGLGFIGSTLFIKGEEVARALVNONLFAERGDLFREKDYYQ ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESTRALFRRARALNELGRIKKEAYECSSRC SLALPIDESSVTQLGGLALAKLGKLVONLFAERGDLFREKDYYQ ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESTRALFRRARALNELGRIKKEAYECSSRC SLALPIDESSVTQLGGLALAKLGLVONLFAERGDLFREKDYYQ ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESTRALFRRARALNELGSRC SLALPHDESSVTQLGGLAGKLGLVANATKAYRPQPELETFSLLENG TAG	1	1		EKGTLDALLAGERDPWTVSSEGVHTVDQVLSEVSRVLVPGGRFI
S579   3   1540   RNSGLARGASALARHGGLAGSVGWDCGACASRCOGWEGLITR   CRALPALATCSRQLSGVVPCRFHHCAPRRGRELLSRVFQCRUL   REDRVLSLQNKSDDLTCKSQCKMLQVGL1YPASPGCYHLLPYTV   RAMEKLUVVLDGEMQAZGGKVMMPSLSPAELMGATTRWDLMGK   GLLEKIRDRHGKSYCLGPTHEAST TAILASGKLSYKQLPFLLYQ   VTRKFRDEPRPRGLLGREFYMKDMYTPDSSPEARQQTYSLVC   DAYCSLFNKLGLFYKVQADVGTIGGTVSKEFGLPVDIGEDRIA   ICPRCSFSAMMETLDLSQMKCPACQGPLTKTKGIEVCHTYLGT   KYSSIFNAQFTNVCGKPLAMMCPACQGPLTKTKGIEVCHTYLGT   KYSSIFNAQFTNVCGKPLAMMCPACQGPLTKTKGIEVCHTYLGT   KYSSIFNAQFTNVCGKPLAMMCPACQGPLTKTKGIEVCHTYLGT   KYSSIFNAQFTNVCGKPLAMMCPACQGPLTKTKGIEVCHTYLGT   KYSSIFNAQFTNVCGKPLAMMCPACQGPLTKTKGIEVCHTYLGT   KYSSIFNAQFTNVCGKPLAMMCPACQGPLTTKGIEVCHTLTARVG   CVRMPSLLAPPQACLIPPKGSKQAASELIGOLYCHITTARVPC   LHGEVLLDDRTHLTIGNRLKDANKFGYPFVIIAGKRALEDPAHF   EVWCQNTGBVAFLTKGWMDLATFTCTV   LHGEVLLDDRTHLTIGNRCKDANKFGYPFVIIAGKRALEDPAHF   EVWCQNTGBVAFLTKGWMDLATFTCTV   ASGRTTLITGNECKLAMAVPAAAMGPSALGQSGCSMAPWCSVSS   GPSRYVLGMQELFRGHSKTEVNISTSMNDMMFFLTHGNGC   INTLSYPELKPVQSIRNAVFRCHOSVDQLCWHPSNDPLFVT   ASGRKTIRIMDVATTKCIATVNTKGBNINICWSPDOGTIAVGMK   DDVVTFTDATTHRSKAEGFENEVISISMNDNMFFLTHGNGC   INTLSYPELKPVQSINAHPSNCICIKDPMGKYFATGSADALVS   LWDVDELVCVCCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA   EVETGKKLWEVQCESFTFTVAMHFKPLLLAFACDDKIGKYDSSR   EAGTVKLIFGLPNDS   GGGGFPAPFSATLLDTGESVAAVASGEDKGIAASAAAAAVFACS   CSPDPQSSTMNPVYSPVQPGAPYGNPKNMAYTGYPTAYAAAPA   YNBSLYPTNSFSYAPEFQFLHSAYATLLMKQAWFONSSCGTAG   TFHLPVDTGTGTHNTYQASSAFATLJAMGQAWFONSSCGTAG   TFHLPVDTGTGTHNTYQASSAFATLJAMGQAWFONSSCGTAG   TFHLPVDTGTGTHNTYQASSAFATLJAMGQAWFONSSCGTAG   TFHLPVDTGTGTHNTYQASSAFTTAGTPYKVYPTQSNTAMPPY   SPSPNPYGTAMYFIRSAYPQQNLYAGGAYTOPVXAAQPHVIHH   TTVQPNSIPSAYPAAPATNAVAMGMAGTTMAMSAGTLL   TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW   TTVQPNSIPSAYSTLAMGARGAYATGPAYSYVPPHW   TTVQPNSIPSAYSTLAMGARGAYATGPAYSYVPPHW   EKGLEFTGGKKAGLIGHTNAAACTTMASAGTLL   TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW   EKGLEFTGGKKAGLIGHTNAAACTTMASAGTLL   EKGLEFTGGKKAGLIGHTNAAACTTMAGATLAWAGATAAACHIALGARHKAAYECSSRC   SALPHDESTOTLGGGLAGACGRAFGFAFARALELGRHKKAAYECSSRC   SALPHDESTOTLGGGTGGKGRAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1		1	SMTSAAPHFRTRHYAQAYYGWSLRHATYGSGFHFHLYLMHKGGK
CRALPALATCSRQLSGYVPCRFHHCAPRRGRRLLLSRVFQPQNL REDRVLSLQDKSDLITCKSQRLMLQVGLIYPASPGCYHLLFYTY RAMRKLWRVIDGEWQAI GGGKVMMPSLSPAELMGATMRUDIMGK BLLKLRDRHGKEYCLGFTHEEAT TALLASGKKLSYKQLPFLLYQ VTRKFRDBPRPFGLLRGRHFYMKDMYTFDSSPEAQQTYSLVC DAYCSLPNKLGJEFFVKVQADVGTIGGTVSHEFGLPVDIGEDRLA ICPRCSSAMMETLDLSQMMCDRACQGPLTKTKGIEVGHTFYLGT KYSSIFMAQFTNVGKPTLABAGGYGLGVTTLABAIEVLSTRD CVRMPSLLAPYQACLIPPKKGSKEQAASELIGQLYDHITEAVPQ LHGEVLLDDTHHITIONRLKDANKFGYPFVITAGKRALEDPAHF EVMCQNTGBVAFITKOGVMDLLTPVQTV  5580 1681 450 ADAGTRCIFGFVVPSGAGYSAPAGGGRRSSGEMEANAPGLTAP EVMCQNTGBVAFITKOGVMDLLTPVQTV  MRLLQCCELEAGELGMAVPAAMAGPSALGQSGPGSMAPWCSVS GPSRYVLGMGELFRGHSKTREFLAHSAKVHSVAMSCLGRRLASG SFDKTASVFLLEKDRLVKENNYRGENINICMSPDGGTIAVGMK DDVVTFIDAKTHRSKABEQFKFEVNEISWNDNNMFFLTNGNGC INTLSYPELKPVGSINAHPSNCCIEKTDPMGKYFATGSADALVS LWDVDELVCVGCFSRLDWPTLSFSHDGKMLASAEDHFIDIA EVETGDKLWEVQCESPFTTVAWHPKRPLLAFACDDKDGKYDSSR EAGTVKLFGLDDDS  5581 54 947 GGGSGPRAPSATLLDTGESVARVASGEDKGIASAAAAAVFACS CSPDPQSSTMNFVYSPVQPGAPYGNFKMAYTGYPTAYPAAPAP YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWPQNSSCGTEG TFHLPVDTGTENRTYQASSAAFRYTAGTFYKVPPTQSNTAPPPY SPSSNPYQTAMYFIRSAYPQQNLYAGGAYTTQPVYAAQPHVIHH TTVVQPNSIJSATYPAVARATTNAMAGATTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW  5582 5775 2739 IITMNNNVIPIVIAVHLSGSAQARGERSPERENDERGKYKADI EKGLGFIGSTLEHKQEFWRAFLLKLVQNNLFAGRONDLFREEDYNQ ALVQYMEGLNVADYAASDOVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGIDESSIRALPRKARALNELGRHKEAYNCSSC CHALDDSSTOTLGGELGKGLEKRALNELGRHKEAYNCSSC SLALPHDESVTOTLGGELGKLGLEKRALNELGRHKEAYNCSSC SLALPHDESVTOTLGGELGKLGLEKRALNELGRHKEAYNCSSC SLALPHDESVTOTLGGELGKLGLEKRALNELGRHKEAYNCSSC SLALPHDESVTOTLGGELGKLGLEKRALNELGRHKEAYNCSSC SLALPHDESVTOTLGGELGKLGLEKRALNELGRHKEAYNCSSC SLALPHDESVTOTLGGELGKLGLEKRALNELGRHKEAYNCSSC SLALPHDESVTOTLGGELGKLGLEKRALNELGRHKEAYNCSSC SLALPHDESVTOTLGGELGKLGLEKRALNELGRHKEAYNCSSC SLALPHDESVTOTLGGELGKLGLEKRALNELGRHKEAYNCSSC SLALPHDESVTOTLGGELGGLDDFDCDDVDFGBEDDTLLDSLSL VQGGLSGSGVPSELPQLIVFFGGTPLLPVVGGSIPVSSPLPP	1	1	1	LSVAQLALGAQILSPPRPPTSPCFLQDSDHEDFLSAIQL
REDRVLSLQDRSDDLTCRSQRIMLQVGLTYPASPGCYHLLPTTY RAMEKLVRVIDQEMQAIGGKVMMPSLSPAELWQATNRWDLMKK BLLRLRDRHGKEYCLGPTHEBAITALIASGKKLSYKQLPFILYQ VTRKFRDBPRPRFGLRGREFYMKDMYTPDSSPEAQQTYSLVC DAYCSLFNKLGLPFVKVQADVGTIGGTVSHEFQLPVDIGEDRLA ICPRCSFSANMETLDLSQMNCPACQSPLTKTKGIEVGHTFYLGT KYSSIFNAQFTNVCGKPTLAEMGCVGLGVTTELLAAAIEVLSTEB CVRMPSLLAPYQACLIPPKKGSKQAASBLIGGLVPHITEAVPQ LHGEVLLDDRTHLTIGNRLKDANKPGYPFVIIAGKRALEDPAHF EVWCQNTGBVAFLTKDGYMDLLTPVQTV ABAGTRCITGFVVPSGAGAPAQRGRRSSGRWRAAAAPGLTAP WRLLQCCELBAGELGMAVPAAAMGPSALGQSGPGSMAPWCSVSS GPSRYVLGMGELFRGHSKTREFLAHSAKVHSVAWSCLOGRLASG SFDKTASVFLLBEKDRLVKHNYRGHGBSVQLCWHBPDDLFVT ASGDKTIRIMDVRTTKCIATVNTKGENINICMSPDGQTIAVGNK DDVVTFIDAKTHSKAEEQFKFEWLSISMNNMFFLINGNGC INILSYPELKEVQSINAHPSNCICIKFDPMGKYPATGSADALVS EVETGDKLWEVQCESPTFTVAWHPKRPLLAFACDDKOKYDSSR EAGTVKLFGLPNDS  5581 54 947 GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAAPAFACS CSPDPQSSTMNPVYSPVQPGAPYGNPKNMAYTGYPTAYPAAAPA YNPSLYPTNSPSYAPEFQFHASAVATLLMKQAWPONSSSCGTEG TFHLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTQSNTAPPPY SPSPNPYQTAMYPIRSAYPQQLYAQGAYYTQPVVAQQPVHIH TTVQPNSISSATYPAFVAAPRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSVPPHW  5582 5775 2739 IITNNNIVIIPLVIAYHLSGSAQARGERSPAERIMERQKRKADI EKGLQFIQSTLPLKQEEYEAFLLKLVONLFREKDYKQ ALVQYMGGLSMSGVPSSLPQLIPVTPGGFPLLDFLYGGSFPLSRILFSTTMFLF EKGLQFIQSTLPLKQEEYEAFLLKLVONLFREKDYKG ALVQYMGGLSMSGVPSSLPQLIPVTPGGFPLLDFLYDGSFPTSTLISNG TAAGVADQGTSNGLGSIDDLETDCYVDPRGSPALLPSTTTPHFLF PHVLDLLAPLDSSRTLPSTDSLDDPSDGDVPGSPELDTLLDSLSL VQGGLSGSGVPSSLPQLIPVPPGGTPLLPPVVGGSIPVSSPLPP	5579	3	1540	RNSGLARGASALARHGGGLAGGVGWDCGACASRCQGVMEGLLTR
RAMEKLVRVIDQEMQAIGGQKVNMPSLSPAELMQATNRWDLMGK ELLRLRDRHGKSYCLGPTHEEAITALIASQKKLSYKQLPFILIYQ VTRKFRDEPRPRFGLLRGREFYMKDMYTDISSPEAAQQTYSLVC DAYCSLFNKLGLPFVKVQADVGTIGGTVSHEFGLPVDIGEDRIA ICPRCSFSANMETLDLSQMCPACQADJETKKGIEVGHTFYLGF KYSSIFNAQFTNVCGKPTLAEMGCYGLGVTRILAAAIEVLSTED CVRMPSLLAPYQACLIPPKKGSKEQASELIGGLYDHITEAVPQ LIGGVLLDDFHTLTIGNEKDANKFGYPFVITAGKRALEDPAHF EVWCQNTGEVAFLTKDGVMDLLTPYQTV  5580  1681  450  ADAGTRCIFGFVVPSGAGYSAPAGKGRRSSGRMRAAAPGLTAP WRLLQCCELRAGELGMAVPAAAMGFSALGQSGPGSMAPWCSVSS GPSRYVLGMOELFRGHSKTREFLAHSAKVHSVAWSCCDGRRLASG SFDKTASVFLLEKDRLVKENNYRGHGDSVDQLCWHPSNPDLFVT ASGKTIRIMDVRTTKCLATVNTKGENINICMSPDGGTIAVGMK DDVVTFIDAKTHRSKAEEQFKFEVHEISMNDNNMFFLINGNGC INILSYPELKPVQSINAHPSNCICIKFDPMGKYFATGSADALVS LWDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA EVETGDKLWEVQCSSPTFTVAWHPKRPLLAFACDDKDGKYDSSR EAGTVKLFGLPNDS  5581  54  947  GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAAVFACS CSDPDGSSTNNPVYSPVQPGAPYCMPKMMAYTGYTAYPAAAPA YNPSLYFINSFSYAPEFGJHSAVATLLMKQAWPONSSCGTEG TFHLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTQSNTAPPPY SPSMPVQTAMYPIRSAYPQQNLVAQGAYYTQPVXAAQPHVLHH TTVVQPNSISPSATPPSGTHSAAYATLMKQAWPONSSCGTEG TFHLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTQSNTAPPPY SPSMPVQTAMYPIRSAYPQQNLVAQGAYYTQPVXAAQPHVLHH TTVVQPNSISPSATPPSGTAPLARGRANGVAGTTMMAGAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSVVPPHW  5582  5775  2739  ITNNNNVITPLVIAYHLSGSQAARGERSPAERIMERQKRKADI EKGLGPTQSTIPLKQEETYPAFLLKUVQNLFAERGNDLFREKDIYQ ALVQYMGGLAVADAYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESTRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGQELGAQKLGLRVRKAYKRPQELETESLLSIG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDPSDGDVPGSPELDTLLDSLSL VQGGLSGSGVPSSLPQLIPVPGGTPLLPPVGGSTPJTSPLIPS	ſ			
BLILRIRORHGREYCLGPTHEBAITALIASGIKILSYKOLPFILLYQ VTRKFRDERPRPERLIRGREFYMKDMYTPDSSPEAAQQTYSLVC DAYCSLENKLGLPFVKVQADVGTIGGTVSHEFQLPVDIGEDRIA ICPRCSFSANNETLDLSQMNCPACQSPLTKTKSIEVGHTFYLGT KYSSIFNAQFTNVCGKPTLAEMGCYGLGVTTLIAAAIEVLSTED CVRMPSLLAPYQACLIPFKKGSKEQAASELIGGLVPHITTAVPG LIGSVLLDDRTHLTIGNELKDANKGYPFVIIAGKRALEDPAHF EVWCQNTGSVAFLTKGGWDLLTFYQTV  5580  1681  450  ADAGTRCIPGFVVPSGAGYSAPAQKGRRSSGRMRAAAAPGLTAP WRLLQCCELBAGELGMAYPAAAMGPSALGQSGPGSMAPMCSVSS GPSRYVLGMQELFRGHSTRELAHSAKVHSVAWSCDGRRLASG GPSRYVLGMQELFRGHSTRELAHSAKVHSVAWSCDGRRLASG GPSRYVLGMYLFRGKAEGKFEVMEISHMNDNMRPFLINGMGC INILSYPELKPVQSINAHPSNCICIKFDPMGKYFATGSADALVS LWDVDFLDAKTHRSKAEGKFEVMEISHMNDNMRPFLINGMGC INILSYPELKPVQSINAHPSNCICIKFDPMGKYFATGSADALVS LWDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA EVERGBALWEVQCSPTFTVAWHPKRPLLAFACDDKDGKYDSSR EAGTVKLFGLPNDS  5581  54  947  GGGSGFRAPSATLLDTGESVAAVASGEDKGIAASAAAAAVFACS CSPDPQSSTMMPVYSPVQPQAPYGMPKMAYTGYPTAYPAAAPA YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWPONSSSCGTEG TFHLPVDTGTENRTYQASSAAFRYTTAGTPYKVPPTQSNTAPPPY SPSPNPYQTAMYPTRSAYQONLVAQGAYYTQPVVAAQPHVIHH TTVQPNSIPSAIYPAPVAAAFRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPYTRAQGTPAYSVPPHW  15582  5775  2739  IITNNNVIIPLVIAYHLSGSAQARGERSPAFERLMERQKRKADI EKGLQFIQSTLPLKQESTRAFLLKLVQNLFARGNDLFREKDVKQ ALVQYMGGLAVVADYAASDOVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGDLSESIRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGQELAQKLGLRVRKYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDLETDCYVDPRGSPALLPSTTTMPLF PHVLDLLAPLDSSRTLPSTDSLDDPSDDVPGPELDTLLDSISL VQGGLSGSGVPSSLPQLIPVPFGGTPLLPPVVGGSIPVSSPLPP	}	}	,	REDRVLSLQDKSDDLTCKSQRLMLQVGLIYPASPGCYHLLPYTV
VTRKPRDEPRPJELLRGREFYMKDMYTPDSSPEAAQQTYSLVC DAYCSLFNKLGLPFYKVQADVGTIGGTVSHEFQLEVDIGEDRILA ICPRCSFSANMETLDLSQNNCDACQGPLTKTKGI EVGHTFYLGT KYSSIFNAQFTMVCGKPTLAEMGCYGLGVTKILAAAIEVISTED CVRWPSLLAPYQACLIPPKKGGREQASELIGQLYDHITEAVPG LHGEVLLDDRTHLITGNRLKDANKFGYPFVIIAGKRALEDPAHF EVWCQNTGEVAPLTKDGVMDLLTPVQTV  ADAGTRCIPGFVVPSGAGYSAFPAQGRERSSGRMEAAAAPGLTAP EVWCQNTGEVAPLTKDGVMDLLTPVQTV ADAGTRCIPGFVVPSGAGYSAFPAQGRERSSGRMEAAAAPGLTAP WRLLQCCELBAGELGMAVPAAAMGPSALGQSGPGSMAPWCSVSS GPSRYVLGMQELFRGHSKTREFLAHSAKVHSVAWSCDGRRLASG SPDKTASVFLLEKDRLVKENNYRGHGDSVDLCWHESNPDLFVTI ASGDKTIR HIDWLTTKLATVNTKGENINICWSPDGQTIAVGNK DDVVTFIDAKTHRSKAEEQFKFEVNEISWNNDNNMFFLTNGNGC INILSYPELKPVQSINAHESNCICIKTDPMKKYFATGSADALVS LWDVDELVVRCFSRLDMPVTTLSFSHDGKNLASASEDHFIDIA EVETGDKLWEVQCESPTFTVAWHPKRPLLAFACDDKDKKYDSSR EAGTVKLFGLDNDS  5581 54 947 GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAAVFACS CSPDPGSSTMNPVYSPVQPGAPYGNEKNMAYTGYPTAYPAAAPA YNPSLYPTNSPSYAPEFOPLHSAYATLLMKGAWPONSSCGTTG TFHLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTQSNTAPPPY SPSENPYQTAMYPIRSAYPQQNLYAQGAYYTQPVYAAQPHVHH TTVVQPNSIBSAIYPAVAPPTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHVYMPYTRAGYPAYSYVPPHW  TTVQPNSIBSAIYPAVSMPYTRAGTPAYSYVPPHW TTVQPNSIBSAIYPAVSMPYTRAGTPAYSYVPPHW EKGLQFIQSTLPLKQEEYEAFLLKLVQNLFABGNDLFREKDYKQ ALVQYMGGLAVADSOVALPRELLCKLHVNRAACYFTMGLY EKGLGFIQSTLPLKQEEYEAFLLKLVVNLFABGNDLFREKDYKQ ALVQYMGGLAVADSOVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESTRALPRKARAINEIGGRKEATECSSRC SLALPHDESVTQLGQELAQKLGLRVKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPPSTOSLDDFSDGDVFGPBLDTLLDSISL VQGGLGSGVPSELPQLIFVPFGGTFLLPPVVGGSIPVSSELPP		Į.		RAMEKLVRVIDQEMQAIGGQKVNMPSLSPAELWQATNRWDLMGK
DAYCSLFNKLGLPFVKVQADVGTIGGTVSHEFQLPVDIGEDRLA ICPRCSFSANMETLDLSQNNCPACQGPLTKTKGIISVGHHFYLGT KYSSIFNAQFTNVCGKPTLABMGCYGLGVTKILAPAIEVLSTED CVRMPSLLAPYQACLIPPKKGSKEQAASELIGQLVDHITEAVPQ LHGEVLLDDRTHLTIGNRLKDANKFGYPFVIIAGKRALEDPAHF EVWCQNTGEVAFLTKDGWDLLTPVQTV  5580 1681 450 ADAGTRCIPGFVVPSGAGYSAPAQRGRRSSGMRAAAAPGLTAP WRLLQCCELEAGELGMAVPAAAMGPSALGQSGGSMAPWCSVSS GPSKYLGMQELFGGLSKTREFLAHSAKVHSVAWSCCDGRLASG SPDKTASVVLLEKDRLVKENNYRGHGDSVDQLCWHPSNPDLFVT ASGDKTIRIWDVRTTKCIATVNTKGENINICWSPDGGTIAVGNK DDVVTFIDAKTHRSKAEEGFKFEVNEISWNNDNNMFFLINGNSC INILSYPBLKPVQSINAHPSNCICIKFDPMGKYFATGSADALVS LWDVDELVCVRCFSRLDWPVRTLSFSHDGKNLASASEDHFIDIA EVETGDKLWEVQCESPTFTVAWHPKRPLLAFACDDKDGKYDSSR EAGTVKLFGLBNDS  5581 54 947 GGGSGPRAPSATLDTGESVAAVASGEDKGIAASAAAAVFACS CSPPPQSSTMMPVYSPVQPGAPYGNPKNMAYTGYPTAVPAAAPA YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWPQNSSSCGTEG TFHLPVDTGTENRTYQASSAARTYAGTPYKVPTQSNTAAPPAY SPSPNPYCTAMYPIRSAYPQONLYAQGAYTYDPVYAAQPHVIHH TTVVQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTTRAQGAYTYDPVYAAQPHVIHH TTVVQPNSIPSAIYPAPVAAPRTNGVAMGWAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTTRAQGTPAYSYVPPHW  5582 5775 2739 IITMINVIJIPUITANTJSGAQARGERSPAERLMERQKRKADI EKGLQFIQSTLPLKQEEYRAFLLKLVONLFABGNDLFREKDYKQ ALVQYMBGLAVADVAASDOVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDESTALDKRARALNELGRIKEAYECSSRC SLALPHDESVTQLGQELAQKLGLRVKKAYKRPQELETTSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDPSDGDVFGPBLDTLLDSISL VQGGLSGSGYPSELPPLILFVPFGGTPLLPPVVGSSIPVSSELPP	1			BLLRLRDRHGKEYCLGPTHEEAITALIASQKKLSYKQLPFLLYQ
ICPRCSFSANMETLDLSQMNCPACQGPLTKTKGIEVGHTFYLGT KYSSIFNAQFTNVCGKPTLAEMGCYGLGVTRILAAAIEVLSTEG CVRMPSLLAPYQACLIPPKKGSKEQAASELIGLYDHTTEAVPQ LHGEVLLDDRTHLTIGNRLKDANKFGYPFVIIAGKRALEDPAHF EVWCQNTGEVAFLTKDGVMDLITFVGTV  ADAGTGCIEFGFVVPSGAGYSAPAQKGRRSSGRMRAAAAPGLTAP WRLLQCCELEAGELGMAVPAAAMGPSALGQSGPGSMAPWCSVSS GPSRYVLGMQBLFRGHSKTREFLAHSAKVHSVAWSCCDGRLASG SFDKTASVVLLEKDRLVKENNYRGHGDSVDQLCWHPSNPDLFVT ASGBKTIRIWDVRTTKCIATVNTKGENINICWSPDGGTLAVGNK DDVVTFIDAKTHRSKABEQFKFEVNEISMNDNMFFLTNGNGC INILSYPELKPVQSINAHPSNCICIKFDPMGKYFATGSADALVS LWDVDELVCVRCFSRLDWPVRTLSFSHDCKMLASASEDHFIDIA EVETGDKLWEVQCESPTFTVAWHPKRPLLAFACDDKDGKYDSSR EAGTVKLFGLPNDS  5581 54 947 GGGSGPRAPSATILDTGESVAAVASGEDKGIAASAAAAAVFACS CSPDPQSSTMNPVYSPVQPGAPYGNPKNMAYTGYPTAYPAAAPA YNBSLYPTNSPSYAPFGFFLHSAVATLLMKQAWPQNSSSCGTEG TFHLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTQSNTAPPY SPSPNPYCTAMYPIRSAYPQONLYAQGAYYTQPVYAAQPHVIHH TTVVQPNSIPSAIYPAPVAAPRTNGVAMMWAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW TTVVQPNSIPSAIYPAPVAAPRTNGVAMMWAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW SKGLQFIQSTLPLKQEEYBAFLLKLVQNLFABGNDLFREKDYKQ ALVQYMBGLNNADYAASDCVALPRELLCKHVWRAACYFTMGLY EKALEDSEKALGLIDSESIRALFRKRALNELGRHKEAYECSSRC SLALPHDESVTQLQGLAQKLGLRVRKAYKRPQELETFSLLSNG TAAGVADQGTSNGLOSIDDIETDCYVDPRGSPALLPSTPTMPLF PHYLDLLAPLDSSRTLPSTDSLDDFSDGDVFGBELDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP	1			VTRKFRDEPRPRFGLLRGREFYMKDMYTFDSSPEAAQQTYSLVC
KYSSIFNAQFTNVCGKPTLAEMGCYGLGVTR:LAAAIEVLSTED CVRWPSLLAPYQACLIPFKKGSKEQAASELIGQLYDHITEAVPQ LIGEVLLDATHLITIGRRLKDANKFGYPFVIIAGKRALEDPAHF EVWCQNTGEVAFLTKGGVMDLLTPVQTV  5580 1681 450 ADAGTRCIPGFVVPSCAGYSAPAQRGRRSSGRMRAAAAPGLTAP WRLLQCCELEAGELGMAVPAAAMGPSALGQSGPGSMAPWCSVSS GPSRYVLGMQELFRGHSKTREFLAHSAKVHSVJWSCDCRRLASG SFDKTASVFLLEKDRLVKENNYRGHGDSVDQLCWHPSNPDLFVT ASGKTIRIWDVRTTKCIATVNTKCENINICWSPDGGTIAVGNK DDVVTFIDAKTRRSKAEQFKFFVUFEISMNDMMFFLINGNGC INILSYPELKPVQSINAHPSNCICIKFDPMGKYFATGSADALVS LWDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA EVETGDKLWEVQCESPTFTVAWHPKRPLLAFACDDKDGKYDSSR EAGTVKLFGLDMDS  5581 54 947 GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAAVFACS CSEDPQSSTMMPVYSPVQPGAPYGNPKNMAYTGYPTAYPAAAPA YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWPQNSSSCGTEG TFHLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTQSNTAPPPY SPSPNPYGTAMYPIRSAYPQONLVAQGAYYTQPVYAAQPHVIHH TTVVQPNSIPSAIYAPPVARPTNGVAMGMVAGTTMAMSAGTLL TTPQHTATGAHPVSMPTYRAQGTPAYSYVPPHW  5582 5775 2739 IITNNNVIIPLVIAYHLSGSAQARGERSPAERIMERQKRKADI EKGLQFTQSTIPLKQEEYBAFLLKLVQNLFAEGNDLFREKDYKQ ALVQYMEGLNVADYAASADQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESIRALFRRARALNELGRHKEAYECSSRC SLALPHDESVTQLQQELAQKLGLRVRKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDRGSPALLPSTPTMPLF PHYLDLLAPLDSSRTLPSTDSLDDFSDRGPSPALLPSTPTMPLF PHYLDLLAPLDSSRTLPSTDSLDDFSDRGPDFEDFELDTLLDSLISL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP	1		į	DAYCSLFNKLGLPFVKVQADVGTIGGTVSHEFQLPVDIGEDRLA
CVRWPSLLAPYQACLIPPKKGSKEQASELIGQLYDHITEAVPQ LHGEVLLDDRTHTIGHRKDANKFGYFFVITAGKRALEDPAHF EWCQNTGEWAFITKDGWMDLITPYQTV  5580  1681  450  ADAGTRCIPGFVVPSGAGYSAPAQRGRRSSGRMRAAAAPGLTAP WRLLQCCELEAGELGMAVPAAMMGPSALGQSGFGSMAPWCSVSS GPSRYVLGMQELFRGHSKTREFLAHSAKVHSVAWSCDCRRLASG SFDKTASVYLLEKDRIVKENNYRGHGDSVQQLCWHBSNPDLFVT ASGDKTIRIWDVRTTKCIATVATKGEBINICMSPDGQTIAVGNK DDVVTFIDAKTHRSKAEEQFKFEVNEISWNDNNMFFLTNGNGC INILSYPELKPVQSINAHPSNCICIKFDPMGXYFATGSADALVS LWDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA EVETGDKLWEVQCESPTFTVAWHPKRFLLAFACDDKDGKYDSSR EAGTVKLFGLPBDS  5581  54  947  GGGSGPRAPSATLLDTGESVAAVASGEDKGTAASAAAAAVFACS CSPDPOSSTMNPVYSPVQPGAPYGNFKNMAYTGYPTAYPAAAPA YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWPQNSSSCGTEG TFHLPVDTGTEINTYQASSAAFRYTAGTPYKVPPTGSNTAPPPY SPSNPYQTAMYPIRSAYPQQNLYAQGAYYTQPVYAAQPHVIHH TTVVQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW  5582  5775  2739  IITMNNNVIIPLVIAYHLSGSAQARGERSPAERLMERQKRKADI EKGLQFIQSTLPILKQEEYEAFLLKLVQNLFABGNDLFREKDYKQ ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESIRALFRKARAINELGRHKEAYECSSRC SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHILDLAPLDSSRTLPSTDSLDDFSDGVPGPELDTLLDSLSL VQGGLSGSGVPSELPQLIPVPPGGTPLLPPVVGGSIPVSSPLPP	ľ			ICPRCSFSANMETLDLSQMNCPACQGPLTKTKGIEVGHTFYLGT
LIGEVLLDDRTHLTIGNRLKDANKFGYPFVIIAGKRALEDPAHF EVWCQNTGRVAFLTKDGYWDLLTPYQTV  ADAGTRCIPGFVVPSGAGYSAPAQRGRRSSGRMRAAAAPGLTAP WRLLQCCELEAGELGMAVPAAAMGPSALGQSGPGSMAPWCSVSS GPSRYVLGMQELFRGHSKTREFLAHSAKVHSVAWSCCGRRLASG SFDKTASVFLLEKDRLVKENNYRGHGDSVDQLCWHPSNPDLFVT ASGDKTIRIWDVRTTKCIATVNTKGENINICWSPDGQTIAVGNK DDVVTFIDAKTHRSKAEEQFKFEVNEISWNDNNMFFLTNGNGC INILSYPELKPVQSINAHPSNCICIKFDPMGKYFATGSADALVS LWDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA EVETGDKLWEVQCESPTFTVAWHPKRPLLAFACDDKDGKYDSSR EAGTVKLPGLPNDS  5581 54 947 GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAAVFACS CSPDPQSSTMNPVYSPVQPGAPYGNPKNMAYTGYPTAYPAAAPA YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWPONSSSCCTEG TFHLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTQSNTAPPPY SPSPNPYQTAMYPIRSAYPQQNLYAQGAYYTQPVXAAQPHVIHH TTVUQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTXRAQGTFAYSYVPPHW  5582 5775 2739 IITNNNVIIPLVIAYHLSGSAQARGERSPAERLMERQKRKADI EKGLQFIQSTLPLKQEEVEAFLLKLVQNLFAEGNDLFREKDYKQ ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESIRALFRKARALMELGRHKEAYECSSRC SLALPHDESVTQLGQELAQKLGLRVKKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDJESDDFSDGDVGPBLDTLLDSLSL VQGGLSGSGVPSELPQLIFVFPGGTPLLPPVVGGSIPVSSPLPP	{			KYSSIFNAQFTNVCGKPTLAEMGCYGLGVTRILAAAIEVLSTED
EVWCQNTGEVAFLTKDGVMDLLTPVQTV  5580  1681  450  ADAGTRCIFGFVVPSGAGYSAPAQRGRRSSGRMRAAAAPGLTAP WRLLQCCELEAGELGMAVPAAAMGPSALGQSGPGSMAPWCSVSS GPSRYVLGMQELFRGHSKTREFLAHSAKVHSVAWSCCGRRLASG SFDKTASVFLLEKDRLVKENNYRGHGDSVDQLCWHPSNPDLFVT ASGDKTIRIWDVRTTKCIATVNTKGENINICWSPDGQTIAVGNK DDVVTFIDAKTHRSKAEEQFKFEVNEISWNNDNNMFFLTNGNGC INILSYPELKPVQSINAHPSNCICIKFDPMGKYFATGSADALVS LWDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA EVETGDKLWEVQCESPTFTVAWHPKRPLLAFACDDKDGKYDGSR EAGTVKLPGLPNDS  5581  54  947  GGGSGPRAPSATLLDTGESVAAVASGEDKGTAASAAAAAVFACS CSPDPQSSTMNPVYSPVQPGAPYGNPKNMAYTGYPTAYPAAAPA YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWPONSSSCGTEG TFHLPVDTGTENRTYQASSAAFRTYAGTPYKVPPTQSNTAPPPY SPSPNPYQTAMYPIRSAYPQQNLYAQGAYYTQPVYAAQPHVHH TTVVQPNSIPSATYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW  5582  5775  2739  IITMNNNVIIPLVIAYHLSGSAQARGERSPAERLMERQKRKADI EKGLQFIQSTLPLKQEEYBAFLLKLVQNLFAEGNDLFREKDYKQ ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESIRALFRKARALNELGRHKEAYECSSRC SLALPHBESVTQLQGELAQKLGLRVRKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP	}			CVRWPSLLAPYQACLIPPKKGSKEQAASELIGQLYDHITEAVPQ
ADAGTRCIPGFVVPSGAGYSAPAGRGRRSSGRMAAAAPGLTAP   WRLLQCCELERGELGMAVPAAAMGPSALGQSGPGSMAPWCSVSS   GPSRYVLGMQELFRGHSKTREFLAHSAKVHSVAWSCDGRRLASG   SFDKTASVFLLEKDRLVKENNYRGHGDSVDQLCWHPSNPDLFVT   ASGDKTIRIWDVRTTKCIATVNTKGENINICWSPDGGTIAVGNK   DDVVTFIDARTHRSKAEQFKFEVNEISWNNDNNMFFLTNGNGG   INILSYPELKPVQSINAHPSNCICIKFDPMGKYFATGSADALVS   LWDVDELVCVCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA   EVETGDKLWEVQCESPTFTVAWHPKRPLLAFACDDKDGKYDSSR   EAGTVKLPGLPNDS   GGGSGPAPSATLLDTGESVAAVASGEDKGIAASAAAAAVFACS   CSPDPQSSTNNPVYSPVQPGAPYGNPKNMAYTGYPTAYPAAAPA   YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWPQNSSSCGTEG   TFHLPVDTGTENRTVQASSAAFRYTAGTPYKVPPTQSNTAPPPY   SPSPNPYQTAMYPIRSAYPQQNLYAQGAYYTQPVYAAQPHVIHH   TTVVQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL   TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW   STRAYPQUSTARAFATLL   TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW   EKGLQFIQSTLPLKQEEYBAFLLKLVQNLFAEGNDLFREKDYKQ   ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY   EKALEDSEKALGLDSESIRALFRKARALNELGRHKEAYECSSRC   SLALPHDESVTQLGGELAQKLGLRVRKAYKRPQELETFSLLSNG   TAAGVADQGTSNGLGSIDDIETDCVVDPRGSPALLPSTPTMPLF   PHVLDLLAFLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL   VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP	1			LHGEVLLDDRTHLTIGNRLKDANKFGYPFVIIAGKRALEDPAHF
WRLLQCCELEAGELGMAVPAAAMGPSALGQSGPGSMAPWCSVSS GPSRYVLGMQELFRGHSKTREFLAHSAKVHSVAWSCDGRRLASG GPSRYVLGMQELFRGHSKTREFLAHSAKVHSVAWSCDGRRLASG SPDKTASVFLLEKDRLVKENNYRGHGDSVDQLCWHPSNPDLFVT ASGDKTIRIWDVRTTKCIATVNTKGENINICWSPDGQTIAVGNK DDVVTFIDAKTHRSKAEEQFKFEVMEISWNNDNNMFFLTNGNGC INILSYPELKPVQSINAHPSNCICIKFDPMGKYFATGSADALVS LWDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA EVETGDKLWEVQCESPTFTVAWHPKRPLLAFACDDKDGKYDSSR EAGTVKLFGLPNDS  5581 54 947 GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAAVFACS CSPDPQSSTMMPVYSPVQPGAPYGNPKNMAYTGYPTAYPAAPA YNPSLYPTNSPSYAPEFCFLHSAYATLLMKQAWPQNSSSCGTEG TFHLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTQSNTAPPPY SPSRNPYQTAMYPIRSAYPQQNLVAQGAYYTQPVYAAQPHVIHH TTVVQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW  5582 5775 2739 IITNNNNVIIPLVIAYHLSGSAQARGERSPAERLMERQKKKADI EKGLQFIQSTLPLKQEEYBAFLLKLVQNLFAEGNDLFREKDYKQ ALVQYMEGLINVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESIRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGQELAQKLGLRVKAYKRPQELETTSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP	i			EVWCQNTGEVAFLTKDGVMDLLTPVQTV
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DDVVTFIDAKTHRSKAEEQFKFEVNEISWNNDNNMFFLTNGNGC INILSYPELKPVQSINAHPSNCICIKFDPMGKYFATGSADALVS LWDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA EVETGDKLWEVQCESPTFTVAWHPKRPLLAFACDDKDGKYDSSR EAGTVKLFGLPNDS  5581 54 947 GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAAVFACS CSPDPQSSTMNPVYSPVQPGAPYGNPKNMAYTGYPTAYPAAAPA YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWPQNSSSCGTEG TFHLPVDTGTERRTYQASSAAFRYTAGTPYKVPPTQSNTAPPPY SPSPNPYQTAMYPIRSAYPQQNLYAQGAYYTQPVYAAQPHVIHH TTVVQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSVYPPHW  5582 5775 2739 IITMNNNVIIPLVIAYHLSGSAQARGERSPAERLMERQKRKADI EKGLQFIQSTLPLKQEEYEAFLLKLVQNLFAEGNDLFREKDYKQ ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESIRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP	1			
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YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWPQNSSSCGTEG TFHLPVDTGTERRTYQASSAAFRYTAGTPYKVPPTQSNTAPPPY SPSPMPYQTAMYPIRSAYPQQNLYAQGAYYTQPVYAAQPHVIHH TTVVQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW  5582 5775 2739 IITMNNNVIIPLVIAYHLSGSAQARGERSPAERLMERQKRKADI EKGLQFIQSTLPLKQEEYEAFLLKLVQNLFAEGNDLFREKDYKQ ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESIRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETFSLLSNG TAAGVADGGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP				
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EKGLQFIQSTLPLKQEEYBAFLLKLVQNLFABGNDLFREKDYKQ ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESIRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPBLDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP	5503	5795	297.5	
ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSES IRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGQELAKOKLGLRVRKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP	3382	5//5	2/39	
EKALEDSEKALGLDSES IRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP	]			
SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP	}			
TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP	]			
PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP	[	[		
VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGS1PVSSPLPP	1	ļ .	ļ	
ASFGLVMDPSKKLAASVLDALDPPGPTLDPLDLLPYSETRLDAL	1		ì	
				ASFGLVMDPSKKLAASVLDALDPPGPTLDPLDLLPYSETRLDAL

SEQ Predicted Predicted end nucleotide nucleotide location corresponding to first amino acid residue of Security amino acid residue of Security amino acid residue of Security amino acid residue of Security amino acid residue of Security amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Ac Glutamic Acid, F=Phenylalanine, G=Gly H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,	id, E= cine,
NO: nucleotide location Glutamic Acid, F=Phenylalanine, G=Gly location corresponding to first location to first amino acid residue of S=Serine, T=Threonine, V=Valine,	cine,
location corresponding to first L=Leucine, M=Methionine, N=Asparagine to first amino acid residue of S=Serine, T=Threonine, V=Valine,	•
corresponding to first L=Leucine, M=Methionine, N=Asparagine to first amino acid P=Proline, Q=Glutamine, R=Arginine, amino acid residue of S=Serine, T=Threonine, V=Valine,	
to first amino acid P=Proline, Q=Glutamine, R=Arginine, amino acid residue of S=Serine, T=Threonine, V=Valine,	
amino acid residue of S=Serine, T=Threonine, V=Valine,	•
residue of amino acid Warryptophan, Yaryrosine, XaUnknown,	*=Stop
amino acid sequence Codon, /=possible nucleotide deletion	,
sequence \=possible nucleotide insertion)	
DSFGSTRGSLDKPDSFMEETNSQDHRPPSGAQKPAPS	
TALLIKNPLAATHEFKQACQLCYPKTGPRAGDYTYREG	
RDILIGRLRSSEDQTWKRIRPRPTKTSFVGSYYLCKDI	
KYGDNCTFAYHQEEIDVWTEERKGTLNRDLLFDPLGG	
IAKLLKEHQGIFTFLCEICFDSKPRIISKGTKDSPSV	
HSFYNNKCLVHIVRSTSLKYSKIRQFQEHFQFDVCRHI REDSCHFAHSFIELKVWLLQQYSGMTHEDIVQESKKY	
AGKASSSMGAPRTHGPSTFDLQMKFVCGQCWRNGQVVI	
YCSAKARHCWTKERRVLLVMSKAKRKWVSVRPLPSIRI	
LC1HAQNGRKCQYVGNCSFAHSPEERDMVTFMKENKI)	
DMWLKKHNPGKPGEGTPISSREGEKQIQMPTDYADIM	
CGKNSNSKKQWQQHIQSEKHKEKVFTSDSDASGWAFRI	
LCDRLQKGKACPDGDKCRCAHGQEELNEWLDRREVLK	
KDMLLCPRDDDFGKYNFLLQEDGDLAGATPEAPAAAA	
5583 3 1265 SSGCRQGRPGRSDRPRPPPRRHKMVKETRYYDILGVK)	PSASPEE
IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPI	KKRDVYD
QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARE	RRGKNVV
HQLSVTLEDLYNGVTKKLALQKNVI CEKCEGVGGKKGS	VEKCPL
CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPH	
SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPEI	
IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIF	
LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILII	
PEKHWLSLEKLPQLEALLP?RQKVRITDDMDQVELKEE WRQHREAYEEDEDGPQAGVQCQTA	CENEON
5584 3 1265 SSGCRQGRPGRSDRPRPPPPRRHKMVKETRYYDILGVK	CACOER
IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDP	1
QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARER	
HOLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGS	
. CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINDR	ORCESC
SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPEI	
IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIK	
LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLBKGILII	
PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEK	CENEON
WRQHREAYEEDEDGPQAGVQCQTA  5585 2619 915 LPAGTPESSLHEALDOCMTALDLFLTNOFSEAYSYLKE	S
5585 2619 915 LPAGTPESSLHEALDQCMTALDLFLTNQFSEALSYLKF YHSLTYATILEMQAMMTFDPQDILLAGNMMKEAQMLCC	
SVTDSFSSLVNRPTLGQFTEEEIHAEVCYAKCLLQRAA	
ENMVSFIKGGIKVRNSYQTYKELDSLVQSSQYCKG3NH	
VKLGVGAFNLTLSMLPTRILRLLEFVGFSGNKDYGLLQ	
GHSFRSVLCVMLLLCYHTFLTFVLGTGNVNIEEAEKLL	
YPKGAIFLFLAGRIEVIKGNIDAAIRRFEECCEAQQHW	
CYWELMWCFTYKGQWKMSYFYADLLSKENCWSKATYIY	
SMFGKEDHKPFGDDEVELFRAVPGLKLKIAGKSLPTEK	
RRYFSSNPISLPVPALEMMYIWNGYAVIGKQPKLTDGI	
AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEA	
ISANEKKIKYDHYLI PNALLELALLIMEQDRNEEAIKL	- 1
NYKNYSMESRTHFRIQAATLQAKSSLBNSSRSMVSSVS 5586 2619 915 LPAGTPESSLHEALDOCMTALDLFLTNOFSEALSYLKP	
YHSLTYATILEMQAMMTFDPQDILLAGNMMKEAQMLCQ SVTDSFSSLVNRPTLGQFTEEEIHAEVCYAKCLLQRAA	
ENMVSFIKGGIKVRNSYQTYKELDSLVQSSQYCKGENH	
VKLGVGAFNLTLSMLPTRILRLLEFVGFSGNKDYGLLQ	,
GHSFRSVLCVMLLLCYHTFLTPVLGTGNVNIBEAEKLL	
YPKGAIFLFLAGRIEVIKGNIDAAIRRFEECCEAQQHW	,
CYWELMWCFTYKGQWKMSYFYADLLSKENCWSKATYIY	
SMFGKEDHKPFGDDEVELFRAVPGLKLKIAGKSLPTEK	
RRYFSSNPISLPVPALEMMYIWNGYAVIGKQPKLTDGI	
ABEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEA	1
ISANEKKIKYDHYLIPNALLELALLLMEQDRNEEAIKL	1
NYKNYSMESRTHFRIQAATLQAKSSLENSSRSMVSSVSI 5587 1768 148 SSAVPDGAVGRPVAVAVGGPDHGCPCRPCCIMAATGVH	
5587 1768 148 SSAVPDGAVGRPVAVAVGGPPHSCRCRPCCLMAAIGVH	LUCISA

SEQ	Predicted	I Predicted end	Amino acid coment containing diseas
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
į	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
-	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	sequence	\=possible nucleotide insertion)
	sequence		CVAVYKDGRAGVVANDAGDRVTPAVVAYSENEEIVGLAAKOSRI
	· ·		
1	1		RNISNTVMKVKQILGRSSSDPQAQKYIAESKCLVIEKNGKLRYE
	!		IDTGEETKFVNPEDVARLIFSKMKETAHSVLGSDANDVVITVPF
			DFGBKQKNALGEAARAAGFNVLRLIHEPSAALLAYGIGQDSPTG
			KSNILVFKLGGTSLSLSVMEVNSGIYRVLSTNTDDNIGGAHFTE
			TLAQYLASEFQRSFKHDVRGNARAMMKLTNSAEVAKHSLSTLGS
1	1	ł	ANCFLDSLYEGQDFDCNVSRARFELLCSPLFNKCIEAIRGLLDQ
1	1	İ	NGFTADDINKVVLCGGSSRIPKLQQLIKDLFPAVELLNSIPPDE
Ī		{	VIPIGAAIEAGILIGKENLLVEDSLMIECSARDILVKGVDESGA
1	j	J	SRFTVLFPSGTPLPARRQHTLQAPGSISSVCLELYESDGKNSAK
1	1		EETKFAQVVLQDLDKKENGLRDILAVLTMKRDGSLHVTCTDQET
	<u> </u>		GKCEAISIEIAS
5588	3	589	TPPPPEQAMVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGK
ſ	[		LVSLEKYRGSVSLVVNVASECGFTDQHYRALQQLQRDLGPHHFN
)	1		VLAFPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG
i			AHPAFKYLAQISGKEPTWNFWKYLVAPDGKVVGAWDPTVSVEEV
L			RPQITALVRKLILLKREDL
5589	1884	553	LRQAWHEGGIGQTDKERGAAALPGEEGDPTRGRSLGRASWESGS
1	i		PRRPRSPFSSFLPRPICLSLEARPCSIEDRRNWSLIGRPGAPAS
1	1		GLNRSSGLWLGPDRCRPRSRCSCRVMENPSPAAALGKALCALLL
	1 .		ATLGAAGQPLGGESICSARAPAKYSITFTGKWSQTAFPKQYPLF
1	1		RPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDFAERGEAWALM
			KEIEAAGEALQSVHAVFSAPAVPSGTGQTSAELEVQRRHSLVSF
Ì	i		VVRIVPSPDWFVGVDSLDLCDGDRWREQAALDLYPYDAGTDSGF
[	J !		TFSSPNFATIPODTVTEITSSSPSHPANSFYYPRLKALPPIARV
			TLLRLRQSPRAFIPPAPVLPSRDNEIVDSASVPETPLDCEVSLW
	<u>.</u>		SSWGLCGGHCGRLGTKSRTRYVRVQPANNGSPCPELEEEAECVP
L		L	DNCV
5590	72	896	LCSSGALRLLPAMVAWRSAFLVCLAFSLATLVQRGSGDFDDFNL
ļ	}		EDAVKETSSVKQPWDHTTTTTTNRPGTTRAPAKPPGSGLDLADA
1	1		LDDQDDGRRKPGIGGRERWNHVTTTTKRPVTTRAPANTLGNDFD
1			LADALDDRNDRDDGRRKPIAGGGGFSDKDLEDIVGGGEYKPDKG
			KGDGRYGSNDDFGSGMVAEPGTIAGVASALAMALIGAVSSYISY
Į.	. 1		QQKKFCFSIQQGLNADYVKGENLEAVVCEEPQVKYSTLHTQSAE
L			PPPPPBPARI
5591	68	1494	AGSSRRAAAERLLVSAGCRSLAGRASGVLLLPAELLPGEEEAMA
	1		LRVTRNSKINAENKAKINMAGAKRVPTAPAATSKPGLRPRTALG
1			DIGNKVSEQLQAKMPMKKEAKPSATGKVIDKKLPKPLEKVPMLV
1			PVPVSEPVPEPEPEPEPEPVKEEKLSPEPILVDTASPSPMETSG
1 .	ĺ		CAPABEDLCQAFSDVILAVNDVDAEDGADPNLCSEYVKDIYAYL
1	]		RQLEEEQAVRPKYLLGREVTGNMRAILIDWLVQVQMKFRLLQET
1			MYMTVSIIDRFMQNNCVPKKMLQLVGVTAMFIASKYEEMYPPBI
1 :			GDFAFVTDNTYTKHQIRQMEMKILRALNFGLGRPLPLHFLRRAS
			KIGEVDVEQHTLAKYLMELTMLDYDMVHFPPSQIAAGAFCLALK
			ILDNGEWTPTLQHYLSYTEESLLPVMQHLAKNAAMVNQGLTKHM
<u></u>			TVKNKYATSKHAKISTLPQLNSALVQDLAKAVAKV
5592	242	924	YGESKDWNQKDLLSALVLTTVNCLPTPIMAKSAEVKLAIFGRAG
{			VGKSALVVRFLTKRFIWEYDPTLESTYRHQATIDDEVVSMEILD
1 1		•	TAGQEDTIQREGHMRWGEGFVLVYDITDRGSFEEVLPLKNILDE
(	{	1	IKKPKNVTLILVGNKADLDHSRQVSTEEGEKLATELACAFYECS
1 1	j		ACTGEGNITEIFYELCREVRRRRMVQGKTRRRSSTTHVKQAINK
[ _ [		ļ	MLTKISS
5593	3	1113	HASGGRAANMAAERGAGQQQSQEMMEVDRRVESEESGDEEGKKH
			SSGIVADLSEQSLKDGEERGEEDPEEEHELPVDMETINLDRDAE
1 1		ł	DVDLNHYRIGKIEGFEVLKKVKTLCLRQNLIKCIENLEELQSLR
j		ļ	BLDLYDNQIKKIENLEALTELEILDISFNLLRNIEGVDKLTRLK
1 1			KLFLVNNKISKIENLSNLHQLQMLELGSNRIRAIENIDTLTNLE
1 1		)	SLFLGKNKITKLQNLDALTNLTVLSMQSNRLTKIEGLQNLVNLR
j			ELYLSHNGIEVIEGLENNNKLTMLDIASNRIKKIENISHLTELQ
t i	1		EFWMNDNLLESWSDLDELKGARSLETVYLERNPLQKDPQYRRKV
L			T A THEWALL A THEWALL AND TAKEN A THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WALL THE WAL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1			
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
)	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Scrine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	i i		
Į.	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			MLALPSVRQIDATFVRF
5594	3	1113	HASGGRAANMAAERGAGQQQSQEMMEVDRRVESEESGDEEGKKH
	ì		SSGIVADLSEQSLKDGEERGEEDPEEEHBLPVDMETINLDRDAB
ł			DVDLNHYRIGKIEGFEVLKKVKTLCLRONLIKCIENLEELOSLR
			•
	)		ELDLYDNQIKKIENLEALTELEILDISFNLLRNIEGVOKLTRLK
1	Ì		KLFLVNNKISKIENLSNLHQLQMLELGSNRIRAIENIDTLTNLE
			SLFLGKNKITKLQNLDALTNLTVLSMQSNRLTKIEGLQNLVNLR
1			ELYLSHNGIEVIEGLENNNKLTMLDIASNRIKKIENISHLTELO
1			EFWMNDNLLESWSDLDELKGARSLETVYLERNPLQKDPQYRRKV
1	1		MLALPSVRQIDATFVRF
	l ————		<u></u>
5595	3	1476	ARWNGRWVQVPAWPGPGCGTNASGERQRQLPRAWRPVGRTLGSE
1			PIALAMSPPLYLFPIPLPSWAVSQPTPTLGTMFADLDYDIEEDK
i			LGIPTVPGKVTLQKDAQNLIGISIGGGAQYCPCLYIVQVFDNTP
1			AALDGTVAAGDEITGVNGRSIKGKTKVEVAKMIQEVKGEVTIHY
1	[		NKLQADPKQGMSLDIVLKKVKHRLVENMSSGTADALGLSRAILC
I			NDGLVKRLEELERTAELYKGMTEHTKNLLRAFYELSQTHRAFGD
1			1-7
ł	1		VFSVIGVREPQPAASEAFVKFADAHRSIEKFGIRLLKTIKPMLT
l			DLNTYLNKAIPDTRLTIKKYLDVKFEYLSYCLKVKEMDDEEYSC
l			IALGEPLYRVSTGNYEYRLILRCRQEARARFSQMRKDVLEKMEL
1			LDOKHVODIVFOLORLVSTMSKYYNDCYAVLRDADVFPIEVDLA
[	[		HTTLAYGLNQEEFTDGEEEEEEEDTAAGEPSRDTRGAAGPLDKG
1	}	•	GSWCDS
5596		- 3-8	
2238	698	219	GAVLAPSSLPAAELAAQGESQSLBDLSNTSRPTSEVYKISFIFP
l			NGDKYDGDCTRTSSGIYERNGIGIHTTPNGIVYTGSWKDDKMNG
1	į l		FGRLEHFSGAVYEGQFKDNMFHGLGTYTFPNGAKYTGNFNENRV
	ĺ	1	KGEGEYTHIQGTRMDVVTFHFTSCSQT
5597	3	731	ISCKMAADGOSSLPASWRSVTLTHVEYPAGDLSGHLLAYLSLSP
			VFVIVGFVTLIIFKRELHTISFLGGLALNEGVNWLIKNVIQEPR
	1		PCGGPHTAVGTKYGMPSSHSQFMWFFSVYSFLFLYLRMHQTNNA
			RFLDLLWRHVLSLGLLAVAPLVSYSRVYLLYHTWSQVLYGGIAG
	i		_
	]		GLMAIAWFIFTQEVLTPLFPRIAAWPVSEFFLIRDTSLIPNVLW
			FEYTVTRAEARNRQRKLGTKLQ
5598	326	2440	GIGPIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL
			VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG
	ĺ		DAKFGERNEGSGARRRRCLNGNPPKRLKRRDRRMMSQLELLSGG
	ļ ļ		EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE
	1		IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR
	i i		15
	ļ i		GHIPGFLQTTADEFCFYYARKDGGLCFPDFPRKQVRGPASNYLD
[	ĺ		QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR
			LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL
1			SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK
	ľ		NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM
			ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS
		ĺ	TNOPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS
		Ì	SARILQIIKGKDYESEPSLLEFKPFSNGPLVGGFVYRGCQSERL
	l i	ļ	YGSYVFGDRNGNFLTLQQSPVTKQWQEKPLCLGTSGSCRGYFSG
		1	HILGFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEE
			CRATVQFAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG
5599	326	2440	GIGPIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL
	-		VPLLGSGVPPHPPAPSPCCSGOTMLKMLSFKLLLLAVALGFFEG
	i		DAKFGERNEGSGARRRRCLNGNPPKRLKRRDRRMMSQLELLSGG
	ļ <b>[</b>	1	EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE
	1	ł	ikcalcsphsqslfhsperevlerdlvlpllckdyckeffytcr
	]	į	GHIPGFLQTTADEFCFYYARKDGGLCFPDFPRKQVRGPASNYLD
ı	i	ł	QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR
}			LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL
l			·-
ļ	1		SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK
j	ŀ		NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM
i	i		ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS
	l j	J	TNOPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	
į	1		P=Proline, Q=Glutamine, R=Arginine,
Į	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	I	\=possible nucleotide insertion)
			SARILQIIKGKDYESEPSLLEFKPFSNGPLVGGFVYRGCQSERL
			YGSYVFGDRNGNFLTLQQSPVTKQWQEKPLCLGTSGSCRGYFSG
1		1	HILGFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEE
1		1	CRATVQPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG
5600	1977	1244	SLRVLSGHLMOTRDLVOPDKPASPKFIVTLDGVPSPPGYMSDOE
5600	19//	1244	
1		Į.	EDMCFEGMKPVNQTAASNKGLRGLLHPQQLHLLSRQLEDPNGSF
1	İ	1	SNAEMSELSVAQKPEKLLERCKYWPACKNGDECAYHHPISPCKA
1			FPNCKFAEKCLFVHPNCKYDAKCTKPDCPFTHVSRRIPVLSPKP
1	1	J	AVAPPAPPSSSQLCRYFPACKKMECPFYHPKHCRFNTQCTRPDC
1	Į.	l	TFYHPTINVPPRHALKWIRPQTSE
5601	1977	1244	SLRVLSGHLMQTRDLVQPDKPASPKFIVTLDGVPSPPGYMSDQE
1		l	EDMCFEGMKPVNQTAASNKGLRGLLHPQQLHLLSRQLEDPNGSF
1	1		SNAEMSELSVAQKPEKLLERCKYWPACKNGDECAYHHPISPCKA
			17
1	Ī	1	FPNCKFAEKCLFVHPNCKYDAKCTKPDCPFTHVSRRIPVLSPKP
1	1	1	AVAPPAPPSSSQLCRYFPACKKMECPFYHPKHCRFNTQCTRPDC
			TFYHPTINVPPRHALKWIRPQTSB
5602	246	766	YHTSCTVWRTAKEALENTEVPVGCLMVYNNEVVGKGRNEVNQTK
	1	İ	NATRHAEMVAIDQVLDWCRQSGKSPSEVFEHTVLYVTVEPCIMC
		i	AAALRLMKIPLVVYGCQNERFGGCGSVLNIASADLPNTGRPFQC
}	1	J	IPGYRAEEAVEMLKTFYKOENPNAPKSKVRKKECOOILNMF
5603	1	565	FRGRTPISGGERGCAQYPIPATPARSGENRTMPGAGDGGKAPAR
	_	1	WLGTGLLGLFLLPVTLSLEVSVGKATDIYAVNGTEILLPCTFSS
ł			CFGFEDLHFRWTYNSSDAFKILIEGTVKNEKSDPKVTLKDDDRI
I			
İ			TLVGSTKEKRNNISIVLRDLEFSDTGKYTCHVKNPKENNLQHHA
			TIFLQVVDRRMQ
5604	1	1506	EDIFPAQLLKLQRHERVWQQEPPVRDHRSWGGSGAGGVAGREWT
!			DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGGDFG
1	ł	ł	GGDFGGGDFGGGGGSFGGHCLDYCESPTAHCNVLNWEQVQ
Į.			RLDGILSETIPIHGRGNFPTLELQPSLIVKVVRRRLAEKRIGVR
	1		KEDGIESELLEINGKONFFILEEQFEELVKVVKKKLAEKKIGVK
1			DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV
			DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV
			DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI
			DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE
			DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG
			DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL
			DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL
			DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLCMHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV
			DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN
5605	35	1821	DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCFRSFSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL
5605	35	1821	DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGSSVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCFRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ
5605	35	1821	DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCFRSFSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVPQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG
5605	35	1821	DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGSSVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCFRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ
5605	35	1821	DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCFRSFSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVPQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG
5605	35	1821	DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFBFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCFRSFSPAPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQFKAGGSGSYWP
5605	35	1821	DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSFSSFAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRNLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQFKAGGSGSVWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE
5605	35	1821	DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCTLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCFRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDBRLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQQPLELRP
5605	35	1821	DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMYKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYEGSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFLDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCFRSFSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSVMP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF
5605	35	1821	DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFBESVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCFRSFSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRHLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQFKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPFGEETAVPGAASAELASEAGVQQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHYHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ
5605	35	1821	DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCFRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALKSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQFKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHYTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFRLKRCGLERRVYLVEEHGSVKNLSLPESTLLQAVTNTQVIDG
5605	35	1821	DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLCMHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLDCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ GALASLRRYPLPLRSGKEAKILGHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVYGAASAELASEAGVQQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFRLKRCGLERRVYLVEEHGSVMNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE
5605	35	1821	DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCTLDFLPEGVNKEKITPLTLKEAYVQKMYKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFRLKCGLERRVYLVEEHGSVHNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG
5605	35	1821	DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFLDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNNIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSFSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSVWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQQPLETRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFRLKCGLERRVYLVEEHGSVNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGMMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL
5605	35	1821	DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCTLDFLPEGVNKEKITPLTLKEAYVQKMYKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFRLKCGLERRVYLVEEHGSVHNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG
5605	35	1821	DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFLDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNNIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSFSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSVWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQQPLETRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFRLKCGLERRVYLVEEHGSVNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGMMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL
		·	DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFBESVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSFSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESP GSSTVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFFLKRCGLERRYYLVEEHGSVINLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL QRNLGPALSRTLSQLYCSYGPLT GRSRCPGPGARGGTMSPRSCLRSLRLLVFAVFSAAASNWLYLAK
		·	DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFBESVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCFRSFSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALKSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQFKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHYTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFRLKRCGLERRVYLVEEHGSVHNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL QRNLGPALSRTLSQLYCSYGPLT GRSRCPGPGARGGTMSPRSCLRSLRLLVFAVFSAAASNWLYLAK LSSVGSISEEETCEKLKGLIQRQVQMCKRNLEVMDSVRRGAQLA
		·	DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCFRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQFKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFRLKRCGLERRVYLVEEHGSVHNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAVDACATPKEQETLLSTIKCGRL QRNLGPALSRTLSQLYCSYGPLT GRSRCPGPGARGGTMSPRSCLRSLRLLVFAVFSAAASNWLYLAK LSSVGSISEEETCEKLKGLIQRQVQMCKRNLEVMDSVRRGAQLA IBECQYQFRNRRWNCSTLDSLPVFGKVVTQGTREAAFVYAISSA
		·	DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMYKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCFRSFSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDBRLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQFKAGGSGSVWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFRLKCGLERRVYLVEEHGSVHNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYCGHTLRSPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL QRNLGPALSRTLSQLYCSYGPLT GRSRCPGPGARGGTMSPRSCLRSLRLLVFAVFSAAASNWLYLAK LSSVGSISEEETCEKLKGLIQRQVQMCKRNLEVMDSVRRGAQLA IBECQYQFRNRRWNCSTLDSLPVFGKVVTQGTREAAFVVAISSA GVAFAVTRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYG
		·	DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGCG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFLDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCFRSFSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSC GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSVMP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFRLKRCGLERRVYLVEEHGSVKNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL QRNLGPALSRTLSQLYCSYGPLT GRSRCPGPGARGGTMSPRSCURSLRLLVFAVFSAAASNWLYLAK LSSVGSISEEETCEKLKGLIQRQVQMCKRNLEVMDSVRRGAQLA IBECQYQFRNRWNCSTLDSLPVFGKVVTQGTREAAFVYAISSA GVAFAVTRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYG VAFSQSFVDVRERSKGASSSRALMNLHNNEAGRKAILTHMRVEC
		·	DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMYKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCFRSFSPAPPWARCSNPDSTTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPPLFVXWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFFLKRCGLERRYYLVEEHGSVHNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL QRNLGPALSRTLSQLYCSYGPLT GRSRCPGPGARGGTMSPRSCLRSLRLLVFAVFSAAASNWLYLAK LSSVGSISEETCEKLKGLIQRQVQMCKRRLEVMDSVRRGAQLA IEECQYQFRNRWNCSTLDSLPVFGKVVTQGTREAAFVYAISSA GVAFAVTRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYG VAFSQSFVDVERRSKGASSSRALMNLHNNEAGRKAILTHMRVEC KCHGVSGSCEVKTCWRAVPPFRQVGHALKEKFDGATEVEPRRVG
		·	DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFBESVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCFRSFSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRHLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFRLKRCGLERRVYLVEEHGSVHNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL QRNLGPALSRTLSQLYCSYGPLT GRSRCPGPGARGGTMSPRSCLRSLRLLVFAVFSAAASNWLYLAK LSSVGSISEEETCEKLKGLIQRQVQMCKRNLEVMDSVRRGAQLA IBECQYQFRNRRWNCSTLDSLPVFGKVVTQGTREAAFVXAISSA GVAFAVTRACSSGELEKCGCDRTVHGVSPQGFQWSCSDNIAYG VAFSQSFVDVRERSKGASSSRALMNLHNNEAGRKAILTHMRVEC KCHGVSGSCEVKTCWRAVPPRQVGTALKEKPDGATEVEPRRVG SSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGR
		·	DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMYKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCFRSFSPAPPWARCSNPDSTTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPPLFVXWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFFLKRCGLERRYYLVEEHGSVHNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL QRNLGPALSRTLSQLYCSYGPLT GRSRCPGPGARGGTMSPRSCLRSLRLLVFAVFSAAASNWLYLAK LSSVGSISEETCEKLKGLIQRQVQMCKRRLEVMDSVRRGAQLA IEECQYQFRNRWNCSTLDSLPVFGKVVTQGTREAAFVYAISSA GVAFAVTRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYG VAFSQSFVDVERRSKGASSSRALMNLHNNEAGRKAILTHMRVEC KCHGVSGSCEVKTCWRAVPPFRQVGHALKEKFDGATEVEPRRVG
		·	DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFBESVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCFRSFSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRHLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFRLKRCGLERRVYLVEEHGSVHNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL QRNLGPALSRTLSQLYCSYGPLT GRSRCPGPGARGGTMSPRSCLRSLRLLVFAVFSAAASNWLYLAK LSSVGSISEEETCEKLKGLIQRQVQMCKRNLEVMDSVRRGAQLA IBECQYQFRNRRWNCSTLDSLPVFGKVVTQGTREAAFVXAISSA GVAFAVTRACSSGELEKCGCDRTVHGVSPQGFQWSCSDNIAYG VAFSQSFVDVRERSKGASSSRALMNLHNNEAGRKAILTHMRVEC KCHGVSGSCEVKTCWRAVPPRQVGTALKEKPDGATEVEPRRVG SSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGR

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lvsine.
l	corresponding	to first	b=Leucine, M=Methionine, N=Asparagine,
- 1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l l	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Ston
ĺ	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
5607	521	141	PPVCNPAEAMPSPGTVCSLLLLGMI.WLDLAMAGSSFLSPEHQRV
1		1	QQRKESKKPPAKLQPRALAGWLRPEDGGQAEGAEDELEVRFNAP
5608			FDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK
2608	2	983	WFQSPLRQADPGPPRHTLFMDFVAGAIGGVCGDAVGYPLDTVKV
1			RIQTEPKYTGIWHCVRDTYHRBRVWGFYRGLLLPVCTVSLVSSE
ı	1		VFGTYRHCLAHICRLRFGNPDAKPTKADITLSGCASGLVRVFLT
ł	1	ļ	SPTEVAKVRLQTQTQAQKQQRRLSASGPLAVPPMCPVPPACPEP
1	,		KYRGPLHCLATVAREEGLCGLYKGSSALVLRDGHSFATYFLSYA
			VLCEWLSPAGHSRPDVPGVLVAGGCAGVLAWAVATPMDVIKSRL
			QADGQGQRYRGLLHCMVTIVREEGPRVLFKGLVLNCCRAFPVN MVVFVAYEAVLRLARGLLT
5609	1628	304	AKGVWVLPSPPPRPGRGALVSGSGLRRGRSGTSWRPRRMNHKSK
1.		]	KRIREAKRSARPELKDSLDWTRHNYYESFSLSPAAVADNVERAD
1	]		ALQLSVEEFVERYERPYKPVVLLNAQEGWSAQEKWTLERLKRKY
			RNQKFKCGEDNDGYSVKMKMKYYIEYMESTRDDSPLYIFDSSYG
1			EHPKRRKLLEDYKVPKFFTDDLFQYAGEKRRPPYRWFVMGPPRS
1			GTGIHIDPLGTSAWNALVQGHKRWCLFPTSTPRELIKVTRDEGG
1 ,			NQQDEAITWFNVIYPRTQLPTWPPEFKPLEILQKPGETVFVPGG
1			WWHYVLNLDTTIAITONFASSTNFPVVWHKTVRGRPKLSRKWYR
1			ILKQEHPELAVLADSVDLQESTGIASDSSSDSSSSSSSSSSDSD
1 .			SECESGSEGDGTVHRRKKRRTCSMVGNGDTTSQDDCVSKERSSS
			R
5610	54	1196	LERTPASADMAWTKYQLFLAGLMLVTGSINTLSAKWADNFMAEG
			CGGSKEHSFQHPFLQAVGMFLGEFSCLAAFYLLRCRAAGOSDSS
1	·		VDPQQPFNPLLFLPPALCDMTGTSLMYVALMMTSASSFOMLRGA
			VIIFTGLFSVAFLGRRLVLSQWLGILATIAGLVVVGLADLLSKH
}			DSQHKLSEVITGDLLIIMAQIIVAIQMVLEEKFVYKHNVHPLRA
;			VGTEGLFGFVILSLLLVPMYYIPAGSFSGNPRGTLEDALDAFCQ
i i			VGQQPLIAVALLGNISSIAFFNFAGISVTKELSATTRMVLDSLR
		ļ	TVVIWALSLALGWEAFHALQILGFLILLIGTALYNGLHRPLLGR
5611	2		LSRGRPLAEESEQERLLGGTRTPINDAS
3611	2	577	FVLPNRLGIPGSTFRGPGACASSSSLAASAKPGAGGSPALAMSG
1	ľ		ELSNRFQGGKAFGLLKARQERRLABINREFLCDQKYSDEENLPE
1. 1	1		KLTAFKEKYMEFDLNNEGEIDLMSLKRMMEKLGVPKTHLEMKKM
1 1		1	ISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMFEGKANESSP
5612	1	721	KPVGPPPERDIASLP ASRDGYMDATIAPHRIPPEMPQYGEENHIFELMQAMWLCKHLNS
	-	,	SLLTLENLILNEFSYTATEARRLYLQRKTVPSALLVQLIQERLA
1		ļ	EEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVL
]	·	1	IERNLGKRIDPQTGEIYHTTFDWPPESEIQNRLMVPEDISELET
, 1		1	AQKLLEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVQS
		1	NHRTNAPFTPRVLLLGPVGS
5613	115	1279	RGVDPALRRAEKMLPLSIKDDEYKPPKFNLFGKISGWFRSILSD
		!	KTSRNLFFFLCLNLSFAFVELLYGIWSNCLGLISDSFHMFFDST
			AILAGLAASVISKWRDNDAFSYGYVRAEVLAGFVNGLFLIFTAF
j i			FIFSEGVERALAPPDVHHERLLLVSILGFVVNLIGIFVFKHGGH
			GHSHGSGHGHSHSLFNGALDQAHGHVDHCHSHEVKHGAAHSHDH
	1		AHGHGHFHSHDGPSLKETTGPSRQILQGVFLHILADTLGSIGVI
	į.	1	ASAIMMONFGLMIADPICSILIAILIVVSVIPLLRESVGILMOR
			TPPLLENSLPQCYQRVQQLQGVYSLQEQHFWTLCSDVYVGTLKL
			IVAPDADARWILSQTHNIFTQAGVRQLYVQIDFAAM
5614	3	1268	LLSRNEHACPLQAGLGLTQRKPKAIRGREGRATNQGQGETQNER
	İ	1	APWGARQRLGVMAELQQLQEFEIPTGREALRGNHSALLRVADYC
	İ		EDNYVQATDKRKALEETMAFTTQALASVAYQVGNLAGHTLRMLD
			LQGAALRQVEARVSTLGQMVNMHMEKVARREIGTLATVORLPPG
			QKVIAPENLPPLTPYCRRPLNFGCLDDIGHGIKDLSTOLSRTGT
1	ļ	1	LSRKSIKAPATPASATLGRPPRIPEPVHLPVVPDGRLSAASSAS
1	ļ	İ	SLASAGSAEGVGGAPTPKGQAAPPAPPLPSSLDPPPPPAAVEVF
ſ			QRPPTLEELSPPPPDEELPLPLDLPPPPPPLDGDELGLPPPPPGF
			GPDEPSWVPASYLEKVVTLYPYTSQKDNELSFSEGTVICVTRRY

SEO	Predicted	Predicted end	I amino agid governt contribution in its
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
j	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ì	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	amino acid	sequence	Codon, /=possible nucleotide deletion,
İ	sequence	Joquanica	\=possible nucleotide insertion)
<b></b>		ļ	SDGWCEGVSSEGTGFFPGNYVEPSC
5615	9	1558	ALGRREPGDPREMEAAATPAAAGAARREELDMDVMRPLINEQNF
1	1	1	DGTSDEEHEQELLPVQKHYQLDDQEGISFVQTLMHLLKGNIGTG
	}		LIGLPLAIKNAGIVLGPISLVFIGIISVHCMHILVRCSHFLCLR
	i	ĺ	FKKSTLGYSDTVSFAMEVSPWSCLQKQAAWGRSVVDFFLVITQL
1			GFCSVYIVFLAENVKQVHEGFLESKVFISNSTNSSNPCERRSVD
	1 .		LRIYMLCFLPFIILLVFIRELKNLFVLSFLANVSMAVSLVIIYQ
	}		YVVRNMPDPHNLPIVAGWKKYPLFFGTAVFAFEGIGVVLPLENQ
1	1	Ì	MKESKRFPQALNIGMGIVTTLYVTLATLGYMCFHDEIKGSITLN
1	Ì		LPQDVWLYQSVKILYSFGIPVTYSIQFYVPAEIIIPGITSKFHT
ŀ			KWKQICEFGIRSFLVSITCAGAILIPRLDIVISFVGAVSSSTLA
			LILPPLVEILTFSKEHYNIWMVLKNISIAFTGVVGFLLGTYITV
			REIIYPTPKVVAGTPQSPFLNLNSTCLTSGLK
5616	1	719	DDFVRCGPQSAAMGASARLLRAVIMGAPGSGKGTVSSRITTHFE
1			LKHLSSGDLLRDNMLRGTEIGVLAKAFIDQGKLIPDDVMTRLAL
İ			HELKNLTQYSWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEV
Į			IKQRLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDD
1			KPETVIKRLKAYEDQTKPVLEYYQKKGVLETFSGTETNKIWPYV
			YAFLQTKVPQRSQKASVTP
5617	176	765	PWRGRGSRPRGAGAMAEEQVNRSAGLAPDCEASATAETTVSSVG
			TCEAAGKSPEPKDYDSTCVFCRIAGRQDPGTELLHCENEDLICF
			KDIKPAATHHYLVVPKKHIGNCRTLRKDQVELVENMVTVGKTIL
}			ERNNFTDFTNVRMGFHMPPFCSISHLHLHVLAPVDQLGFLSKLV
5618	3	1692	YRVNSYNFITADHLIEKLRT
1 3010	,	1032	YLNYINLKSENKLSGKEDLWEKLQYLWKSTLNLPEDLLRVPDES
1			LFLNSGGDSLKSIRLLSEIEKLVGTSVPGLLEIILSSSILEIYN HILQTVVPDEDVTFRKSCATKRKLSNINQEBASGTSLHOKAIMT
1			FTCHNEINAFVVLSRGSQILSLNSTRFLTKLGHCSSACPSDSVS
1	i		QTNIQNLKGLNSPVLIGKSKDPSCVAKVSEEGKPAIGTOKMELH
1 .			VRWRSDTGKCVDASPLVVIPTFDKSSTTVYIGSHSHRMKAVDFY
	]		SGKVKWEQILGDRIESSACVSKCGNFIVVGCYNGLVYVLKSNSG
1 1			EKYMMFTIEDAVKSSATMDPTTGLIYIGSHDQHAYALDIYRKKC
1	i		VWKSKCGGTVFSSPCLNLIPHHLYFATLGGLLLAVNPATGNVIW
1			KHSCGKPLFSSPQCCSQYICIGCVDGNLLCFTHFGEQVWQFSTS
			GPIFSSPCTSPSEQKIFFGSHDCFIYCCNMKGHLOWKFETTSRV
1 1			YATPFAFHNYNGSNEMLLAAASTDGKVWILESQSGQLQSVYELP
			GEVFSSPVVLESMLIIGCRDNYVYCLDLLGGNQK .
5619	2160	1477	DSPVLPTSGNVISTAQPAQPWSAVEAALRSLGSPPGAGRGCPCP
]			AQSLHSHQLAAWDPLKPSLRSYPPHLLQHPQLRSLTASSGHLGR
j i			RSCPQPRPLEELLRAGSSTRPQPLTSSCCGMSCMYSFLGHCSVL
1			LWGTKGRGSGSPSSPGCCLHPPAQHSQDLPLVHVDVGWQPPLGP
	ļ		TVGLRPGLLGERQRGALRAGDPQCQCPLPATVREDLGVPSPWAA
E230	030		ECSPPATP
5620	930	182	PLPPPTLAMFLTRSEYDRGVNTFSPEGRLFQVEYAIEAIKLGST
			AIGIQTSEGVCLAVEKRITSPLMEPSSIEKIVEIDAHIGCAMSG
	Ì		LIADAKTLIDKARVETQNHWFTYNETMTVESVTQAVSNLALQFG
1 1	1		EEDADPGAMSRPFGVALLFGGVDEKGPQLFHMDPSGTFVQCDAR
1	i		AIGSASEGAQSSLQEVYHKSMTLKEAIKSSLIILKQVMEEKLNA
5621	3	819	TNIELATVQPGQNFHMFTKEELEEVIKDI
	-	017	VVEFVEYTATDANVKNESLSSVQQLGIKMTVRYGKFLSLLKDGA ENDLTWVLKHCERFLKOOOTSIKSSLLCLQGNYAGHDWFVSSLF
, I			MIMLGDKEKTFQFLHQFSRLLTSAFLWLPRLHISSYLPNDTVES
[	1		GIHPVYFCSTHYIEMLLKAELPLVFSAFHMSGFAPSQICLOWIT
1 1	į	İ	QCFWNYLDWIEICHYIATCVFLGPDYQVYICIAVFKHLQQDILQ
} 1			HTQTQDLQVFLKEEALHGFRVSDYFEYMEILEQNYRTVLLRDMR
			NIRLQST
5622	1122	456	AASTKDAVSRKRSHSASEKSGTGTSISKRLNMNPOIRNPMKAMY
			PGTFYFQFKNLWEANDRNETWLCFTVEGIKRRSVVSWKTGVFRN
]			QVDSETHCHAERCFLSWFCDDILSPNTKYQVTWYTSWSPCPDCA
L i		}	GEVAEFLARHSNVNLTIFTARLYYFQYPCYQEGLRSLSQEGVAV

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
į	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
•	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
Į	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
i i	sequence		\=possible nucleotide insertion)
	1		BIMDYEDFKYCWENFVYNDNEPFKPWKGLKTNFRLLKRRLRESL
1			O O
5623	3	954	FLPFFIRAPKISRNGQWLFTFTTPFPFANKALPGWEGIVPACFW
		334	RKKILTPSTGTMELLQVTILFLLPSICSSNSTGVLEAANNSLVV
ł			TTTKPSITTPNTESLQKNVVTPTTGTTPKGTITNELLKMSLMST
ŀ			ATFLTSKDEGLKATTTDVRKNDSIISNVTVTSVTLPNAVSTLQS
	l .		SKEWPETOGGT VERRETEGGIA ODDA CEGARORI MODELLE
	1		SKPKTETQSSIKTTEIPGSVLQPDASPSKTGTLTSIPVTIPENT
			SQSQVIGTEGGKNASTSATSRSYSSIILPVVIALIVITLSVFVL VGLYRMCWKADPGTPENGNDQPQSDKESVKLLTVKTISHESGEH
	<b>(</b>		SAQGKTKN
5624	159	898	PGVAAAAGALPQYHGPAPALVSCRRELSLSAGSLQLERKRRDFT
1		0,00	SSCSPKI.VPDTHALUCI.I.EDMC@X@OONETTUOX
1	J		SSGSRKLYFDTHALVCLLEDNGFATQQAEIIVSALVKILEANMD
ĺ			IVYKDMVTKMQQEITFQQVMSQIANVKKDMIILEKSEFSALRAE NEKIKLELHQLKQQVMDEVIKVRTDTKLDFNLEKSRVKBLYSLN
1	ļ		EKKLLELRTEIVALHAQQDRALTQTDRKIETEVAGLKTMLESHK
1	1		LDNIKYLAGSIFTCLTVALGFYRLWI
5625	1	1180	TIPSSAAAQRAGPPAGALEALSPGGARAHAERRGEMRATPLAAP
1			AGSLSRKKRLELDDNLDTERPVQKRARSGPQPRLPPCLLPLSPP
j			TAPDRATAVATASRLGPYVLLEPEEGGRAYQALHCPTGTEYTCR
}			VYPVQEALAVLEPYARLPPHKHVARPTEVLAGTQLLYAFFTRTH
1	1		GDMHSLVRSRHRIPEPEAAVLFRQMATALAHCHQHGLVLRDLKL
			CRFVFADRERKKLVLENLEDSCVLTGPDDSLWDKHACPAYVGPE
1			ILSSRASYSGKAADVWSLGVALFTMLAGHYPFQDSEPVLLFGKI
			RRGAYALPAGLSAPARCLVRCLLRREPAERLTATGILLHPWLRO
Li			DPMPLAPTRSHLWEAAQVVPDGLGLDEAREEEGDREVVLYG
5626	3123	2011	PPRALGSVAMENQVLTPHVYWAQRHRELYLRVELSDVQNPAISI
1			TENVLHFKAQGHGAKGDNVYEFHLEFLDLVKPEPVYKLTQRQVN
l i			ITVQKKVSQWWBRLTKQEKRPLFLAPDFDRWLDESDAEMELRAK
	Į		EEERLNKLRLESEGSPETLTNLRKGYLFMYNLVQFLGFSWIFVN
	1		LTVRFCILGKESFYDTFHTVADMMYFCQMLAVVETINAAIGVTT
	ļ <b>!</b>		SPVLPSLIQLLGRNFILFIIFGTMEEMQNKAVVFFVFYLWSAIE
			IFRYSFYMLTCIDMDWKVLTWLRYTLWIPLYPLGCLAEAVSVIQ
1			SIPIFNETGRFSFTLPYPVKIKVRFSFFLQIYLIMIFLGLYINF
			RHLYKQRRRRYGQKKKKIH
5627	3123	2011	PPRALGSVAMENQVLTPHVYWAQRHRELYLRVELSDVQNPAISI
, j	1		TENVLHFKAQGHGAKGDNVYEFHLEFLDLVKPEPVYKLTQRQVN
1	1		ITVQKKVSQWWERLTKQEKRPLFLAPDFDRWLDESDAEMELRAK
1	i		EEERLNKLRLESEGSPETLTNLRKGYLFMYNLVQFLGFSWIFVN
1			LTVRFCILGKESFYDTFHTVADMMYFCQMLAVVETINAAIGVTT
			SPVLPSLIQLLGRNFILFIIFGTMEEMQNKAVVFFVFYLWSAIE
	1		IFRYSFYMLTCIDMDWKVLTWLRYTLWIPLYPLGCLAEAVSVIQ
, 1			SIPIFNETGRFSFTLPYPVKIKVRFSFFLQIYLIMIFLGLYINF
5628	75	1455	RHLYKQRRRRYGQKKKKIH  VAGAMASKCLKAGFSSGSLKSPGGASGGSTRVSAMYSSSPCKT,P
1			SLSPVARSFSACSVGLGRSSYRATSCLPALCLPAGGFATSYSGG
1 1			
[		ļ	GGWFGEGILTGNEKETMQSLNDRLAGYLEKVRQLEQENASLESR IREWCEQQVPYMCPDYQSYFRTIEELQKKTLCSKAENARLVVEI
1 1	1		DNAKLAADDFRTKYETEVSLRQLVESDINGLRRILDDLTLCKSD
		1	LEAQVESLKEELLCLKKNHEEEVNSLRCQLGDRLNVEVDAAPPV
	1		DLNRVLEEMRCQYBTLVENNRRDAEDWLDTQSEELNQQVVSSSE
	ľ	i	QLQSCQABIIELRRTVNALEIELQAQHSMRDALESTLAETEARY
1		Í	SSQLAQMQCMITNVEAQLAEIRADLERQNQEYQVLLDVRARLEC.
1	l	-	BINTYRGLLESEDSKLPCNPCAPDYSPSKSCLPCLPAASCGPSA
	1	ĺ	ARTNCSARPICVPCPGGRF
5629	2287	938	GRPRSSSDNRNFLRERAGLSSAAVQTRIGNSAASRRSPAARPPV
			PAPPALPRGRPGTEGSTSLSAPAVLVVAVAVVVVVVSAVAWAMA
i i	1	ĺ	NYIHVPPGSPEVPKLNVTVQDQEEHRCREGALSLLQHLRPHWDP
1			QEVILQLFIDGITNKLIGCYVGNTMEDVVLVRIYGNKTELLVDR
			DBEVKSFRVLQAHGCAPQLYCTFNNGLCYEFIQGEALDPKHVCN
		)	PAIFRLIARQLAKIHAIHAHNGWIPKSNLWLKMGKYFSLIPTGF
			The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s

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	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			ADEDINKRFLSDIPSSQILQEEMTWMKEILSNLGSPVVLCHNDL
		[	LCKNIIYNEKQGDVQFIDYEYSGYNYLAYDIGNHFNEFAGVSDV
			DYSLYPDRELQSQWLRAYLEAYKEFKGFGTEVTEKEVEILFIQV
			NQFALASHFFWGLWALIQAKYSTIEFDFLGYAIVRFNQYFKMKP
5630	1104		EVTALKVPE
3630	1194	278	GFWAIAQTCAHHLPPGSPWLVPASPWRLPEMSSFGYRTLTVALF
			TLICCPGSDEKVFEVHVRPKKLAVEPKGSLEVNCSTTCNQPEVG
1			GLETSLDKILLDEQAQWKHYLVSNISHDTVLQCHFTCSGKQESM
]			NSNVSVYQPPRQVILTLQPTLVAVGKSFTIECRVPTVEPLDSLT
1			LFLFRGNETLHYETFGKAAPAPQEATATFNSTADREDGHRNFSC
į			LAVLDLMSRGGNIFHKHSAPKMLEIYEPVSDSQMVIIVTVVSVL LSLFVTSVLLCFIFGQHLRQQRMGTYGVRAAWRRLPQAFRP
5631	1053	290	SRVDDFVRPEPSRAEPSRSGRRRPARRAATMSVFGKLFGAGGGK
			AGKGGPTPQEAIQRLRDTEEMLSKKQEFLEKKIEQELTAAKKHG
	,		TKNKRAALQALKRKKRYEKQLAQIDGTLSTIEFQREALENANTN
1			TEVLKNMGYAAKAMKAAHDNMDIDKVDELMQDIADQQELAEEIS
			TAISKPVGFGBEFDEDELMAELEELEQEELDKNLLEISGPETVP
			LPNVPSIALPSKPAKKKEEEDDDMKELENWAGSM
5632	3	952	VVLGWSPPRRLWWGSLGAAQRPAVPVSGLARSLHVETRRPHRRA
			SVRVARGRLGVWAQPQPLLPRPVGSRREMQPPGPPPAYAPTNGD
			FTFVSSADAEDLSGSIASPDVKLNLGGDFIKESTATTFLRQRGY
1 1			GWLLEVEDDDPEDNKPLLEELDIDLKDIYYKIRCVLMPMPSLGF
			NRQVVRDNPDFWGPLAVVLFFSMISLYGQFRVVSWIITIWIFGS
}			LTIFLLARVLGGEVAYGQVLGVIGYSLLPLIVIAPVLLVVGSFE
1 1			VVSTLIKLFGVFWAAYSAASLLVGEEFKTKKPLLIYPIFLLYIY
5633	771	460	FLSLYTGV
] }		*00	QGCSKTMSVGRPFYRSSEFMEQLLSSHLHQVPFFCCFTVVCLCN CLFENSVSKLYMLCFNFFMSIFFYSLSITKLNLIYLWGLSYQSL
1 1	ì		LLLLLSGHRPWGSSMV
5634	1446	855	PRATGRIRSRAAASRPRAGAGASGAEPRSGRERSRLSGRRAPAM
1			ARNTLSSRFRRVDIDEFDENKFVDEQEEAAAAAAEPGPDFSEVD
1			GLLRQGDMLRAFHAALRNSPVNTKNQAVKERAQGVVLKVLTNFK
1 1	į		SSEIEQAVQSLDRNGVDLLMKYIYKGFEKPTENSSAVLLQWHEK
			ALAVGGLGSIIRVLTARKTV
5635	3	· 943	DRGPRSTATDTGRARVSFWRFPLDPGVKNSNVQISGEKRRFRTL
}			RSLFHPFPVTRSGAPRAVLVGSSWPAKMVAPAVKVARGWSGLAL
1			GVRRAVLQLPGLTQVRWSRYSPEFKDPLIDKEYYRKPVEELTEE
	1		EKYVRELKKTQLIKAAPAGKTSSVFEDPVISKFTNMMMIGGNKV
1 1			LARSLMIQTLEAVKRKQFEKYHAASAEEQATIERNPYTIFHQAL
1 1		ļ	KNCEPMIGLVPILKGGRFYQVPVPLPDRRRRFLAMKWMITECRD
	,		KKHQRTLMPEKLSHKLLEAFHNQGPVIKRKHDLHKMAEANRALA
5636	2253	1143	HYRWW
		****	LEDTICQHPPAEKKLYLYHRKLREVERNGIPRLPKDVPMDTHQG
1	1		LTDVRAKUTGFSEGVVDSVKGGFSSFSQATHSAAGAVVSKPREI ASLIRNKFGSADNIPNLKDSLEEGQVDDAGKALGVISNFQSSPK
1 1	1	1	YGSEEDCSSATSGSVGANSTTGGIAVGASSSKTNTLDMQSSGFD
1 1	1	1	ALLHEIQEIRETQARLEESFETLKEHYQRDYSLIMQTLQEERYR
1		ĺ	CERLEEQLNDLTELHQNEILNLKQELASMEEKIAYQSYERARDI
	!	1	QEALEACQTRISKMELQQQQQQVVQLEGLENATARNLLGKLINI
]	1	1	LLAVMAVLLVFVSTVANCVVPLMKTRNRTFSTLFLVVFIAFLWK
			HWDALFSYVERFFSSPR
5637	948	2532	MSFCGARANAKMMAAYNGGTSAAAAGHHHHHHHHLPHLPPPHLH
1		ļ	HHHHPQHHLHPGSAAAVHPVQQHTSSAAAAAAAAAAAAAAMLNPG
]			QQQPYFPSPAPGQAPGPAAAAPAQVQAAAAATVKAHHHQHSHHP
		1	QQQLDIEPDRPIGYGAFGVVWSVTDPRDGKRVALKKMPNVFQNL
			VSCKRVFRELKMLCFFKHDNVLSALDILQPPHIDYFEBIYVVTE
[	1	İ	LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD
i 1	•		IKPGNLLVNSNCVLKICDFGLARVEELDESRHMTQEVVTQYYRA
	1		PEILMGSRHYSNAIDIWSVGCIFAELLGRRILFQAQSPIQQLDL
			ITDLLGTPSLEAMRTACEGAKAHILRGPHKQPSLPVLYTLSSQA

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	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
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i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			THEAVHLLCRMLVFDPYKRISAKDALAHPYLDEGRLRYHTCMCK
1			CCFSTSTGRVYTSDFEPVTNPKFDDTFEKNLSSVRQVKEIIHQF
1	,		ILEQQKGNRVPLCINPQSAAFKSFISSTVAQPSEMPPSPLVWE
5638	125	1155	DRKMSELDQLRQEAEQLKNQIRDARKACADATLSQITNNIDPVG
			RIQMRTRRTLRGHLAKIYAMHWGTDSRLLVSASQDGKLIIWDSY
1	Ì		TTNKVHAIPLRSSWVMTCAYAPSGNYVACGGLDNICSIYNLKTR
			EGNVRVSRELAGHTGYLSCCRFLDDNQIVTSSGDTTCALWDIET
1	•		GQQTTTFTGHTGDVMSLSLAPDTRLFVSGACDASAKLWDVREGM
1			CRQTFTGHESDINAICFFPNGNAFATGSDDATCRLFDLRADQEL
			MTYSHDNIICGITSVSFSKSGRLLLAGYDDFNCNVWDALKADRA
1			GVLAGHDNRVSCLGVTDDGMAVATGSWDSFLKIWN
5639	125	1155	DRKMSELDQLRQEAEQLKNQIRDARKACADATLSQITNNIDPVG
		1	RIQMRTRRTLRGHLAKIYAMHWGTDSRLLVSASQDGKLIIWDSY
1			TTNKVHAIPLRSSWVMTCAYAPSGNYVACGGLDNICSIYNLKTR
1			EGNVRVSRELAGHTGYLSCCRFLDDNQIVTSSGDTTCALWDIET
1			GQQTTTFTGHTGDVMSLSLAPDTRLFVSGACDASAKLWDVREGM
i i			CRQTFTGHESDINAICFFPNGNAFATGSDDATCRLFDLRADOEL
1			MTYSHDNIICGITSVSFSKSGRLLLAGYDDFNCNVWDALKADRA
			GVLAGHDNRVSCLGVTDDGMAVATGSNDSFLKIWN
5640	280	1092	QQGNKKTMLSHNTMMKQRKQQATAIMKEVHGNDVDGMDLGKKVS
			IPRDIMLEELSHLSNRGARLFKMRQRRSDKYTFENFQYQSRAQI
			NHSIAMQNGKVDGSNLEGGSQQAPLTPPNTPDPRSPPNPDNIAP
			GYSGPLKEIPPEKFNTTAVPKYYQSPWEQAISNDPELLEALYPK
			LFKPEGKAELPDYRSFNRVATPFGGFEKASRMVKFKVPDFELLL
	·		LTDPRFMSFVNPLSGRRSFNRTPKGWISENIPIVITTEPTDDTT
			VPESEDL
5641	27	332	CRHNCNGDVKLLSNQMDKLFAFHLFTFHGLLHFLDGSIQKLIQA
į l			EIILSDNSSILVLENNFLFKVKSKQFIHLIAKKFYISITIVSAS
			NGESFVLSMIVTG
5642	199	1247	ITPCRMDFLVLFLFYLASVLMGLVLICVCSKTHSLKGLARGGAO
			IFSCI TPECLQRAMHGLLHYLFHTRNHTFIVLHLVLQGMVYTEY
Į.			TWEVFGYCQELELSLHYLLLPYLLLGVNLFFFTLTCGTNPGIIT
			KANELLFLHVYEFDEVMFPKNVRCSTCDLRKPARSKHCSVCNWC
1 1			VHRFDHHCVWVNNCIGAWNIRYFLIYVLTLTASAATVAIVSTTF
1 1	ĺ		LVHLVVMSDLYQETYIDDLGHLHVMDTVFLIQYLFLTFPRIVFM
i I	1		LGFVVVLSFLLGGYLLFVLYLAATNQTTNEWYRGDWAWCQRCPL
!!			VAWPPSAEPQVHRNIHSHGLRSNLQEIFLPAFPCHERKKQE
5643	1	847	PSGGVRDVETRGPGSRAARGPRVVMFRRGVGAGAIAKKKLAEAK
1 1			YKERGTVLAEDQLAQMSKQLDMFKTNLEEFASKHKQEIRKNPEF
			RVQFQDMCATIGVDPLASGKGFWSEMLGVGDFYYELGVQIIEVC
[ i			LALKHRNGGLITLEELHQQVLKGRGKFAQDVSQDDLIRAIKKLK
j l			ALGTGFGIIPVGGTYLIQSVPAELNMDHTVVLOLAEKNGYVTVS
i !			EIKASLKWETERARQVLEHLLKEGLAWLDLQAPGEAHYWLPALF
1			TDLYSQEITAEEAREALP
5644	83	1138	PRRMGSWVQLITSVGVQQNHPGWTVAGQFQEKKRFTEEVIEYFQ
	ł		KKVSFVHLKILLTSDEAWKRFVRVAELPREEADALYEALKNLTP
f			YVAIEDKDMQQKEQQFREWFLKEFPQIRWKIQESIERLRVIANE
]			1EKVHRGCVIANVVSGSTGILSVIGVMLAPFTAGLSLSITAAGV
	ļ		GLGIASATAGIASSIVENTYTRSAELTASRLTATSTDOLEALRD
		i	ILHDITPNVLSFALDFDEATKMIANDVHTLRRSKATVGRPLIAW
	1		RYVPINVVETLRTRGAPTRIVRKVARNLGKATSGVLVVLDVVNL
ļ l		i i	VQDSLDLHKGEKSESAELLRQWAQELEENLNELTHIHQSLKAG
5645	537	799	VQSVRDLKRLSPTDPPGDSGNRDVTREDPVTGPLNSASSQVPTL
			YLCLQNSLLGHSSVEDARATMELYOISORIRARRGLPRLAVSD
5646	3745	3328	AEQYGTSPHLLPTMLLSSCLPPANVTTKAATPPPLVLSLTTADP
	5,43	3320	
			AGKPAPCRVTLTLLRASIPATKRASFLSSFIKMFFEELEYILGF
1			LSLLKFHVHVSVYSAICHFQKEGTGNSRSFTCTPELFPRLQTHL RAEGGAO
5647	288	800	
		555	GVIMATSELSCEVSEENCERREAFWAEWKDLTLSTRPEEGCSLH EEDTQRHETYHQQGQCQVLVQRSPWLMMRMGILGRGLQEYQLPY
<u>.</u>			

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-{	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence	1	\=possible nucleotide insertion)
			QRVLPLPIFTPAKMGATKEEREDTPIQLQELLALETALGGQCVD
Ĺ	_		RQEVAEITKQLPPVVPVSKPGALRRSLSRSMSQEAQRG
5648	7	1518	VLSELCGRHEALREVGAEWPPPTCSPNICSGLOOAGNTDWSLTM
			APQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPEK
1			SSTKETERKETKAEEBLDAEVLEVFHPTHEWQALQPGQAVPAGS
1			HVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTNTYTSQDLKS
1			ALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVV
	]		IETDMQIMVRLINKFNSSSSSLEEKIAALFDLEYYVHQMDNAQD
			LLSFGGLQVVINGLNSTEPLVKEYAAFVLGAAFSSNPKVQVEAI
	ł		EGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQROFLK
			LGGLQVLRTLVQEKGTEVLAVRVVTLLYDLVTEKMFABEEAELT
	1		QEMSPEKLQQYRQVHLLPGLWEQGWCEITVHLLALPEHDAREKV
	j		LQTLGVLLTTCRDRYRQDPQLGRTLASLQAEYQVLASLELQDGE
1 '			DEGYFQELLGSVNSLLKELR
5649	1172	3006	MLQEQLDAINEEIRMIQEEKESTELRAEEIETRVTSGSMEALNL
			KQLRKRGSIPTSLTDLSLASASPPLSGRSTPKLTSRSAAQDLDR
1			MGVMTLPSDLRKHRRKLLSPVSREENREDKATIKCETSPPSSPR
1			TLRLEKLGHPALSQEEGKSALEDQGSNPSSSNSSQDSLHKGAKR
1			KGIKSSIGRLFGKKEKGRLIQLSRDGATGHVLLTDSEFSMQEPM
I			VPAKLGTQAEKDRRLKKKHQLLEDARRKGMPFAQWDGPTVVSWL
i			ELWVGMPAWYVAACRANVKSGAIMSALSDTEIQREIGISNALHR
			LKLRLAIQEMVSLTSPSAPPTSRTSSGNVWVTHEEMETLETSTK
1	}		TDSEEGSWAQTLAYGDMNHEWIGNEWLPSLGLPQYRSYFMECLV
1			DARMLDHLTKKDLRVHLKMVDSFHRTSLQYGIMCLKRLNYDRKE
1			LEKRREESQHEIKDVLVWTNDQVVHWVQSIGLRDYAGNLHESGV
]			HGALLALDENFDHNTLALILQIPTQNTQARQVMEREFNNLLALG
ì			TDRKLDDGDDKVFRRAPSWRKRFRPREHHGRGGMLSASABTLPA
			GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD
5650	1172	3006	MLQEQLDAINEEIRMIQEEKESTELRAEEIETRVTSGSMEALNL
1			KQLRKRGSIPTSLTDLSLASASPPLSGRSTPKLTSRSAAQDLDR
			MGVMTLPSDLRKHRRKLLSPVSREENREDKATIKCETSPPSSPR
1			TLRLEKLGHPALSQEEGKSALEDQGSNPSSSNSSQDSLHKGAKR
1	<u> </u>		KGIKSSIGRLFGKKEKGRLIQLSRDGATGHVLLTDSEFSMQEPM
1 1			VPAKLGTQAEKDRRLKKKHQLLEDARRKGMPFAQWDGPTVVSWL
1			ELWYGMPAWYVAACRANVKSGAIMSALSDTEIQREIGISNALHR
j j	i j		LKLRLAIQEMVSLTSPSAPPTSRTSSGNVWVTHEEMETLETSTK TDSEBGSWAQTLAYGDMNHEWIGNEWLPSLGLPQYRSYFMECLV
			DARMLDHLTKKDLRVHLKMVDSFHRTSLQYGIMCLKRLNYDRKE
1 1			LEKRREESQHEIKDVLVWTNDQVVHWVQSIGLRDYAGNLHESGV
			HGALLALDENFOHNTLALILQIPTQNTQARQVMEREFNNLLALG
1 1	. 1		TDRKLDDGDDKVFRRAPSWRKRFRPREHHGRGGMLSASAETLPA
1 1	1		GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD
5651	646	1869	ARQGQRQPWG*EARAKGPASESPRV*EGSGWEGPASP*TPGSTL
1		-	AWGEGAGIR+ASGLTAAGAASAAAA/PPPTRGGPAPAGCGRAPP
1	j		WPAPLRVPTHGRAPAPRSRAAPRAPALSHGTAAAALSPASPAGP
] [		i	ADP*LPGHSSQSPPRG*RWGRSRSAPAPAHPEHPAPAGSASASQ
			QTPGWPGSCCLAQGWQAEPLGAPGAEDG\PVPPQRGFPLGTLGS
	I		PAGSWAGLAGYG*AGAPGTQATAPRAAGQTPVAAAPNCRV*GSA
1 1			PALHRAPAAADPGSPLQAPPRAWASPAAAGPGLSSSDYCGGLGA
, !	j	j	GWRAGISPELLGAAGLSDNWARCPGPGPAE*GGQPGCRTIPASA
	[		CMPSPPVEGSLGLSRKGHGDLPSQAR+GWHECRRARHLVPLPRL
			LGPRGRTGRPSSPS
5652	735	343	HHKKYQHIHQKSFSCPEPACGKSFNFKKHLKEHMKLHSDTRDYI
]		1	CEFCARSFRTSSNLVIHRRIHTGEKPLQCEICGFTCRQKASLNW
L /			HORKHAETVAALRFPCEFCGKRFEKPDSVAAHRSKSHPALLLA
5653	66	1401	RGRLQSRGRLTLGLVLLLLDILGARQHGQRVSHGWKGGFLTAPL
			CFPQPCQPGTRRGRRRSLKEATEPQLAMAEEFVTLKDVGMDFTL
			GDWEQLGLEQGDTFWDTALDNCQDLFLLDPPRPNLTSHPDGSED
[ [	1	1	LEPLAGGSPEATSPDVTETKNSPLMEDFFEEGFSQEI/SRDVIQ
			GWLLELQFRRSLYRGHLVR+FARRSRKSSEV+YCHQRGKSHGMQ

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
İ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
J	sequence		\=possible nucleotide insertion)
	† <del></del>	<del> </del>	ES*IKERTQSCVHRFHGRRFHG\DNVSEKTLTPAKSKEYRGEFF
			SYSDHSQQDSVQEGEKPYQCSECGKSFSGSYRLTOHWITHTREK
l .			PTVHQECEQGFDRKASHSGYPKTHTGYKFYVCNEYGTPFSQSTY
1			LWHQKTHAGEKPCKSQDSDHPPSHDTQSGEHQKTHTDSKSYNCN
			ECGKAFTRIFHLTRHQKIHTRKRYECSKCQATFNLRKHLIQHQK
1			THAANV
5654	3	598	TLPLFPGRRFRGWRRCGAVAARKNSTGGNVSINORRDSVRMSAL
	ì		NWKPFVYGGLASITAECGTFPIDLTKTRFQIQGQTNDAKFKEII
	}	ļ	YRGMLHALVRIGREEGLKALYSG*VGLHAFLCHCSLFHMGIDFR
ĺ	1	1	PRLHRSQVKSLRCV*KEQIA**/MFSLLISTLISKYIYYAADVL
			EKLFYYIQVQTDNNKKICLFKNI
5655	2	867	RPPGIRAPRQLHPAAGRRPDASARPRFRPTVLLHDPFQLSFPPP
	_	1	PLSYPSVFPAVARVLPQRSGDYRAAGMPQLSGGGGGGGGGDPELC
1	1	1	ATDEMIPFKDEGDPQ\REKIFABIVNPEEEGDLADIKSSLVNES
1			EIIPASNGHEVAROAOTSOEPYHDKAREHPDDGKHPDGGLYNKG
1	į	-	PSYSSYSGYIMMPNMNNDPYMSNGSLSPPIPRTSNKVPVVQPSH
ĺ		İ	AVHPLTPLITYSDEHFSPGSHPSHIPSDVNSKQGMSRHPPAPDI
			PTFYPLSPGGGGQITPPLGWQGQP
5656	228	1066	PRRVPPLPEFASGPGAAFFHSGRLQRSLTKDSAGCFSQCRSRAM
			LVLRSGLTKALASRTLAPQVCSSFATGPRQYDGTFYEFRTYYLK
1		1	PSNMNAFMENLKKNIHLRTSYSELVGFWSVEFGGRTNKVFHIWK
1			YDNFPHRAEVRKALANCKEWOEOSIIPNLARIDKOETEITYLIP
			WSKLQKPPKEGVYELAVFQMKPGGPALWGDAFERAINAHVNLGY
		1	TKVVGVFHTEYGELNRVHVLWWNESADSRAAVRHKSHEDPISWG
]		}	GVRESVNYL\VSQQNM
5657	105	1052	1
			T GORLOSPRVOMPVOPPSKDTEEMEAEGDSAAKMNGEEEESEEER
333,	105	1052	GORLOSPRVOMPVOPPSKOTEEMEAEGDSAAEMNGEEEESEEER SGSOTESEEESSEMDDEDYERRRSECVSEMLDLEKOFSELKEKT
]	105	1052	SGSQTESEEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEKL
	105	1032	
	105	1054	SGSQTESEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEXL FRERLSQLRLRLEEVGABRAPEYTEPLGGLQRSLKIRIQVAGIY
	105	1052	SGSQTESEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEXL FRERLSQLRLRLEEVGAERAPEYTEPLGGLQRSLKIRIQVAGIY KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLQGELQERIQR
	105	1052	SGSQTESEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEXL FRERLSQLRLRLEEVGAERAPEYTEPLGGLQRSLKIRIQVAGIY KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLQGELQERIQR LEEDRQSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG
	103	1052	SGSQTESEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEXL FRERLSQLRIRLEEVGABRAPEYTEPLGGLQRSLKIRIQVAGIY KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLQGELQBRIQR LEEDRQSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG PYIVYMLQEIDILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ
5658	2346	3541	SGSQTESEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEXL FRERLSQLRIRLEEVGABRAPEYTEPLGGLQRSLKIRIQVAGIY KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLQGELQBRIQR LEEDRQSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG PYIVYMLQEIDIILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ GDPQSSWHCTQDSRLPPADRRTHRPLRVCPARLLWCCWALPLHL
			SGSQTESEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEXL FRERLSQLRLRLEEVGAERAPEYTEPLGGLQRSLKIRIQVAGIY KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLGGELQBRIQR LEEDRQSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG PYIVYMLQEIDILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ GDPQSSWHCTQDSRLPPADRRTHRPLRVCPARLLWCCWALPLHL ALVWTPPL
			SGSQTESEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEXL FRERLSQLRLRLEEVGAERAPEYTEPLGGLQRSLKIRIQVAGIY KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLQGELQBRIQR LEEDRQSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKAPLVSG PYIVYMLQEIDILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ GDPQSSWHCTQDSRLPPADRRTHRPLRVCPARLLWCCWALPLHL ALVWTPPL TERRVYNPWPEPDPD\CIQEDPWNLFNSIKTLVDNIQRYVEDGK
			SGSQTESEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEXL FRERLSQLRIRLEEVGABRAPEYTEPLGGLQRSLKIRIQVAGIY KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLQGELQBRIQR LEEDRQSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG PYIVYMLQEIDIILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ GDPQSSWHCTQDSRLPPADRRTHRPLRVCPARLLWCCWALPLHL ALVWTPPL  TERRYYNPWPEPDPD\CIQEDPWNLPNSIKTLVDNIQRYVEDGK NQLLLALLKCTDTELQLRRDAIFCQALVAAVCTFSEQLLAALGY RYNNNGEYEESSRDASRKWLEQVAATGVLLHCQSLLSPATVKEE RTMLEDIWVTLSELDNVTFSFKQLDENYVANTNVFYHIEGSRQA
			SGSQTESEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEXL FRERLSQLRLRLEEVGAERAPEYTEPLGGLQRSLKIRIQVAGIY KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLGGELQBRIQR LEEDRQSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG PYIVYMLQEIDILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ GDPQSSWHCTQDSRLPPADRRTHRPLRVCPARLLWCCWALPLHL ALVWTPPL TERRVYNPWPEPDPD\CIQEDPWNLFNSIKTLVDNIQRYVEDGK NQLLLALLKCTDTELQLRRDAIFCQALVAAVCTFSEQLLAALGY RYNNNGEYEESSRDASRKWLEQVAATGVLLHCQSLLSPATVKEE RTMLEDIWVTLSELDNVTFSFKQLDENYVANTNVFYHIEGSRQA LKVIFYLDSYHFSKLPSRLEGGASLRLHTALFTKVLENVEGLPS
			SGSQTESEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEXL FRERLSQLRLRLEEVGAERAPEYTEPLGGLQRSLKIRIQVAGIY KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLGGELQBRIQR LEEDRQSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG PYIVYMLQEIDILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ GDPQSSWHCTQDSRLPPADRRTHRPLRVCPARLLWCCWALPLHL ALVWTPPL TERRVYNPWPEPDPD\CIQEDPWNLFNSIKTLVDNIQRYVEDGK NQLLLALLKCTDTELQLRRDAIFCQALVAAVCTFSEQLLAALGY RYNNNGEYEESSRDASRKWLEQVAATGVLLHCQSLLSPATVKEE RTMLEDIWVTLSELDNVTFSFKQLDENYVANTNVFYHIEGSRQA LKVIFYLDSYHFSKLPSRLEGGASLRLHTALFTKVLENVEGLPS PGSQAAEDLQQDINAQSLEKVQQYYKLRAFYLERSNLPTDAST
			SGSQTESEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEXL FRERLSQLRIRLEEVGABRAPEYTEPLGGLQRSLKIRIQVAGIY KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLQGELQBRIQR LEEDRQSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG PYIVYMLQEIDILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ GDPQSSWHCTQDSRLPPADRRTHRPLRVCPARLLWCCWALPLHL ALVWTPPL TERRVYNPWPEPDPD\CIQEDPWNLFNSIKTLVDNIQRYVEDGK NQLLLALLKCTDTELQLRRDAIFCQALVAAVCTFSEQLLAALGY RYNNNGEYEESSRDASRKWLEQVAATGVLLHCQSLLSPATVKEE RTMLEDIWVTLSELDNVTFSFKQLDENYVANTNYFYHIEGSRQA LKVIFYLDSYHFSKLPSRLEGGASLRLHTALFTKVLENVEGLPS PGSQAAEDLQQDINAQSLBKVQQYYRKLRAFYLERSNLPTDAST TAVKIDQLIRPINALDELCRLMKSPVHPKPGAAGSVGAGLIPIS
			SGSQTESEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEXL FRERLSQLRIRLEEVGABERAPEYTEPLGGLQRSLKIRIQVAGIY KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLQGELQBRIQR LEEDRQSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG PYIVYMLQEIDILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ GDPQSSWHCTQDSRLPPADRRTHRPLRVCPARLLWCCWALPLHL ALVWTPPL TERRVYNPWPEPDPD\CIQEDPWNLFNSIKTLVDNIQRYVEDGK NQLLLALLKCTDTELQLRRDAIFCQALVAAVCTFSEQLLAALGY RYNNNGEYEESSRDASRKWLEQVAATGVLLHCQSLLSPATVKEE RTMLEDIWVTLSELDNVTFSFKQLDENYVANTNVFYHIEGSRQA LKVIFYLDSYHFSKLPSRLEGGASLRLHTALFTKVLENVEGLPS PGSQAAEDLQQDINAQSLBKVQQYYRKLRAPYLERSNLPTDAST TAVKIDQLIRPINA_DELCRLMKSFVHPKPGAAGSVGAGLIP_IS SELCYRLGACQMVMCGTGMQRSTLSVSLEQAAILARSHGLLPKC
			SGSQTESEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEXL FRERLSQLIRLEEVGABERAPEYTEPLGGLQRSLKIRIQVAGIY KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLQGELQBRIQR LEEDRQSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG PYIVYMLQEIDILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ GDPQSSWHCTQDSRLPPADRRTHRPLRVCPARLLWCCWALPLHL ALVWTPPL TERRYYNPWPEPDPD\CIQEDPWNLFNSIKTLVDNIQRYVEDGK NQLLLALLKCTDTELQLRRDAIFCQALVAAVCTFSEQLLAALGY RYNNNGEYEESSRDASRKWLEQVAATGVLLHCQSLLSPATVKEE RTMLEDIWVTLSELDNVTFSFKQLDENYVANTNVFYHIEGSRQA LKVIFYLDSYHFSKLPSRLEGGASLRLHTALFTKVLENVEGLPS PGSQAAEDLQQDINAQSLEKVQQYYKKLRAPYLERSNLPTDAST TAVKIDQLIRPINALDELCRLMKSFVHPKPGAAGSVGAGLIPIS SELCTRLGACQMVMCGTGMQRSTLSVSLEQAATLARSHGLLPKC IMQATDIMRKQGPRVEILAKNLRVKDQMPQGAPRLYRLCQPKMN
5658	2346	3541	SGSQTESEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEXL FRERLSQLRIRLEEVGABRAPEYTEPLGGLQRSLKIRIQVAGIY KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLGBELQBRIQR LEEDRQSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG PYIVYMLQEIDILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ GDPQSSWHCTQDSRLPPADRRTHRPLRVCPARLLWCCWALPLHL ALVWTPPL TERRYNPWPEPDPD\CIQEDPWNLFNSIKTLVDNIQRYVEDGK NQLLLALKCTDTELQLRRDAIFCQALVAAVCTFSEQLLAALGY RYNNNGEYEESSRDASRKWLEQVAATGVLLHCQSLLSPATVKBE RTMLEDIWVTLSELDNVTFSFKQLDENYVANTNVFYHIEGSRQA LKVIFYLDSYHFSKLPSRLEGGASLRLHTALFTKVLENVEGLPS PGSQAAEDLQQDINAQSLEKVQQYYRKLRAPYLERSNLPTDAST TAVKIDQLIRPINALDELCRLMKSPVHPKPGAAGSVGAGLIPIS SELCYRLGACQMVMCGTGMQRSTLSVSLEQAAILARSHGLLPKC IMQATDIMRKQGPRVEILAKNLRVKDQMPQGAPRLYRLCQPKMN GDL
			SGSQTESEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEXL FRERLSQLRIRLEEVGAERAPEYTEPLGGLQRSLKIRIQVAGIY KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLGGELQBRIQR LEEDRQSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG PYIVYMLQEIDILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ GDPQSSWHCTQDSRLPPADRRTHRPLRVCPARLLWCCWALPLHL ALVWTPPL TERRVYNPWPEPDPD\CIQEDPWNLENSIKTLVDNIQRYVEDGK NQLLLALLKCTDTELQLRRDAIFCQALVAAVCTFSEQLLAALGY RYNNNGEYEESSRDASRKWLEQVAATGVLLHCQSLLSPATVKEE RTMLEDIWVTLSELDNVTFSFKQLDENYVANTNVFYHIEGSRQA LKVIFYLDSYHFSKLPSRLEGGASLRLHTALFTKVLENVEGLPS PGSQAAEDLQQDINAQSLEKVQQYYRKLRAFYLERSNLPTDAST TAVKIDQLIRPINA-DELCRLMKSFVHPKPGAAGSVGAGLIPIS SELCYRLGACQMVMCGTGMQRSTLSVSLEQAAILARSHGLLPKC IMQATDIMRKQGPRVEILAKNLRVKDQMPQGAPRLYRLCQPKMN GDL WKRSGEVSFKGELGAWRGNSGRPKIIGRAAEAENEDRTLGRLLP
5658	2346	3541	SGSQTESEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEXL FRERLSQLRIRLEEVGABRAPEYTEPLGGLQRSLKIRIQVAGIY KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLQGELQBRIQR LEEDRQSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG PYIVYMLQEIDILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ GDPQSSWHCTQDSRLPPADRRTHRPLRVCPARLLWCCWALPLHL ALVWTPPL TERRVYNPWPEPDPD\CIQEDPWNLFNSIKTLVDNIQRYVEDGK NQLLLALLKCTDTELQLRRDAIFCQALVAAVCTFSEQLLAALGY RYNNNGEYEESSRDASRKWLEQVAATGVLLHCQSLLSPATVKEE RTMLEDIWVTLSELDNVTFSFKQLDENYVANTNVFYHIEGSRQA LKVIFYLDSYHFSKLPSRLEGGASLRLHTALFTKVLENVEGLPS PGSQAAEDLQQDINAQSLBKVQQYYRKLRAFYLERSNLPTDAST TAVKIDQLIRPINALDELCRLMKSFVHPKPGAAGSVGAGLIPIS SELCYRLGACQMVMCGTGMQRSTLSVSLEQAAILARSHGLLPKC IMQATDIMRKQGPRVEILAKNLRVKDQMPQGAPRLYRLCQPKMN GDL WKRSGEVSPKGELGAWRGNSGRPKIIGRAARAENEDRTLGRLLP GNERSQPRSPLRLLAPQLKAEAAADKGLAPVPPPFSSGHSGPC\
5658	2346	3541	SGSQTESEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEXL FRERLSQLRIRLEEVGABRAPEYTEPLGGLQRSLKIRIQVAGIY KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLQGELQBRIQR LEEDRQSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG PYIVYMLQEIDILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ GDPQSSWHCTQDSRLPPADRRTHRPLRVCPARLLWCCWALPLHL ALVWTPPL TERRVYNPWPEPDPD\CIQEDPWNLFNSIKTLVDNIQRYVEDGK NQLLLALLKCTDTELQLRRDAIFCQALVAAVCTFSEQLLAALGY RYNNNGEYEESSRDASRKWLEQVAATGVLLHCQSLLSPATVKEE RTMLEDIWVTLSELDNVTFSFKQLDENYVANTNVFYHIEGSRQA LKVIFYLDSYHFSKLPSRLEGGASLRLHTALFTKVLENVEGLPS PGSQAAEDLQQDINAQSLBKVQQYYRKLRAPYLERSNLPTDAST TAVKIDQLIRPINA-DELCRLMKSFVHPKPGAAGSVGAGLIP:S SELCYRLGACQMVMCGTGMQRSTLSVSLEQAAILARSHGLLPKC IMQATDIMRKQGPRVEILAKNLRVKDQMPQGAPRLYRLCQPKMN GDL WKRSGEVSPKGELGAWRGNSGRPKTIGRAARAENEDRTLGRLLP GNERSQPRSPLRLLAPQLKAEAAADKGLAPVPPPFSSGHSGPC\ EREGEGQQRGRGRSRRGAHLELKPSPGLRAGAPTDRGRGGPAEVA
5658	2346	3541	SGSQTESEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEXL FRERLSQLRIRLEEVGABRAPEYTEPLGGLQRSLKIRIQVAGIY KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLQGELQBRIQR LEEDRQSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG PYIVYMLQEIDILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ GDPQSSWHCTQDSRLPPADRRTHRPLRVCPARLLWCCWALPLHL ALVWTPPL TERRYYNPWPEPDPD\CIQEDPWNLFNSIKTLVDNIQRYVEDGK NQLLLALLKCTDTELQLRRDAIFCQALVAAVCTFSEQLLAALGY RYNNNOEYEESSRDASRKWLEQVAATGVLLHCQSLLSPATVKEE RTMLEDIWVTLSELDNVTFSFKQLDENYVANTNVFYHIEGSRQA LKVIFYLDSYHFSKLPSRLEGGASLRLHTALFTKVLENVEGLPS PGSQAAEDLQQDINAQSLEKVQQYYRKLAFYLERSNLPTDAST TAVKIDQLIRPINALDELCRLMKSFVHPKPGAAGSVGAGLIPIS SELCTRLGACQMVMCGTGMQRSTLSVSLEQAATLARSHGLLPKC IMQATDIMRKQGPRVEILAKNLRVKDQMPQGAPRLYRLCQPKMN GDL WKRSGEVSPKGELGAWRGNSGRPKIIGRAAEAENEDRTLGRLLP GNERSQPRSPLRLLAPQLKAEAAADKGLAPVPPPFSSGHSGPC\ EREGEGQRGRGRSRRGAHLELKPSPGLRAGAPTDRGRGGPAEVA AAGGRRMVQKESQATLEERESELSSNPAASAGASLEPPAAPAPG
5658	2346	3541	SGSQTESEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEXL FRERLSQLIRLEEVGABRAPEYTEPLGGLQRSLKIRIQVAGIY KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLQGELQBRIQR LEEDRQSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG PYIVYMLQEIDILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ GDPQSSWHCTQDSRLPPADRRTHRPLRVCPARLLWCCWALPLHL ALVWTPPL TERRYYNPWPEPDPD\CIQEDPWNLFNSIKTLVDNIQRYVEDGK NQLLLALLKCTDTELQLRRDAIFCQALVAAVCTFSEQLLAALGY RYNNNGEYEESSRDASRKWLEQVAATGVLLHCQSLLSPATVKEE RTMLEDIWVTLSELDNVTFSFKQLDENYVANTNVFYHIEGSRQA LKVIFYLDSYHFSKLPSRLEGGASLRLHTALFTKVLENVEGLPS PGSQAAEDLQQDINAQSLEKVQQYYRKLRAPYLERSNLPTDAST TAVKIDQLIRPINALDELCRLMKSFVHPKPGAAGSVGAGLIPIS SELCTRLGACQMVMCGTGMQRSTLSVSLEQAATLARSHGLLPKC IMQATDIMRKQGPRVEILAKNLRVKDQMPQGAPRLYRLCQPKMN GDL WKRSGEVSFKGELGAWRGNSGRPKIIGRAAEAENEDRTLGRLLP GNERSQPRSPLRLLAPQLKAEAAADKGLAPVPPPFSSGHSGPC\ EREGEGQRGRGRSRRGAHLELKPSFGLRAGAPTDRGRGGPAEVA AAGGRRMVQKESQATLEERESELSSNPAASAGASLEPPAAPAPG EDNPAGAGG\AAVAGAAGGARRFLCGVVEGFYGRPWVMEQRKEL
5659	2346	3541 696	SGSQTESEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEXL FRERLSQLRIRLEEVGABRAPEYTEPLGGLQRSLKIRIQVAGIY KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLGBELQBRIQR LEEDRQSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG PYIVYMLQEIDIILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ GDPQSSWHCTQDSRLPPADRRTHRPLRVCPARLLWCCWALPLHL ALVWTPPL TERRYNPWPEPDPD\CIQEDPWNLFNSIKTLVDNIQRYVEDGK NQLLLALKCTDTELQLRRDAIFCQALVAAVCTFSEQLLAALGY RYNNNGEYEESSRDASRKWLEQVAATGVLLHCQSLLSPATVKEE RTMLEDIWVTLSELDNVTFSFKQLDENYVANTNVFYHIEGSRQA LKVIFYLDSYHFSKLPSRLEGGASLRLHTALFTKVLENVEGLPS PGSQAAEDLQQDINAQSLEKVQQYYRKLRAPYLERSNLPTDAST TAVKIDQLIRPINALDELCRLMKSPVHPKPGAAGSVGAGLIPIS SELCYRLGACQMVMCGTGMQRSTLSVSLEQAAILARSHGLLPKC IMQATDIMRKQGPRVEILAKNLRVKDQMPQGAPRLYRLCQPKMN GDL WKRSGEVSPKGELGAWRGNSGPPKIIGRAAEAENEDRTLGRLLP GNERSQPRSPLRLLAPQLKAEAAADKGLAPVPPFFSSGHSGPC\ EREGEGQRGRGRSRRGAHLELKPSPGLRAGAPTDRGRGGPAEVA AAGGRRMVQKESQATLEERESELSSNPAASAGASLEPPAAPAPG EDNPAGAGG\AAVAGAAGGARRFLCGVVEGFYGRPWVMEQRKEL FRRLQKWELNTYL
5658	2346	3541	SGSQTESEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEXL FRERLSQLRIRLEEVGABRAPEYTEPLGGLQRSLKIRIQVAGIY KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLQGELQBRIQR LEEDRQSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG PYIVYMLQEIDILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ GDPQSSWHCTQDSRLPPADRRTHRPLRVCPARLLWCCWALPLHL ALVWTPPL TERRVYNPWPEPDPD\CIQEDPWNLFNSIKTLVDNIQRYVEDGK NQLLLALLKCTDTELQLRRDAIFCQALVAAVCTFSEQLLAALGY RYNNNGEYEESSRDASRKWLEQVAATGVLLHCQSLLSPATVKEE RTMLEDIWVTLSELDNVTFSFKQLDENYVANTNYFYHIEGSRQA LKVIFYLDSYHFSKLPSRLEGGASLRLHTALFTKVLENVEGLPS PGSQAAEDLQQDINAQSLBKVQQYYRKLRAFYLERSNLPTDAST TAVKIDQLIRPINA_DELCRLMKSPVHPKPGAAGSVGAGLIPIS SELCYRLGACQMVMCGTGMQRSTLSVSLEQAAILARSHGLLPKC IMQATDIMRKQGPRVEILAKNLRVKDQMPQGAPRLYRLCQPKMN GDL WKRSGEVSFKGELGAWRGNSGRPKIIGRAAEAENEDRTLGRLLP GNERSQPRSPLRLLAPQLKAEAAADKGLAPVPPPFSSGHSGPC\ EREGEGQGGGRGRSRRGAHLELKPSFGLRAGAPTDRGRGGPAEVA AAGGRRMVQKESQATLEERESELSSNPAASAGASLEPPAAPAPG EDNPAGAGG\AAVAGAAGAAGGARRFLCGVVEGFYGRPWVMEQRKEL FRRLQKWELNTYL PVTMWAFSELPMPLLINLIVSLLGFVATVTLIPAFRGHFIAARL
5659	2346	3541 696	SGSQTESEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEXL FRERLSQLRIRLEEVGABRAPEYTEPLGGLQRSLXIRIQVAGIY KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLQGELQBRIQR LEEDRQSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG PYIVYMLQEIDILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ GDPQSSWHCTQDSRLPPADRRTHRPLRVCPARLLWCCWALPLHL ALVWTPPL TERRVYNPWPEPDPD\CIQEDPWNLFNSIKTLVDNIQRYVEDGK NQLLLALLKCTDTELQLRRDAIFCQALVAAVCTFSEQLLAALGY RYNNNGEYEESSRDASRKWLEQVAATGVLLHCQSLLSPATVKEE RTMLEDIWVTLSELDNVTFSFKQLDENYVANTNVPYHIEGSRQA LKVIFYLDSYHFSKLPSRLEGGASLRLHTALFTKVLENVEGLPS PGSQAAEDLQQDINAQSLBKVQQYYKKLRAPYLERSNLPTDAST TAVKIDQLIRPINALDELCRLMKSFVHPKPGAAGSVGAGLIPIS SELCYRLGACQMVMCGTGMQRSTLSVSLEQAAILARSHGLLPKC IMQATDIMRKQGPRVEILAKNLRVKDQMPQGAPRLYRLCQPKMN GDL WKRSGEVSPKGELGAWRGNSGRPKIIGRAAEAENEDRTLGRLLP GNERSQPRSPLRLLAPQLKAEAAADKGLAPVPPFFSSGHSGPC\ EREGEGQRGRGRSRRGAHLELKPSPGLRAGAPTDRGRGGPAEVA AAGGRRMVQKESQATLEERESELSSNPAASAGASLEPPAAPAPG EDNPAGAGG\AAVAGAAGGARRFLCGVVEGFYGRWVMEQRKEL FRRLQKWELNTYL PVTMWAFSELPMPLLINLIVSLLGFVATVTLIPAFRGHFIAARL CGQDLNKTSRQQIPESQGVISGAVFLIILFCFIPFFFLNCFVKE
5659	2346	3541 696	SGSQTESEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEXL FRERLSQLRIRLEEVGABRAPEYTEPLGGLQRSLXIRIQVAGIY KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLQGELQBRIQR LEEDRQSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG PYIVYMLQEIDILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ GDPQSSWHCTQDSRLPPADRRTHRPLRVCPARLLWCCWALPLHL ALVWTPPL TERRVYNPWPEPDPD\CIQEDPWNLFNSIKTLVDNIQRYVEDGK NQLLLALLKCTDTELQLRRDAIFCOALVAAVCTFSEQLLAALGY RYNNNGEYEESSRDASRKWLEQVAATGVLLHCQSLLSPATVKEE RTMLEDIWVTLSELDNVTFSFKQLDENYVANTNVFYHIEGSRQA LKVIFYLDSYHFSKLPSRLEGGASLRLHTALFTKYLENVEGLPS PGSQAAEDLQQDINAQSLBKVQQYYKKLRAFYLERSNLPTDAST TAVKIDQLIRPINA_DELCRLMKSFVHPKPGAAGSVGAGLIPIS SELCYRLGACQMVMCGTGMQRSTLSVSLEQAAILARSHGLLPKC IMQATDIMRKQGPRVEILAKNLRVKDQMPQGAPRLYRLCQPKMN GDL WKRSGEVSPKGELGAWRGNSGRPKIIGRAAEAENEDRTLGRLLP GNERSQPRSPLRLLAPQLKAEAAADKGLAPVPPPFSSGHSGPC\ EREGEGQRGRGRSRRGAHLELKPSPGLRAGAPTDRGRGGPAEVA AAGGRRMVQKESQATLEERESELSSNPAASAGASLEPPAAPAPG EDNPAGAGG\AAVAGAAGGARRFLCGVVEGFYGRPWVMEQRKEL FRRLQKWELNTYL PVTMWAFSELPMPLLINLIVSLLGFVATVTLIPAFRGHFIAARL CGQDLNKTSRQQIPESQGVISGAVFLIILFCFIPFFFLNCFVKE QRKAFPHHEFVALIGALLAICCMIFLGFADDVLNLRWRHKLLLP
5659	2346	3541 696	SGSQTESEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEXL FRERLSQLRIRLEEVGABRAPEYTEPLGGLQRSLKIRIQVAGIY KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLQGELQBRIQR LEEDRQSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG PYIVYMLQEIDILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ GDPQSSWHCTQDSRLPPADRRTHRPLRVCPARLLWCCWALPLHL ALVWTPPL TERRYYNPWPEPDPD\CIQEDPWNLFNSIKTLVDNIQRYVEDGK NQLLLALLKCTDTELQLRRDAIFCQALVAAVCTFSEQLLAALGY RYNNNOEYEESSRDASRKWLEQVAATGVLLHCQSLLSPATVKEE RTMLEDIWVTLSELDNVTFSFKQLDENYVANTNVFYHIEGSRQA LKVIFYLDSYHFSKLPSRLEGGASLRLHTALFTKVLENVEGLPS PGSQAAEDLQQDINAQSLBKVQQYYRKLAFYLERSNLPTDAST TAVKIDQLIRPINALDELCRLMKSFVHPKPGAAGSVGAGLIPIS SELCYRLGACQMVMCGTGMQRSTLSVSLEQAATLARSHGLLPKC IMQATDIMRKQGPRVEILAKNLRVKDQMPQGAPRLYRLCQPKMN GDL WKRSGEVSPKGELGAWRGNSGRPKIIGRAAEAENEDRTLGRLLP GNERSQPRSPLRLLAPQLKAEAAADKGLAPVPPPFSSGHSGPC\ EREGEGQRGRGRSRRGAHLELKPSPGLRAGAPTDRGRGGPAEVA AAGGRRMVQKESQATLEERESELSSNPAASAGASLEPPAAPAPG EDNPAGAGG\AAVAGAAGGARRFLCGVVEGFYGRPWVMEQRKEL FRRLQKWELNTYL PVTMWAFSELPMPLLINLIVSLLGFVATVTLIPAFRGHFIAARL CGQDLNKTSRQQIPESQGVISGAVFLIILFCFIPFPFLNCFVKE QRKAFPHHEFVALIGALLAICCMIFLGFADDVLNLRWRHKLLLP TAASLPLLMVYFTNFGNTTIVVPKPFRPILGLHLDLGR*SYHCC
5659 5660	2346	696	SGSQTESEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEXL FRERLSQLRIRLEEVGABRAPEYTEPLGGLQRSLKIRIQVAGIY KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLQGELQBRIQR LEEDRQSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG PYIVYMLQEIDILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ GDPQSSWHCTQDSRLPPADRRTHRPLRVCPARLLWCCWALPLHL ALVWTPPL TERRYYNPWPEPDPD\CIQEDPWNLFNSIKTLVDNIQRYVEDGK NQLLLALLKCTDTELQLRRDAIFCQALVAAVCTFSEQLLAALGY RYNNNGEYEESSRDASRKWLEQVAATGVLLHCQSLLSPATVKEE RTMLEDIWVTLSELDNVTFSFKQLDENYVANTNVFYHIEGSRQA LKVIFYLDSYHFSKLPSRLEGGASLRLHTALFTKVLENVEGLPS PGSQAAEDLQQDINAQSLEKVQQYYRKLRAPYLERSNLPTDAST TAVKIDQLIRPINALDELCRLMKSFVHPKPGAAGSVGAGLIPIS SELCYRLGACQMVMCGTGMQRSTLSVSLEQAATLARSHGLLPKC IMQATDIMRKQGPRVEILAKNLRVKDQMPQGAPRLYRLCQPKMN GDL WKRSGEVSFKGELGAWRGNSGRPKIIGRAAEAENEDRTLGRLLP GNERSQPRSPLRLLAPQLKAEAAADKGLAPVPPPFSSGHSGPC\ EREGEGQRGRGRSRRGAHLELKPSFGLRAGAPTDRGRGGPAEVA AAGGRRMVQKESQATLEERESELSSNPAASAGASLEPPAAPAPG EDNPAGAGG\AAVAGAAGGARRFLCGVVEGFYGRPWVMEQRKEL FRRLQKWELNTYL PVTWMAFSELPMPLLINLIVSLLGFVATVTLIPAFRGHFIAARL CGQDLNKTSRQQIPESQGVISGAVFLIILFCFIPFFFLNCFVKE QRKAFPHHEFVALIGALLAICCMIFLGFADDVLNLRWRHKLLLP TAASLPLLMVYFTNFGNTTIVVPKPFRPILGIHLDLGR*SYHCC PYGTYFREPFLVLHILLQVFLFCLCVFPDPFW
5659	2346	3541 696	SGSQTESEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEXL FRERLSQLRIRLEEVGABRAPEYTEPLGGLQRSLKIRIQVAGIY KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLQGELQBRIQR LEEDRQSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG PYIVYMLQEIDIILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ GDPQSSWHCTQDSRLPPADRRTHRPLRVCPARLLWCCWALPLHL ALVWTPPL TERRYYNPWPEPDPD\CIQEDPWNLFNSIKTLVDNIQRYVEDGK NQLLLALLKCTDTELQLRRDAIFCQALVAAVCTFSEQLLAALGY RYNNNGEYEESSRDASRKWLEQVAATGVLLHCQSLLSPATVKEE RTMLEDIWVTLSELDNVTFSFKQLDENYVANTNVFYHIEGSRQA LKVIFYLDSYHFSKLPSRLEGGASLRLHTALFTKVLENVEGLPS PGSQAAEDLQQDINAQSLBKVQQYYRKLRAPYLERSNLPTDAST TAVKIDQLIRPINALDELCRLMKSFVHPKPGAAGSVGAGLIPIS SELCYRLGACQMVMCGTGMQRSTLSVSLEQAATLARSHGLLPKC IMQATDIMRKQGPRVEILAKNLRVKDQMPQGAPRLYRLCQPKMN GDL WKRSGEVSPKGELGAWRGNSGRPKIIGRAAEAENEDRTLGRLLP GNBRSQPRSPLRLLAPQLKAEAAADKGLAPVPPPFSSGHSGPC\ EEGEGQRGRGRSRRGAHLELKPSPGLRAGAPTDRGRGGPAEVA AAGGRRMVQKESQATLEERESELSSNPAASAGASLEPPAAPAPG EDNPAGAGG\AAVAGAAGGARRFLCGVVEGFYGRPWVMEQRKEL FRRLQKWELNTYL PYTWWAFSELPMPLLINLIVSLLGFVATVTLIPAFRGHFIAARL CGQDLNKTSRQQIPESQGVISGAVFLIILFCFIPFPFLNCFVKE QRKAFPHHEFVALIGALLAICCMIFLGFADDVLNLRWRHKLLLP TAASLPLLMVYFTNFGNTTIVVPKPFRPILGHLDLGR*SYHCC PYGTYFREPFLVHILLLQVFLFCLCVFPDPFW LNLYFSPCGGIPKLPGLPREAAAALGASFLAEAPLPVTVRGSGL
5659 5660	2346	696	SGSQTESEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEXL FRERLSQLRIRLEEVGABRAPEYTEPLGGLQRSLXIRIQVAGIY KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLQGELQBRIQR LEEDRQSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG PYIVYMLQEIDILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ GDPQSSWHCTQDSRLPPADRRTHRPLRVCPARLLWCCWALPLHL ALVWTPPL TERRVYNPWPEPDPD\CIQEDPWNLFNSIKTLVDNIQRYVEDGK NQLLLALLKCTDTELQLRRDAIFCQALVAAVCTFSEQLLAALGY RYNNNGEYEESSRDASRKWLEQVAATGVLLHCQSLLSPATVKEE RTMLEDIWVTLSELDNVTFSFKQLDENYVANTNVFYHIEGSRQA LKVIFYLDSYHFSKLPSRLEGGASLRLHTALFTKVLENVEGLPS PGSQAAEDLQQDINAQSLBKVQQYYRKLRAFYLERSNLPTDAST TAVKIDQLIRPINALDELCRLMKSFVHPKPGAAGSVGAGLIP_S SELCYRLGACQMVMCGTGMQRSTLSVSLEQAAILARSHGLLPKC IMQATDIMRKQGPRVEILAKNLRVKDQMPQGAPRLYRLCQPKMN GDL WKRSGEVSPKGELGAWRGNSGRPKIIGRAAEAENEDRTLGRLLP GNBRSQPRSPLRLLAPQLKAEAAADKGLAPVPPPFSSGHSGPC\ EREGEGQRGRGRSRRGAHLELKPSPGLRAGAPTDRGRGGPAEVA AAGGRRMVQKESQATLEERESELSSNPAASAGASLEPPAAPAPG EDNPAGAGG\AAVAGAAGGARRFLCGVVEGFYGRPWVMEQRKEL FRRLQKWELNTYL PVTMWAFSELPMPLLINLIVSLLGFVATVTLIPAFRGHFIAARL CGQDLNKTSRQQIPESQGVISGAVFLIILFCFIPFFFLNCFVKE QRKAPPHHEFVALIGALLAICCMIFLGFADDVLNIRWRHKLLLP TAASLPLLMVYFTNFGNTTIVVPKPFRPILGHLDLGR*SYHCC PYGTYFREPFLVLHILLQVFLFCLCVFPDPFW LNLYFSPCGGIPKLPGLPREAAAALGASFLAEAPLPVTVRGSGL AGMAVTCDPKAFLSICFVTLVFLQLPLASICQN*GTDSCASRGK
5659 5660	2346	696	SGSQTESEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEXL FRERLSQLRIRLEEVGABRAPEYTEPLGGLQRSLKIRIQVAGIY KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLQGELQBRIQR LEEDRQSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG PYIVYMLQEIDILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ GDPQSSWHCTQDSRLPPADRRTHRPLRVCPARLLWCCWALPLHL ALVWTPPL TERRVYNPWPEPDPD\CIQEDPWNLFNSIKTLVDNIQRYVEDGK NQLLLALLKCTDTELQLRRDAIFCQALVAAVCTFSEQLLAALGY RYNNNGEYEESSRDASRKWLEQVAATGVLLHCQSLLSPATVKEE RTMLEDIWVTLSELDNVTFSFKQLDENYVANTNVFYHIEGSRQA LKVIFYLDSYHFSKLPSRLEGGASLRLHTALFTKVLENVEGLPS PGSQAAEDLQQDINAQSLBKVQQYYKKLRAPYLERSNLPTDAST TAVKIDQLIRPINA-DELCRLMKSFVHPKPGAAGSVGAGLIP:3 SELCYRLGACQMVMCGTGMQRSTLSVSLEQAAILARSHGLLPKC IMQATDIMRKQGPRVEILAKNLRVKDQMPQGAPRLYRLCQPKMN GDL WKRSGEVSPKGELGAWRGNSGRPKIIGRAAEAENEDRTLGRLLP GNERSQPRSPLRLLAPQLKAEAAADKGLAPVPPPFSSGHSGPC\ EREGEGQRGRGRSRRGAHLELKPSPGLRAGAPTDRGRGGPAEVA AAGGRRMVQKESQATLEERESELSSNPAASAGASLEPPAAPAPG EDNPAGAGG\AAVAGAAGGARRFLCGVVEGFYGRPWVMEQRKEL FRRLQKWELNTYL PVTWMAFSELPMPLLINLIVSLLGFVATVTLIPAFRGHFIAARL CGQDLNKTSRQQIPESQGVISGAVFLIILFCFIPFPFLNCFVKE QRKAFPHHEFVALIGALLAICCMIFLGFADDVLNLRWRHKLLLP TAASLPLLMVYFTNFGNTTIVVPKPFRPILGLHLDLGR*SYHCC PYGTYFREPFLVLHILLQVFLFCLCVFPDPFW LNLYPSPCGGIPKLPGLPREAAAALGASFLEAPLPVTVRGSGL AGMAVTCDPKAFISICFVTLVFIQLPLASICQN*GTDSCASRGK ADPDVTGPHAPILAMAGGHVELQCQLFPNISAEDMELRWYRCQP
5659 5660	2346	696 853	SGSQTESEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEXL FRERLSQLRIRLEEVGABERAPEYTEPLGGLQRSLKIRIQVAGIY KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLQGELQBRIQVE LEEDRQSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG PYIVYMLQEIDILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ GDPQSSWHCTQDSRLPPADRRTHRPLRVCPARLLWCCWALPLHL ALVWTPPL TERRVYNPWPEPDPD\CIQEDPWNLFNSIKTLVDNIQRYVEDGK NQLLLALLKCTDTELQLRRDAIFCQALVAAVCTFSEQLLAALGY RYNNNGEYEESSRDASRKWLEQVAATGVLLHCQSLLSPATVKEE RTMLEDIWVTLSELDNVTFSFKQLDENYVANTNVFYHIEGSRQA LKVIFYLDSYHFSKLPSRLEGGASLRLHTALFTKYLENVEGLPS PGSQAAEDLQQDINAQSLBKVQQYYKKLRAFYLERSNLPTDAST TAVKIDQLIRPINALDELCRLMKSFVHPKPGAAGSVGAGLIPIS SELCYRLGACQMVMCGTGMQRSTLSVSLEQAAILARSHGLLPKC IMQATDIMRKQGPRVEILAKNLRVKDQMPQGAPRLYRLCQPKMN GDL WKRSGEVSFKGELGAWRGNSGRPKIIGRAAEAENEDRTLGRLLP GNERSQPRSPLRLLAPQLKAEAAADKGLAPVPPPFSSGHSGPC\ EREGEGQRGRGRSRRGAHLELKPSPGLRAGAPTDRGRGGPAEVA AAGGRRMVQKESQATLEERESELSSNPAASAGASLEPPAAPAPG EDNPAGAGG\AAVAGAAGGARRFLCGVVEGFYGRPWVMEQRKEL FRRLQKWELNTYL PVTMWAFSELPMPLLINLIVSLLGFVATVTLIPAFRGHFIAARL CGQDLNKTSRQQIPESQGVISGAVFLIILFCFIPFFFLNCFVKE QRKAFPHHEFVALIGALLAICCMIFLGFADDVLNLRWRHKLLLP TAASLPLLMVYFTNFGNTTIVVPKPFRPILGLHLDLGR*SYHCC PYGTYFREPFLUHTILLQVFLFCLCVFPDPFW LNLYFSPCGGIPKLPGLPREAAALGASFLAEAPLPVTVRGSGL AGMAVTCDPKAFLSICFVTLVFLQLPLASICQN*GTDSCASRGK ADFDVTGPHAPILAMAGGHVELQCQLFPNISAEDMELRWYRCQP SLAVHMHERGMDMDGEQKWQYRGRT
5659 5660	2346	696	SGSQTESEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEXL FRERLSQLRIRLEEVGABRAPEYTEPLGGLQRSLKIRIQVAGIY KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLQGELQBRIQR LEEDRQSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG PYIVYMLQEIDILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ GDPQSSWHCTQDSRLPPADRRTHRPLRVCPARLLWCCWALPLHL ALVWTPPL TERRVYNPWPEPDPD\CIQEDPWNLFNSIKTLVDNIQRYVEDGK NQLLLALLKCTDTELQLRRDAIFCQALVAAVCTFSEQLLAALGY RYNNNGEYEESSRDASRKWLEQVAATGVLLHCQSLLSPATVKEE RTMLEDIWVTLSELDNVTFSFKQLDENYVANTNVFYHIEGSRQA LKVIFYLDSYHFSKLPSRLEGGASLRLHTALFTKVLENVEGLPS PGSQAAEDLQQDINAQSLBKVQQYYKKLRAPYLERSNLPTDAST TAVKIDQLIRPINA-DELCRLMKSFVHPKPGAAGSVGAGLIP:3 SELCYRLGACQMVMCGTGMQRSTLSVSLEQAAILARSHGLLPKC IMQATDIMRKQGPRVEILAKNLRVKDQMPQGAPRLYRLCQPKMN GDL WKRSGEVSPKGELGAWRGNSGRPKIIGRAAEAENEDRTLGRLLP GNERSQPRSPLRLLAPQLKAEAAADKGLAPVPPPFSSGHSGPC\ EREGEGQRGRGRSRRGAHLELKPSPGLRAGAPTDRGRGGPAEVA AAGGRRMVQKESQATLEERESELSSNPAASAGASLEPPAAPAPG EDNPAGAGG\AAVAGAAGGARRFLCGVVEGFYGRPWVMEQRKEL FRRLQKWELNTYL PVTWMAFSELPMPLLINLIVSLLGFVATVTLIPAFRGHFIAARL CGQDLNKTSRQQIPESQGVISGAVFLIILFCFIPFPFLNCFVKE QRKAFPHHEFVALIGALLAICCMIFLGFADDVLNLRWRHKLLLP TAASLPLLMVYFTNFGNTTIVVPKPFRPILGLHLDLGR*SYHCC PYGTYFREPFLVLHILLQVFLFCLCVFPDPFW LNLYPSPCGGIPKLPGLPREAAAALGASFLEAPLPVTVRGSGL AGMAVTCDPKAFISICFVTLVFIQLPLASICQN*GTDSCASRGK ADPDVTGPHAPILAMAGGHVELQCQLFPNISAEDMELRWYRCQP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion,
<b> </b>	sequence	L	\=possible nucleotide insertion) LHVNDGSSLESLQVVADSGLDSRELTFGSSVEVQGQLIKSPSKR
1			QNVELKAEKIKVIGNCDAKDFPIKYKERHPLEYLRQYPHFRCRT
		1	NVLGSILRIRSEATAAIHSFFKDSGFVHIHTPIITSNDSEGAGE
i			LFQLEPSGKLKVPEENFFNVPAFLTVSGQLHLEVMSGAFTQVFT
		1	FGPTFRAENSQSRRHLAEFYMIEAEISFVDSLQDLMQVIEELFK
1		1	ATTMMVLSKCPEDVELCHKFIAPGQKDRL*HMLKNNFLIISYTE
			AVEILKQASQNFTFTPEWGADLRTEHEKYLVKHCGNIPVFVINY
			PLTLKPFYMRDNEDGPQELEGSVA*HSLGLMILLSIVVIGQP
5663	119	698	PADIGRSTAKTPGPPRSLEMDDPRYGMCPLKGASGCPGAERSLL
1.		Ì	VQSYFEKGPLTFRDVAIEFSLEEWQCLDSAQQGLYRKVMLENYR
1			NLVFLGIALTKPDLITCLEQGKEPWNIKRHEMVAKPPVICSHFP
1			QDLWAEQDIKDSFQEAILKKYGKYGHANFQLQKGCKSVDECKVH KEHDNKLNQCLIPKKKK
5664	118	572	SLSMESNHKSGDGLSGTQKEAALRALVQRTGYSLVQENGQRKYG
			GPPPGWDAAPPERGCEIFIGKLPRDLFEDELIPLCEKIGKIYEM
			RMMMDFNGNNRGYAFVTFSNKVEAKNAIKQLNNYEIRNGRLLGV
1	}	İ	CASVDNCRLFVGGIPKTKK
5665	347	702	VVQHLIILLHCERTSPAMITSELPVLQDSTNETTAHSDAGSELE
i		İ	ETEVKGKRKRGRPGRPPSTNKKPRKSPGEKSRIEAGIRGAGRGR
			ANGHPQQNGEGEPVTLPEVVKLGKSAMQRC
5666	213	540	VSCLPTSCKMITLNNQDQPVPFNSSHPDEYKIAALVFYSCIFII
			GLFVNITALWVFSCTTKKRTTVTIYMMNVALVDLIFIMTLPFRM
5667			FYYAKDEWPFGEYFCQILGA
3667	1	695	HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKRRRARVGSP
			SGDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFLTGLARSKGFR VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD
i			ISWLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAWMPAYACOR
			PTPLTHHNTGLSEALEILAEAAGFEGSEGRLLTFCRAASVLKAL
			PSPVTTLSQLQ
5668	691	894	CSFLFCIPDLFLQFLLGRKEEBAVLVGGEWSPSLDGLDPQADPQ
			VLVRTAIRCAQAQTGIDLSGCTKW
5669	407	1	DSGAPEGLSPLMSTQEGLSMHAHPQAYTPFIYLHARKRRGEIGD
			ADSRFNDRYAHKSAQLYFLYFVCWIFQDVYYFTIKEKNHFFFPK
1			ARGAPTKYSGSPIGSPTTTPPTRPPSFNLHPAPHLLASMQLQKL
5670	3	373	SSECLTMAWIPLLLPLLILCTVSVASYELAQPSSVSVSPGQTAK
] 55.5	_	3/3	ITCSGDVLAKKYARWFQQKPGQAPVLVIYKDTERPSGIPERFSG
			STSGTTVTLTISGAQVEDEADYFCYSATDNFLWVF
5671	280	524	KFPPKKTPPHLGMESAITLWQFLLQLLLDQKHEHLICWTSNDGE
	<u> </u>		FKLLKAKKVAKLWGLRKNKTNMNYDKLSRALRLLFMT
5672	2	557	FVPATPDPGVWLPPSRDPAMAKRSSLYIRIVEGKNLPAKDITGS
			SDPYCIVKVDNBPIIRTATVWKTLCPFWGEEYQVHLPPTFHAVA
			FYVMDEDALSRDDVIGKVCLTRDTIASHPKGKFSLPSHTGLPSP
		į	WPPSHSETSPLGSVWSPAQGKPFLLSPEAGATFCTPGLCSAACS
5673	327	696	QAWLLLPLP
30/3	341	070	ITVÄDQISHWSAGRIKNRTRIPECIHSSAATTLAGPHTMEGESV KLSSQTLIQAGDDEKNQRTITVNPAHMGKAFKVMNELRSKQLLC
		·	DVMIVAEDVEIEAHRVVLAACSPYFCAMFTGDMS
5674	17	984	GGGSMEGESTSAVLSGFVLGALAFOHLNTDSDTEGFLLGEVKGE
			AKNSITDSQMDDVEVVYTIDIQKYIPCYQLFSFYNSSGEVNEQA
j	l		LKKILSNVKKNVVGWYKFRRHSDQIMTFRERLLHKNLQEHFSNQ
			DLVFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLG
			MSEQLGYKTVSGSCMSTGFSRAVQTHSSKFFEEDGSLKEVHKIN
Į			EMYASLQEELKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRGA
			QIQAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKID
			MFLKVAVTTTISM
5675	80	753	EGSRRGPTRLARLSARAGRLHFPPGFSSRLIHFRGVSECRRPPG
			KSGVPVSAPGSDGKWWEERPGMFSLMASCCGWFKRWREPVRKVT
			LLMVGLDNAGKTATAKGIQGEYPEDVAPTVGFSKINLRQGKFEV
			TIFDLGGGIRIRGIWKNYYAESYGVIFVVDSSDEERMEETKEAM

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	corresponding to first	H=Histidine, T=Isoleucine, K=Lysine,
Ì	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid		P=Proline, Q=Glutamine, R=Arginine,
	residue of	residue of	S=Serine, T=Threonine, V=Valine,
Į.	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	1	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	1	•	SEMLRHPRISGKFILVLANKQDKEGALGEADVIECLSLEKLVNE
F282			HKCL
5676	2	930	FVSSPPPRPVQPARPGGFGLSGRRSLLCQVASTPAHVGVMRSPV
[	!		RDLARNDGEESTDRTPLLPGAPRAEAAPVCCSARYNLAILAFFG
ľ	1		PFIVYALRVNLSVALVDMVDSNTTLEDNRTSKACPEHSAPIKVH
			HNQTGKKYQWDAETQGWILGSFFYGYIITQIPGGYVASKIGGKM
1			LLGFGILGTAVLTLFTPIAADLGVGPLIVLRALEGLGEGVTFPA
			MHAMWSSWAPPLERSKLLSISYAGAQLGTVISLPLSGIICYYMN
	1		WTYVFYFFGTIGIPWFLLWIWLVSDTPQKHKRISHYEKEYILSS
1			L L
5677	1	1028	PPRDGFLELRRLSVPLCSGPCPLTSLSRQGERSGGHLVAAARAA
		4020	VTAETHPLPLLAPLAVCQSVKSPAACQVRPRPRAVALPAALGGP
			GPSLDGI TARTMEGRERGAL EVEL GREEN GREEN GREEN
1			GRSLPGLTAATMSSFSESALEKKLSELSNSQQSVQTLSLWLIHH
1			RKHAGPIVSVWHRELRKAKSNRKLTFLYLANDVIQNSKRKGPEF
1			TREFESVLVDAFSHVAREADEGCKKPLERLLNIWQERSVYGGEF
]			IQQLKLSMEDSKSFPPKATEEKKSLKRTFQQIQEEEDDDYPGSY.
1 1			SPQDPSAGPLLTEELIKALQDLENAASGDATVRQKIASLPQEVQ
5678	3		DVSLLEKITDKEAAERLSKTVDEACLRNRGPGTS
1 3073	,	593	SSSPPSSTPSLPLPFYLLLGQLRLQLLWGTAHLSGAGEAAPCPG
			GSGRTAAPRTRADPAAQSLMIMNKMKNFKRRFSLSVPRTETIEE
i i	i		SLAEFTEQFNQLHNRRNENLQLGPLGRDPPQECSTFSPTDSGER
			PGQLSPGVQFQRRQNQRRFSMEVRASGALPRQVAGCTHKGVHRR
5679	2	<b></b>	AAALQPDFDVSKRLSLPMDI
1 30,3	2	623	LNSRVDDFVAVPGAIMDEDYYGSAAEWGDEADGGQQEDDSGEGE
1 1	l l		DDAEVQQECLHKFSTRDYIMEPSIFNTLKRYFQAGGSPENVIQL
1	í		LSENYTAVAQTVNLLAEWLIQTGVEPVQVQETVENHLKSLLIKH
	į		FDPRKADSIFTEEGETPAWLEQMIAHTTWRDLFYKLAEAHPDCL
5680	258		MLNFTVKVGRVLELRRKVFMNVYFWLLVCFL
1 3000	256	592	RRLTSTSEKLONRNSHTPLESLIHPQPSYKGFGIMFGKKKKKIE
. !	ŧ		ISGPSNFEHRVHTGFDPQEQKFTGLPQQWHSLLADTANRPKPMV
5681	45		DPSCITPIQLAPMKTIVRGNKPC
3681	45	869	LLCAKTLGVRTKESQAEGYNRSGINNHQAEDPRFCPSFCWMRSA
1	Į.		RQTRPQRLRKEAARPPTPGSCPGGTGMDGKKCSVWMFLPLVFTL
J I	1		FTSAGLWIVYFIAVEDDKILPLNSAERKPGVKHAPYISIAGDDP
1 1		*	PASCVFSQVMNMAAFLALVVAVLRFIQLKPKVLNPWLNISGLVA
	·		LCLASFGMTLLGNFQLTNDEEIHNVGTSLTFGFGTLTCWTOAAL.
}	i		TLKVNIKNEGRRVGIPRVILSASITLCVGPLLHPHGPKHPHVCS
			QGPVGPGHVL
5682	3.9	622	PSRSCLGTMRKWRHREVNLPEVTQQDAVCPAPIPSPGLSAQTGL
	İ	į	QKIWGTIHCQVCPGAPAWPGSPWHEEMGLLLLVPLLLLPGSYGT.
1 1		ĺ	PFYNGFYYSNSANDONLGNGHGKDLLNGVKLVVETPERTLFTYO
			GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIG
<u> </u>			LRHRSFGDYQGRVHLRQD
5683	89	778	GSCGATALITRCLAWSVLISRLAMATYTCITCRVAFRDADMQRA
	1		HYKTDWHRYNLRRKVASMAPVTAEGFOERVRAORAVAEEESKGS
			ATYCTVCSKKFASFNAYENHLKSRRHVELEKKAVQAVNRKVEMM
1		l	NEKNLEKGLGVDSVDKDAMNAAIQQAIKAQPSMSPKKAPPAPAK
	ĺ	Į.	EARNVVAVGTGGRGTHDRDPSEKPPRLQWFEQQAKKLAKHSEDD
		ĺ	SEDEEHDLC
5684	195	677	TWCFRGYLGPRVIMKALDEPPYLTVGTDVSAKYRGAFCEAKIKT
		1	AKRLVKVKVTFRHDSSTVEVQDDHIKGPLKVGAIVEVKNLDGAY
	ļ	į	QEAVINKLTDASWYTVVFDDGDEKTLRRSSLCLKGERHFAESET
·		1	LDQLPLTNPEHFGTPVIGKKTNRGRRYE
5685	779	1262	LLLQQPVVHCFLLFPPFRFSHHMIPGPPGPHTTGIPHPAIVTPQ
!	-		VKQEHPHTDSDLMHVKPQHEQRKEQEPKRPHIKKPLNAFMLYMK
1			EMDANTARECTIVES DA INOTI CORREST CORREST
ı	į		EMRANUVAECTLKESAAINQILGRRWHALSREEQAKYYELARKE
5686	128		ROLHMOLYPGWSARDNYVSPSSIPVALHS
- 1		****	CTWWQVNITLLDINDNHPTWKDAPYYINLVEMTPPDSDVTTVVA
- 1	1	1	VDPDLGENGTLVYSIQPPNKFYSLNSTTGKIRTTHAMLDRENPD
		<del></del>	PHEAELMRKIVVSVTDCGRPPLKATSSATVFVNLLDLNDNDPTF

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
No:	nucleotide	location	Glutamic Acid, F≈Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Tysine
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *-Ston
ŀ	amino acid	sequence	Codon, /=possible nucleotide deletion.
<u> </u>	sequence		\=possible nucleotide insertion)
ì			QNLPFVAEVLEGIPAGVSIYQVVAIDLDEGLNGLVSYRMPVCMP
1			RMDFLINSSSGVVVTTTELDRERIAEYOLRVVASDAGTDTKSST
		}	STLTIHVLDVNDETPTFFPAVYNVSVSEDVPR\GSGWSG*AARN
			NDVGLNAELSYFITGGNVDGKFSVGYRDAVVRTVVGLDRETTAA
L.,	<u> </u>		YMLILEAIDNGPVGKRHTGTATVFVTVLDVNDKRPIILOSSYV
5687	17	917	AAPPAPPDG/PPP/PPPAPPT/PGPAA/APASSCOPRLSAGRAA
		Į	QGDGGAAAVGHVLVVPAVGPVRVNPGLOTPVPRPELLPGP\SSS
1		1	LHSDSSYPPDAGLSDDEEPPDASLPPDPPPLTVP/ADA/PMPVT
1			SGCRMPSTSASE/AAGGOGACTHAKGSETPPPASPOTSEPAPSP
			LPPHLTGGPGMYSSEAKLPNSFSCLGLAGTGAGI *GTASAHGTG
[			PPVLPHVCTPSLANPQP\AVGPEASSLPLGVSGIGMSA/SAPIS
			SSPFVAIGSCWLRGIPPPGSGFLCPGRAPGPVPITTHGQEGQGP
			VLDI
5688	1	420	LTKWDLFGNCYRLLKTGIEHGAMPEQVGVYWYS/CLYDSRKLFF
1	[		*SHMIIRSLL*KVIDDSLGOLPLLRELLL**LNVIDRCIILAVV
1	1		LRVEKTFAITYLKNFTVKVDFSLLGEIPLISMAAILKLWIMKID
F 500			DGYIPAVF
5689	1504	3	HELSGKHISMVSGNTCNWHPGGHSPGGGGGGEITSKDRGEIPAL
1	[		IWA/RKPIGTWTATKPTHRAG*GGAEEYOPPFOPCEGPRSTSRG
1			GEG*GHAVGPGREIGKEGSLPFLGPKALGF*SASCORAFEGGAH
	1		GSTARKPAPATPGTRHPRTMETREVAOGWPAGPRSOFWDOHPHS
			PGEHRPSG\SPLPACPPRAWPKAGAVASATGTG\PQLPGSRGKQ
1			KLPRTREPPLLQAGWAVRKPPWSEAKEGLGQAGRPSGMDSSAS\
1			PQTPGGRGSLEWGLPLYLGPHHDVK*RSDRLG*PP*GGQGGGGH
			GAPSTPGPGGEAW*LPQQTSRPKPGPQAY*GE\GSPGLQCPCSK
i			EL*RVPPGSLGPSTQCMYEPTDKHS\GGADAQLEVSTAGSRSTF
ŀ			GQELKGPLDAGRLWPGAPSASSSHR*GG*ERARAGAGHRGST*A
1	1		SSKIEQGRPRPGPTSDALADVEGGAES/GPHPWPLPGTLPNR/P
5690	1424	58	GSPPPA*ASAGRKGTVSTLGGGLL PSPPAGVCAAPAPLPLLALARRDRRPCSPGAEAAPWQTGGPAID
1		••	GAWRTSVSALRRGATG/APCSPGAEAAPWQTGGPAIDG CAWRTSVSALRRGATG/APCSPGAEAAPWQTGGPAIDG CALP
	· 1	•	*VRSEEAPRGCGAEGGGPGSGPVRRPGAGRGAHAGQGRQQDPEP
			DGLRHRQHGAASHARHRLQRLRPGHHQNRHVRRDPQAPPGGPAP
i			GHAAALPERTRGVAEPPAWAHAGSDAWRAGR*SQRT*ERARPRH
1 1			PTFQGRAGS\GQPGYQPPNPHPGPSSPPAAP\GPRGA*GNPQLE
1 1			KAPRSDRNPSQGLRTRIRRPETPDCGPPSPAGSSASASTFRCTS
i l	,	i	SLSLLGP/PGAHNLDTAPQDR*HGP*GDKRGAPGVAGEDPRPP*
	·		GNFVR*LLLMP/GVA*RHGTSPFLGPSLGENGGQWDSGNLFGTP
]			KG*SHPAFTKST*SMEAEKSYWNHPHR\DRGROGVRINCLRVGE
1	ł		SEMWGPYSAPRPGTVFLSSFLSPASEEH\PEGSSSFNTPFPPAG
			PEGDPGLNSPGLLP
5691	107	550	ISNDPSPGYNIEQMAKRGKKLVELPYTVKGMDVSFSG_LSFIED
1	1		VAHRMLATGECTPEDLCFSLQVMO*KTGTESWG*RFYIVEON*S
1			GDAPLIFSPYLSLTGNCGFAMLVEITERAMAH\CGSPGGPSLWG
<b> </b>			GVGVYVLLESVPLSYS
5692	1193	548	TQAWTRAEKDRKGSVRALRLHLERGPPT*RGSHPL\QSVPCIQK
1	·	l	PSIFSSYPI/GLPQSGGEPGPVGEQQPVRRPEQPSCGPASRMPL
			TSRSVPPGRGALPPDSLSTRKGLPRPSTAGHRVRESGHKVPVSO
		ł	RLNLPVMGATRSNLQPPRKVAVPGPTR*RDQDSKODFSSKPLOS
			VPGLASTQQTLTPADSGPGTGGRDATRAGLPGVETMGNGVD
5693	1258	1330	ALTVVPVRKGTTWWAQPHGCSNLVSRARLDLSSRPSONTEPOAP
j		ĺ	*QAGPPSSLRPP\SRRR*APEWPKRATGSRCRGLSAPPWPWPAA
] [	ľ	ļ	RGE/PGSAPSHAP/PNSPRPSGTRHP/PGPSSRVLYSPSLPRNS
<u> </u>			PEAIVWRSSRFPLWFPLRCCFWVSGFKDPNPVLRFF
5694	3	1338	GSKEPARSLHRRGSGHKSSAGKWGSVTLSTAGALG*KOLHO*WT
			QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVLRTDSEKR
į į		i	SLAESGLSWFSESEBKAPKKLEYDSGSLKMEPGTSKWRRERPES
1	· I	1	CDDSSKGGELKKPISLGHPGSLKKGKTPPVAVTSPITHTAOSAL
	1		KVAGKPEGKATDKGKLAVKNTGLQRSSSDAGRDRLSDAKKPPSG
LL			IARPSTSGSFGYKKPPPATGTATVMQTGGSATLSKIQKSSGIPV

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ļ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
Ĺ	sequence		\=possible nucleotide insertion)
			KPVNGRKTSLDVSNSAEPGFLAPGARSNIQYRSLPRPAKSSSMS
			VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLKEPTKVASGRTT
1	Ì		PAPVNQTDREKEKAKAKAVALDSDNISLKSIGSPESTPKNQASH
1			PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS
L	1		DTTQCI
5695	3	1338	GSKEPARSLHRRGSGHKSSAGKWGSVTLSTAGALG*KQLHQ*WT
1			QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVLRTDSEKR
1	]		SLAESGLSWFSESEEKAPKKLEYDSGSLKMEPGTSKWRRERPES
1			CDDSSKGGELKKPISLGHPGSLKKGKTPPVAVTSPITHTAQSAL
1			KVAGKPEGKATDKGKLAVKNTGLQRSSSDAGRDRLSDAKKPPSG
1			IARPSTSGSFGYKKPPPATCTATVMQTGGSATLSKIQKSSGIPV
}			KPVNGRKTSLDVSNSAEPGFLAPGARSNIQYRSLPRPAKSSSMS
			VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLKEPTKVASGRTT
İ			PAPVNQTDREKEKAKAKAVALDSDNISLKSIGSPESTPKNQASH
			PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS
			DTTOCI
5696	3	1338	GSKEPARSLHRRGSGHKSSAGKWGSVTLSTAGALG*KQLHQ*WT
1 1			QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVLRTDSEKR
1			SLAESGLSWFSESEEKAPKKLEYDSGSLKMEPGTSKWRRERPES
			CDDSSKGGELKKPISLGHPGSLKKGKTPPVAVTSPITHTAQSAL
1 1			KVAGKPEGKATDKGKLAVKNTGLQRSSSDAGRDRLSDAKKPPSG
1 1			IARPSTSGSFGYKKPPPATGTATVMQTGGSATLSKIQKSSGIPV
1			KPVNGRKTSLDVSNSAEPGFLAPGARSNIQYRSLPRPAKSSSMS
1 1			VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLKEPTKVASGRTT
1 1	,		PAPVNQTDREKEKAKAKAVALDSDNISLKSIGSPESTPKNQASH
ììì	i	i	PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS
	_		DTTQCI
5697	1147	47	PSEALSPPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPAA
] }			QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAAQQDS
1 1			DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL
1			SSEEEAEVAAPTKGPAPAPQQCSEPETKWSSIPASKPRRGTAPT
1 1	l		RTAAPPWPGGVSVRTGPEKRSSTRPPAEMEPGKGEQASSSESDP
1	İ		EGPIAAQMLSFVMDDPDFESEGSDTORRADDFPVRDDPSDVTDE
			DEGPAEPPPPPKLPLPAFRLKNDSDLFGLGLEEAGPKESSEEGK
1 1	ł		EGKTPSKENKKKKKKGKEEEEKAAKKKSKHKKSKDKEEGKEERR
			RRQQRPPRSRERTAA
5698	2	666	GARAAEPQEDLPPLSQSSRFFQEQQKMNKSLGPVSFKDVAVDFT
1			QEEWQQLDPEQKITYRDVMLENYSNLVSVGYHIIKPDVISKLEO
j	'		GEEPWIVEGEFLLQSYPDEVWQTDDLIERIQEEENKPSRQTVFI
			ETLI*R/ERGNVPGNTFDVETNPVPSRKIAYTHSLCNSCER\GF
		l l	NASSEYISSDGRYARMKADECSGCGKSLLHIKLEKTHPGDQAYE
5699			FNQ
6696	2	1448	RVRQPPGLWVRRTVPAMQCPAGLSRVPGVAG/DPSLPSFRGPRD
1 1	1	1	EAAHRGTIQTARHTRKLYVQGPASGPPLPRVSTOVAI*DEKPLA
		. 1	RPS/GRTNAPFPQGQKPAGKAAPGPAAAGRVAMR\PGHPGLLAS
ļ ļ			DSQRSSSKGSGWETPVPWS*AQPGWVSGLLLLGDPSGPGSL*RS
1 1	1	1	TWLVGGARGPEGSGVRGSGWPSGCSDIGWALAGWNHS+HLDPNT
	1	l	WTQKWTGE/SPAPGEEG\VAPAPRGPTAEHGHCELTTESOYSNN
		İ	VPILFQNPSGALRSRRTEPAGWVPPTRHE*DDG*TAAPASGGAP
j İ	<u> </u>	i	VSTPTWAGTP/LNASLGPTDPQGKPGCRPPCALPKPAGPERSA*
		Ī	GGSLGCR/SMLPASSGPPPAPGPRRLAAGAHTSASARCPPAAAA
1	1	]	GNQPRRPGFAGRAALPGPPHPPSS*RELGGLPGPGW*TLDPLPA
	ŀ	İ	HPAHPPGSAPPWGALGGWAAARASLPWSPSLCLSFPAVTPVAGL
		<u></u>	FPPGRG
5700	923	597	NGHKGVWEINIY*RRSNIHKNSKSESHLNQDHSFPPPTPNSARS
ļ .			KLHSTGTAKNTGLPLSGAPRQRAVFSGRTICQEFSSCLQCAYLD
			E*CSIASSLIKAILRVSVLSE
5701	59	410	IFEKICSDTQEFISPEINPQICSWLIFDKGAK/NHATGKDSLFN
			KWSWKNWLSTCR*MRPGPYFTPYTKINSK*IK/DANIRCETVKL
		ľ	LEENTGENLHDTGLGNVFLDMTPKTQPTKQK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Asparcic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ŀ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
}	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	Beneditie, Memechionine, Neasparagine,
- [	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
į.	residue of	1	S=Serine, T=Threonine, V=Valine,
1	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
5702	. 3	1517	ETFVDPSQCGGIPSDSPHPVITPSRASESSASSDGPHPVITPSR
- 1	1	J	ASESSASSDGPHPVITPSRASESSASSDGLHPVITPSRASESSA
ľ	1	i	SSDGPHPVITPSRASESSASSDGPHPVITPSRASESSASSDGLH
i	ı	1	PVITPSRASESSASSDGPHPVITPSWSPGSDVTLLAEALVTVTN
	1		IEVINCSITEIETTTSSIPGASDTDLIPTEGVKASSTSDPPALP
ľ	1	1 ,	DSTEAKPHITEVTASAETLSTAGTTESAAPHATVGTPLPTNSAT
	1	1	EREVTAPGATTLSGALVTVSRNPLEETSALSVETPSYVKVSGAA
	1		PVSIEAGSAVGKTTSFAGSSASSYSPSEAALKNFTPSETLTMDI
	İ		TTKGPFPTSRDPLPSVPPTTTNSSRGTNSTLAKITTSAKTTMKP
ı			PTATPITARTRPTT\A*VQVKNEVSSSCG*VWLPRKTSLTPEWQ
1			KG*CSSSTGNSTPTRLTSRSPYCVSGEANG/PSAAARHVPYAKR
			GCCD+DCDDDTDCCCUTUU DOTOVUDWCGCUCVCV TRANCO
1			GCCP+PGPPPTDCSCVTVLRGTQKVPMKGSMSKPLTPDVATGPS
5703	14		LTSTGVYVWGGASPVPRGVLGLTLAHVLCFSKEKT
1 3,03		1117	HHKDSRSQGLPRTQECARPELRPLLCPRALWPVTRLSYRCPWQA
1	1		PKAGIGTKAKPSESHLKLHPGWPSLDRQGEPATLGTGTGHCSDS
	}		RILRWHP*HTAAR*PRWRRLPSSHRWTRHLGVLRVQDKS**VSL
	1.		DPSCRPRFLRTC**YGMRSVASSSNPPPGWSGPGASVFPARPVS
	i		ALPTGPRCW*APRGRTRQPCGWPRLSSPHATADWGPGCPLSPSR
1	1		GSWETAPGS*WCPWL*AARWTGWRTASGASAGLGRAADRPSAWA
İ			RRVAGLLPGQGLTVRR*H*TAGAPASVRSSQGATRSPAPGGDQC
	i		ACGRGPGSC*HPPPWPVSPSSPVPCPSGR*HLRGPLLSAARPRA
			AGWPRHSPHDTQTPEP
5704	23	562	GDYEFDSPYWDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWI
			SGNAASDKNIKDGVCAQIEKNPARAKWKKAVRVTTLMKRLRAPE
	į		QSSTAAAQSASATOTATPGAAGGATAAAASGATSAPEGDAARAA
	1		KSDNVAPRRP+LPPQPQMEVPPQPLMAVSPQPPMEASLQPLMGE
1	i l		SPOP
5705	23	562	GDYEFDSPYWDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWI
1			SGNAASDKNIKDGVCAQIEKNFARAKWKKAVRVTTLMKRLRAPE
1	ľ		QSSTAAAQSASATDTATPGAAGGATAAAASGATSAPEGDAARAA
			VSD I MANGOADAT DI INDODONEUDO DE VALIGO DO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE VALIGO DE
			KSDNVAPRRP*LPPQPQMEVPPQPLMAVSPQPPMEASLQPLMGE SPOP
5706	1161	610	
0.00	1 1	010	QLGRFXAQDTVAIRKVKEVFGTGAMRHVVILFTHKED*GGQALD
			DYVANTDNCSLKDLVRECERRYCAFNNWGSVEEQRQQQAELLAV
			IERLGREREGSFHSNDLFLDAQLLQRTGAGACQEDYRQYQAKVE
			WQVEKHKQELRENESNWAYKALLRVKHLMLLHYEIFVFLLLCSI
5707			LPPIIFLF
1 3/0/	28	609	GSPAPTPGFRRPGRGTPSPGTRHHQGRABPEPDAPERAPLRR*
	1		MFAIQPGLAEGGQFLGDPPPGLCQPELQPDSNSNFMASAKDANE
	<b>!</b>	,	NWHGMPGRVEPILRRSSSESPSDNQAFQAPGSPEEGVRSPPEGA
] ]			EIPGAEPEKMGGAGTVCSPLEDNGYASSSLSIDSRSSSPRPACG
			TPRGPGPPDPLLPSVAQA
5708	44	1925	SFSWEETISPCFPKMPAEPWWLSPVSLGAAGWPGQPRPYLDLPA
} I		ļ	QASVSRPHDRA*GEAVSLSLSSGDVCGHTDGGGAGSDPQAKPKP
	1	!	PRCPFTAMPSPRTKQKVRNKVCLLIAIRYSDIPSDVSKAP\GPA
	ļ		GNPHDRSSTAA*LHRRAGAGSLCLSASLLPPSFSLGAPGAPSPL
	•		RVSPASGGPRKEGRQGSGG+AGGGGP\ARTHADLPCVGFVCSPP
		ł	LLK*SDSPVKQLPA\SGQGSGAGMPPVGSSDILRPRPTSVSGTG
	i		RAAG*CSWQPAACCTPRSQ*WAVARSPSRCSRW*RQSGR*RG*S
[ ]			SRRRRGP*AAGRSTPAVP*PCS*GGAGRRAYACRTGWGYAPSR*
1 1		}	LEPSGPTSGSAL*TWASHSTGA**SRLCGTAGTGPLCSQSSRS*
			AG*RCCCTAASPCGGSGPSHPGSPSAHCLSWSGGRTQPRAPSAH
1		1	GRAMGSRCVCTCTGLPCPGIPLSGASPGGSGETGAGRSHTLK
1 1			
1	i	I	AARSRLSPRPGSGSRGSY*SHNDNWGTWPAPPSAGHLLVGG*NS
	1	1	QRTSSDH*YTGTRRPWAGPGTRCSTAPSRAAPPVSRCRPPPPPP
	1	ļ	PPRPPRLPAAAS/SGGASGSPAASCSCSCRAPAKPASS/GEAPA
5709			PPPRPEPPPPPARRP
1 2,03	2	2031	ITLCPLPQTEKCLNVVTEAATPLGIYLKARVEAGGLKELEISWG
1	1	į	LHQIVVRWGAVVMRAGMGGCRCWGVMAPFAPK/NALSFLVNDCS
			LIHNNVCMAAVFVDRAGEWKLGGLDYMYSAQGNGGGPPRKGIPE

SEQ ID NO:			
	Predicted	Predicted end	Amino acid segment containing signal peptide
i Mo:	beginning nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	to first	L=Leucine, M=Methionine, N=Asparagine,
	amino acid		P=Proline, Q=Glutamine, R=Arginine,
1	residue of	residue of	S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	5	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
}			LEQYDPPELADSSGRVVREKRSADMWRLGCLIWEVFNGPLPRAA
1		1	ALRNPGKIPKTLVPHYCELVGANPKVRPNPARFLQNCRAPGGFM
			SNRFVETNLFLEEIQIKEPAEKQKFFQELSKSLDAFPEDFCRHK
		Ī	VLPQLLTAFEFGNAGAVVLTPLFKVGKFLSAEEYQQKIIPVVVK
l l			MFSSTDRAMRIRLLQQMEQFIQYLDEPTVNTQIFPHVVHGFLDT
1			NPAIREQTVKSMLLLAPKLNEANLNVELMKHFARLQAKDEQGPI
1			RCNTTVCLGKIGSYLSASTRHRVLTSAFSRATRDPFAPSRVAGV
			LGFAATHNLYSMNDCAQKILPVLCGLTVDPEKSVRDQAFKAIRS
1			FLSKLESVSEDPTQLEEVEKDVHAASSPGMGGAAASWAGWAVTG
ł			VSSLTSKLIRSHPTTAPTETNIPQRPTPEGVPAPAPTPVPATPT
1			TSGHWETQEEDKDTAEDSSTADRWDDEDWGSLEQEAESVLAOOD
1	1		DWSTGGQVSRASQVS\TPTTNPPNPQSPTGAAGK\RGLLGTGLA
			GAKLPGATS*RYTAGQRV
5710	1	562	IFGSTISCEVELMARMAKTIDSFTQNQTRLVVIIDGLDACEQDK
1			VLQMLDTVRVLFSKGPFIAIFASDPHIIIKAINQNLNSVPSGFK
į			\LNGHDYMRNIVHLPVFLNSRGL/RQ/LQENFS*LQQQMETFHA
			QILQGYRKMLTEEFHRTALGR*QNLVARQPSIDG*DAIGFELYV
			CIAIQFNTNKDDAT
5711	1526	1130	RRHPFQWTTVTQEAFSHHDVAFTSTPVLFYPDSAQPFIVKSESS
1	Ì		SQIAKAVLSQQRPSLFHECAFHFFS*SLQRHTINLDQGIF*LLM
1			LSEBROHLFESS/IWTTPHNLK*/FEIHEHLGSHEGHWTLFFLL
		4	OIL
5712	3	1391	GRKLFQSLDISERLKFLLTLDCVDDTLIVLAEEHGCLDIIKELP
i			ETVIDI.I.NKCLTFHPSKRPTPDELMKDKVFSEVSPLYTPFTKPA
1			SLFSSSLRCADLTLPEDISQLCKDINNDYLAERSIEEVYYLWCL
[			AGGDLEKELVNKEIIRSKPPICTLPNFLFEDGESFGQGRDRSS/
			TFR*YHWDIVVMPAKK*IERCWGRSILPITLKMTSLILPYSNSN
	l i		NELSAAATLPLIIREKDTEYQLNRIILFDRLLKAYPYKKNQIWK
			EARVDIPPLMRGLTWAALLGVEGAIHAKYDAIDKDTPIPTDRQI
1	i i		EVDIPRCHQYDELLSSPEGHAKFRRVLKAWVVSHPDLVYWQGLD
]			SLCAPFLYLNFNNEALVYACMSAFIPKYLYNFFLKDNSHVIQEY
İ			LTVFSQMIAFHDPELSNHLNEIGFIPDLYAIPWFLTMFTHVFPL
			HKIFHLW\DTLLLGEFLFPILYWE
5713	634	284	PVCAVPVDRWPVLPREDQEGQQL*AKLPRDFRR*FQILGPMEGH
ŀ			TACRCSRRGAQVQHLPREDIRAAE*DFHLREVWPGLPTSSATSP
			*RAVLTSPCSHLGSADAASSHWLCGVSFH
5714	212	613	WGLGLGPTMSSLGGGSQDAGGSSSSSTNGSGGSGSSGPKAGAAD
1			
			KSAVVAAAAPASVADDTPPPERRNKSGIISEPLNKSLRRSRPLS
			HYSSFGSSGGSGGSMMGGESADKATAAAAASLLANGHDLAAA
5715	131	1970	HYSSFGSSGGSGGSMMGGESADKATAAAAASLLANGHDLAAA MA
5715	131	1979	HYSSFGSSGGSGGSMMGGESADKATAAAAAASLLANGHDLAAA MA ESASQQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE
5715	131	1979	HYSSFGSSGGSGGSMMGGESADKATAAAAASLLANGHDLAAA MA ESASQQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE QTPPASKLQGGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\
5715	131	1979	HYSSFGSSGGSGGSMMGGESADKATAAAAASLLANGHDLAAA MA ESASQQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE QTPPASKLQGGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\ GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN
5715	131	1979	HYSSFGSSGGSGGSMMGGESADKATAAAAAASLLANGHDLAAA MA ESASQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE QTPPASKLQGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\ GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS
5715	131	1979	HYSSFGSSGGSGGSMMGGESADKATAAAAAASLLANGHDLAAA MA ESASQQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE QTPPASKLQGGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\ GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS PRPPGS/SDLDGPRPQMHLKAFPAAHGGPVNTPHGGEEKTFMSS
5715	131	1979	HYSSFGSSGGSGGSMMGGESADKATAAAAAASLLANGHDLAAA MA ESASQQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE QTPPASKLQGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\ GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS PRPPGS/SDLDGPRPQMHLKAFPAAHGGPVNTPHGGEEKTFMSS QIRRKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR
5715	131	1979	HYSSFGSSGGSGGSMMGGESADKATAAAAAASLLANGHDLAAA MA ESASQQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE QTPPASKLQGGGGGLQTGWGLHPVPVTAASFLPRWCLFGAVAK\ GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS PRPPGS/SDLDGPRPQMHLRAFPAAHGGPVNTPHGGEEKTFMSS QIRRKETKPL*RKTPAG\NYYQSNSIPVSQSPQLTVDLLPSAGR TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL
5715	131	1979	HYSSFGSSGGSGGGMMGGESADKATAAAAAASLLANGHDLAAA MA ESASQQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE QTPPASKLQGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\ GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS PRPFGS/SDLDGPRPQMHLKAFPAAHGGPVNTPHGGEEKTFMSS QIRKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL YPKTPKQRRWRRPL/LLGPSQ*GSRQSTC*EV\GALGBEVRIPG
5715	131	1979	HYSSFGSSGGSGGSMMGGESADKATAAAAAASLLANGHDLAAA MA  ESASQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE QTPPASKLQGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\ GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS PRPFGS/SDLDGPRPQMHLRAFPAAHGGPVNTPHGGEEKTFMSS QIRRKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL YPKTPKQRRWRRPL/LLGPSQ*GSRQSTC*EV\GALGEEVRIPG L*PDLSCILSNGSKHRREGLSFPRSLGPGRRGPAGLQSLGCSPT
5715	131	1979	HYSSFGSSGGSGGSMMGGESADKATAAAAAASLLANGHDLAAA MA  ESASQQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE QTPPASKLQGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\ GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS PRPFGS/SDLDGPRPQMHLRAFPAAHGGPVNTPHGGEEKTFMSS QIRRKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL TYPKTPKQRRWRRPL/LLGPSQ*GSRQSTC*EV\GALGEPVRIPG L*PDLSCILSNGSKHRREGLSFPRSLGPGRRGPAGLQSLGCSPT PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP
5715	131	1979	HYSSFGSSGGSGGSMMGGESADKATAAAAAASLLANGHDLAAA MA  ESASQQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE QTPPASKLQGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\ GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVBNN DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS PRPPGS/SDLDGPRPQMHLRAFPAAHGGPVNTPHGGEEKTFMSS QIRRKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGG*PPGL YPKTPKQRRWRRPL/LLGPSQ*GSRQSTC*EV\GALGEPVRIPG L*PDLSCILSNGSKHRREGLSFPRSLGPGRRGPAGLQSLGCSPT PKNTACHSSGHVALQAGHDSTQDVGRP VWRWIPLE*LGLSRETGQATRKGLVWISPGRAAAACVACAQALE
5715	131	1979	HYSSFGSSGGSGGSMMGGESADKATAAAAAASLLANGHDLAAA MA  ESASQQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE QTPPASKLQGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\ GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS PRPFGS/SDLDGPRPQMHLRAFPAAHGGPVNTPHGGEEKTFMSS QIRKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL YPKTPKQRRWRPL/LLGPSQ*GSRQSTC*EV\GALGEPVRIPG L*PDLSCILSNGSKHREGLSFPRSLGPGRRGPAGLQSLGCSPT PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP VWRWIPLE*LGLSRETGOATRRGLVWISPGRAAAACVACAQALE EGPLRLPGQDRGAQPCSHCPGRAAAQPEPGAGAPCRE/GG*DPT
5715	131	1979	HYSSFGSSGGSGGSMMGGESADKATAAAAAASLLANGHDLAAA MA  ESASQQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE GYPPASKLQGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\ GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS PRPFGS/SDLDGPRPQMHLRAFPAAHGGPVNTPHGGEEKTFMSS QIRKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL YPKTPKQRRWRRPL/LLGPSQ*GSRQSTC*EV\GALGFPVRIPG L*PDLSCILSNGSKHRREGLSFPRSLGPGRRGPAGLQSLGCSPT PKNTACHSSGHVALQAGHDSTQDVGRP VWRWIPLE*LGLSRETGQATRKGLVWISPGRAAAACVACAQALE EGPLRLPGQORGAQPCSHCPGRAAGQPFPGAGAPCRE/GG*DPT GLT/GVPGTDPKRGGRKPGQSGQETQGPTVWSGPESPLQPKP*E
5715	131	1979	HYSSFGSSGGSGGSMMGGESADKATAAAAAASLLANGHDLAAA MA  ESASQQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE QTPPASKLQGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\ GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS PRPFGS/SDLDGPRPQMHLRAFPAAHGGPVNTPHGGEEKTFMSS QIRKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL YPKTPKQRRWRPL/LLGPSQ*GSRQSTC*EV\GALGEPVRIPG L*PDLSCILSNGSKHREGLSFPRSLGPGRRGPAGLQSLGCSPT PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP VWRWIPLE*LGLSRETGOATRRGLVWISPGRAAAACVACAQALE EGPLRLPGQDRGAQPCSHCPGRAAAQPEPGAGAPCRE/GG*DPT
			HYSSFGSSGGSGGSMMGGESADKATAAAAAASLLANGHDLAAA MA  ESASQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE QTPPASKLQGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\ GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS PRPFGS/SDLDGPRPQMHLRAFPAAHGGPVNTPHGGEEKTFMSS QIRRKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL L*PDLSCILSINGSKHRREGLSFPRSLGPGRRGPAGLQSLGCSPT PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP VWRWIPLE*LGLSRETGQATRRGLVWISPGRAAAACVACAQALE EGPLRLPGQDRGAQPCSHCPGRAAGQPBPGAGAPCRE/GG*DPT GLT/GVPGTDPKRGGRKPGQSGQETQGPTVWSGPESPLQPKP*E RQE/VGAGASSGVGLSRGRAGGPSSAWEVAAMLLLLRHGSHSEL TDLTEAQTSQH
5715	131	1979	HYSSFGSSGGSGGSMMGGESADKATAAAAAASLLANGHDLAAA MA  ESASQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE QTPPASKLQGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\ GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS PRPFGS/SDLDGPRPQMHLRAFPAAHGGPVMTPHGGEEKTFMSS QIRRKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL YPKTPKQRRWRRPL/LLGPSQ*GSRQSTC*EV\GALGEPVRIPG L*PDLSCILSNGSKHRREGLSFPRSLGPGRRGPAGLQSLGCSPT PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP VWRWIPLE*LGLSRETGQATRRGLVWISPGRAAACVACAQALE EGPLRLPGQDRGAQPCSHCPGRAAGQPEPGAGAPCRE/GG*DPT GLT/GVPGTTPKRGGRKPGQSGQETQGPTVWSGPESPLQPKP*E RQE/VGAGASSGVGLSRGRAGGPSSAWEVAAMLLLLRHGSHSEL
			HYSSFGSSGGSGGSMMGGESADKATAAAAAASLLANGHDLAAA MA  ESASQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE QTPPASKLQGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\ GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS PRPFGS/SDLDGPRPQMHLRAFPAAHGGPVNTPHGGEEKTFMSS QIRRKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL L*PDLSCILSINGSKHRREGLSFPRSLGPGRRGPAGLQSLGCSPT PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP VWRWIPLE*LGLSRETGQATRRGLVWISPGRAAAACVACAQALE EGPLRLPGQDRGAQPCSHCPGRAAGQPEPGAGAPCRF/GG*DPT GLT/GVPGTDPKRGGRKPGQSGQETQGPTVWSGPESPLQPKP*E RQE/VGAGASSGVGLSRGRAGGPSSAWEVAAMLLLLRHGSHSEL TDLTEAQTSQH
5716	1711		HYSSFGSSGGSGGSMMGGESADKATAAAAAASLLANGHDLAAA MA  ESASQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE QTPPASKLQGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\ GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS PRPFGS/SDLDGPRPQMHLRAFPAAHGGPVNTPHGGEEKTFMSS QIRKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL L*PDLSCILGNGSKHRREGLSFPRSLGPGRRGPAGLQSLGCSPT PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP VWRWIPLE*LGLSRETGQATRRGLVWISPGRAAAACVACAQALE EGPLRLPGQDRGAQPCSHCPGRAAGQPEPGAGAPCRE/GG*DPT GLT/GVPGTDPKRGGRKPGQSGQETQGPTVWSGPESPLQPKP*E RQE/VGAGASSGVGLSRGRAGGPSSAWEVAAMLLLRHGSHSEL TDLTEAQTSQH RVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD
			HYSSFGSSGGSGGSMMGGESADKATAAAAAASLLANGHDLAAA MA  ESASQQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE QTPPASKLQGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\ GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS PRPPGS/SDLDGPRPQMHLRAFPAAHGGPVNTPHGGEEKTFMSS QIRRKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR TQAPSGRGDACKPTPGHG\LPKASVILTPNCPCSLAGGG*PPGL YPKTPKQRRWRRPL/LLGPSQ*GSRQSTC*EV\GALGEPVRIPG L*PDLSCILSNGSKHRREGLSFPRSLGPGRRGPAGLQSLGCSPT PKNTACHSSGHVALQAGHDSTQDVGRP VWRWIPLE*LGLSRETGQATRKGLVWISPGRAAAACVACAQALE EGPLRLPGQDRGAQPCSHCPGRAAGQPEPGAGAPCRE/GG*DPT GLT/GVPGTTDKRGGRKPGQSGQETQGFTVWSGPESPLQPKP*E RQE/VGAGASSGVGLSRGRAGGPSSAWEVAAMLLLRHGSHSEL TDLTEAQTTSQH RVFSLLCEGPGHCYQGAVCREACAAASFGLDSAAEPHRLCEHTD *LPK*GPGYIQHFHCDSNILCILYNISFNLFSYSF*GVARYAC*

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Tweine
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
i	to first	amino acid	P=Proline, O=Glutamine, R=Arginine
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence		\=possible nucleotide insertion)
1			GDSLGARPGLPYGLSDDESGGGRALSAESEVEEPARGPGEARGE
			RPGPACQLCGGPTGEGPCCGAGGPGGGPLLPPRLLYSCRLCTFV
		]	SHYSSHLKRHMQTHSGEKPFRCGRCPYASAQLVNLTRHTRTHTG
			EKPYRCPHCPFACSSLGNLRRHQRTHAGPPTPPCPTCGFRCCTP
		1	RPARPPSPTEQEGAVPRRPEDALLLPDLSLHVPPGGASFLPDCG
1	1		Q\CGVKGRASAGLDQNHCQS/SLFPWTCRGCGQELEEGEGSRLG
Ī			AAMCGRCMRGEAGGASGGPQGPSDKGFACSLCFFATHYPNHLA RHMKTHSGEKPFRCARCPYASAHLDNLKRHQRVHTGEKPYKCPL
1			CPYACGNLANLKRHGRIHSGDKPFRCSLCNYSCNQSMNLIRHM
5718	120	284	VAHALSLPAESYGNDVSMTHPQLPPTQLAWDLCRTCLPLSYNFT
			S**STADPLHL
5719	48	428	ELNNGPFQMPLCNGGNLAVTGSWADRSPLHEAASQGRLLALRTL
	l i		LSQGYNVNAVTLDHVTPLHEACLGDHVACARTLLEAGANVNAIT
			IDGVTPLFNACSQGSPSCAELLLEYGAKAQP\ESCLPSP
5720	1	1051	LQAFRNASEVPMVLVGTQDAISAA\NPRVYRRTSRARKLSTDLK
1			\RCT\YYE\TCGGTYGLQMWSVSFQDVAQKVVAL\RKKQQ\LAI
	1		GPCK\SLPN\SPSH\SAVSAASIPARAPINQGHE/SGGGSAFSD
1			Y\SSSVPSTPSISQRELRIETIAASSTPTPIRKQSKRRSNIFTS
1			RKGADP\DREKKAAGCKVDSIGSGRAIPIKQGILLKRSGKSLNK
1			EWKKKYVTLCDNGLLTYHPSLHDYMONIHGKEIDLLRTTVKVPG
1 :			KRLPRATPATAPGTSPRANGLSVERSNTOLGGGTGAPHSASSAS
			LHSERPLSSSAWAGPRPEGLHQRSCSVSSADQWSEATTSLPPGM
			QHPASG
5721	97	192	RHSSPCCSLRRTERSSNAAVST/TTVQQFKRFIENYRRHIGCVA
			VFYAIAGGLFLERAYYYAFAAHHTGITDTTRVGIILSRGTAASI
5722	88	1040	SFMFSYILLTMCRNLITFLRETFLNRYVPFDAAVDFHRLIASTA
1 3,22	0.0	1043	VALDVLAGSSPGGGMAGALLGPRVHGIRAVLRVARGGVQAPGAP
			GSLGVSHAAAPPARPQGAAQSPHRGRRHGGGGAGLPPPRSPRFP
1 1			QESVPASTSTARGPRRVSRRLPPQHPGPRGRRRRPGAGVGAPRR GRARGQAGLLGRQGQGGRGAERERAALQARRGRRPGPEPDQSCG
			GRPRRAAAAPGRAPADPQPPAPRPAPAPDVRPPADAPAPAPAPA
1 1		İ	PPPPPHLGALTAGSGEERQSQPRAETLRLGRGAPLP\PRAERGG
1 1			RPKQAEQQQ\PKRPTPPARGPQSSGDPAMLPQRAGLRTGGLAGT
		ì	KSSTREIPEMI
5723	88	1043	VALDVLAGSSPGGGMAGALLGPRVHGIRAVLRVARGGVQAPGAP
l ł		•	GSLGVSHAAAPPARPOGAAOSPHRGRRHGGGGAGLPPPRSPRFP
1 1	į.		QESVPASTSTARGPRRVSRRLPPQHPGPRGRRRRPGAGVGAPRR
1	1		GRARGQAGLLGRQGQGGRGAERERAALQARRGRRPGPEPDOSCG
	ľ		GRPRRAAAAPGRAPADPQPPAPRPAPAPDVRPPADAPAPAPA
1 1	}	1	PPPPPHLGALTAGSGEERQSQPRAETLRLGRGAPLP\PRAERGG
	İ		RPKQAEQQQ\PKRPTPPARGPQSSGDPAMLPQRAGLRTGGLAGT
5724	3		KSSTREIPEMI
- /	3	1841	FINEAPPAPLPDASASPLSPHRRAKSLDRRSTEPSVTPDLLNFK
	j		KGWLTKQYEDGQWKKHWFALADQSLRYYRDSVAEEAADLDGEID .
1	į.		LSACYDVTEYPVQRNYGFQIHTKEGEFTLSAMTSGIRRNWIQTI
1 1		İ	MKHVHPTTAPDVTSSLPEEKNKSSCSFETCPRPTEKQEAELGEP
1		į	DPEQKRSRARE\RREGRSKTFDWAEFRPIQQALAQERVGGVGP
) [	1	ĺ	ADTH\DPWRPEAEHGELERBRARREERRKRFGMLDATDGPGTE
	1	ļ	DAALRMEVDRSPGLPMSDI.KTHNVHVEIEQRWHQVETTPLREEK
	[		QVPIAPVHLSSEDGGDRLSTHELTSLLEKELEQSQKEASDLLEQ
			NRLLQDQLRVALGREQSAREGYVLQATCERGFAAMEETHQKKIE
	ļ		DLQRQHQRELEKLREEKDRLLAEETAATISAIEAMKNAHREEME RELEKSQRSQISSVNSDVEALRRQYLEELQSVQRELEVLSEQYS
	1		OKCLENATI AOALEA PROAL ROCORENOET NATURALE VISEOUS
			QKCLENAHLAQALEAERQALRQCQRENQELNAHNQBLNNRLAAE ITRLRTLLTGDGGGEATGSPLAQGKDAYELEVPSGARPCLTQLC
	ĺ		TREET TO TED TED TED TED TED TED TED TED TED TED
5725	3		VNGHSEETSQSPNRTEPHDSDCSVDLGISKSTEDLSPOKSGPVG
	·		SVVKSHSITNMEIGGLKIYDILSDN\DLSSHLQPLK/FTSAVDG
ļ		1	KNIVRSKAATLLYDQPLQVFTGSSSSSDLISGTKAIFKFDSNHN
			PE/GAKYNKRPHKWAHNLHLKYMVLHSIISNTVAV\RSQRHFVA
	<u></u>		Jones Ave

Degaming   nocation   corresponding   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   cont	SEQ	Predicted	Predicted end	Amino acid gogment containing of
Noticetide   Cocation   Corresponding to first amino acid residue of seizet amino acid sequence   P-P-P-Coline, Q-Gultumine, R-Asparagine, P-P-P-Coline, Q-Gultumine, R-Asparagine, P-P-P-Coline, Q-Gultumine, R-Asparagine, P-P-P-Coline, Q-Gultumine, R-Asparagine, P-P-P-Coline, Q-Gultumine, R-Asparagine, M-T-Typ Coban, Y-Typ Coline, Y-Typ Coline, Q-Gultumine, R-Asparagine, M-T-Typ Coban, Y-Typ Coline, Q-Gultumine, R-Asparagine, M-T-Typ Coban, Y-Typ Coline, Q-Gultumine, R-Asparagine, M-T-Typ Coban, Y-Typ Coline, Q-Gultumine, R-Asparagine, M-T-Typ Coban, Y-Typ Coline, Q-Gultumine, R-Asparagine, M-T-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ Coban, Y-Typ		1		Amino acid segment containing signal peptide
Cocation   Cocresponding   Cofirst   amino acid   sequence   Severine, Perboline, Qedlutamine, Rahginine, Sequence   Severine, Territorine, Vavaline, Securine, Vavaline, Sequence   Codon, Possible nucleotide insertion)   Lorispano   Codon, Possible nucleotide insertion   Lorispano   Codon, Possible nucleotide insertion   Lorispano   Codon, Possible nucleotide insertion   Lorispano   Codon, Possible nucleotide insertion   Lorispano   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Possible nucleotide   Codon, Poss			1	(A=Aranine, C=Cysteine, D=Aspartic Acid, E=
corresponding to first amino acid residue of mino acid residue of mino acid residue of mino acid residue of amino acid sequence				Grutamic Acid, F=Phenylalanine, G=Glycine,
amino acid residue of amino acid residue of servine, Tenheconiae, Vervaline, amino acid sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of se		1		H=Histidine, I=Isoleucine, K=Lysine,
amino acid residue of amino acid sequence should be amino acid sequence should be amino acid sequence should be amino acid sequence should be amino acid sequence should be amino acid sequence should be amino acid sequence should be amino acid sequence should be amino acid sequence should be amino acid sequence should be amino acid sequence should be amino acid sequence should be amino acid sequence should be amino acid sequence should be amino acid sequence should be amino acid sequence should be amino acid sequence should be amino acid sequence should be amino acid sequence should be amino acid sequence should be amino acid sequence should be amino acid sequence should be amino acid sequence should be amino acid sequence should be amino acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid sequence should be acid seq				L=Leucine, M=Methionine, N=Asparagine,
residue of amino acid sequence con. X-Dycosine. X-Sudnown. *-Stop con. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide delecion. /-possible nuclectide d			1	P=Proline, Q=Glutamine, R=Arginine,
amino acid sequence    Codon, /=possible nuclectide details.com sequence			· ·	S=Serine, T=Threonine, V=Valine,
Sequence   Codon, /-possible nucleotide deletion,	1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Sequence   A-possible nucleotide insertion	1	amino acid	sequence	Codon, /=possible nucleotide deletion.
LOTKSPRRPCGFSSSAPS/VGCRAQ/INGSYAGISANNINFININRANATAYHLIGALGPARHGEWAL SENDRLI PATRSTIGRGS SYSTASVILIDPGSTRRAGIFEGOVIA: STREPHSAGETPPHMIGE SCRLSARTYS LIGORASPOSARS INSIDERATISTICRGS SYSTASVILIDPGSTRRAGIFEGOVIA: STREPHSAGETPPHMIGE SCRLSARTYS CONTROL OF THE STREET STREET STREET STREET STREET STREET TSP  5726  2 486  SSLSJWMNISGLFSSKSKLPVTVGFSGCVKILRIHGRPLAGA GSSPGGGGGGGTFLFAGATAGGCVKALRIHGRPLAGA GSSPGGGGGGFPHAGATAGGVALLAGADG COSPGGGGGGFPHAGATAGGSVALLAGADG COSPGGGGGGFPHAGATAGGVALLAGADG COSPGGGGGGFPHAGATAGGVALLAGADG STREET THE STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET	1	sequence	ł	\=possible nucleotide insertion)
S726 2 486 SSLSJWINGSCHARPGEWALTSFRIDELPAYTRSTEDGE SGRPLSARTYSIDGENARRQSARPSINSIPERTMSVSDFNYSR TSP  FIRMAGVIPCILIGELERGLEFFGGGGUTUL/SSURGIPGERGE GGSPGGGGGGGGFFLSSPSGFFDLADLGGATLFDVGLELEVTPLAVT GLIPHLGGARTPYLOLQUTERGGGVULRADDG GGSPGGGGGFFTLSPVGLQUTERGUTULRADG GGSPGGGGGFFTLSPVGLQUTERGUTULRADG GGSPGGGGGFFTLSPVGLQUTERGUTULRADG GGSPGGGGGFFTLGGARTPYLOLQUTERGUTULRADG GGSPGGGGGFFTLGGARTPPLAVT GLIPHLGGARTPYLOLQUTERGUTULRADG GGSPGGGGGGGGGGGFTLSPSGGGTTLGSGARGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG				LOTKSPNRPCOFSSSAPS/VDORAG/TNGSVAKUGAMMNPCMUN
SYSTASVILOPICSTRAQTIFEQUIVATERISAGRITPIMMES SORPLISARTYS IDGINASRIGOSARS INISIERISAGRITPIMMES 5726 2 4866 SESISJWWINSGLFASSHSKLFVTVGFSGCVKLRIHGRFLGAP TEMAGVTPCILGFLEAGLFFEGGGVITL/SSVGAGIOPISAGR QGSPGGGGGGPTSSSSSQLFADLGATLFPVSLLEVERLANG GLIPHLGGARTPFVLOLGVTEKQULKRADDG 5727 21 221 RPILILKETRELSSSSSQLFADLGATLFADGASCEVUTVKKK AGAUTSTTRINSSKRSSLSUNGE 2 877 GTRGGFFFREGGAREGSAGGLFAFGANAGGFGVQFREGG/LDG NAIRAGVNFGGGFFFREGGAREGSAGGLFAFGANAGGFGVQFREGG/LDG NAIRAGVNFGGGSAFFENDLSLPHDLNPPPTDIADADPDFSGG GGPAGAGGDA/LPGRCPSAPWRAGSRPAASCPDWIPDGADAPD HARAGRAPPWSGVLGRKVCOPTYSTSSAGPG/SGGLPAPG GGPAGAGGDA/LPGRCPSAPWRAGSRPAASCPDWIPDGGDAPA GRAGARSVUTLUJGHFAGSVGALARGSRPAASCPDWIPDGGDAPA GGPAGAGGDA/LPGRCPSAPWRAGSRPAASCPDWIPDGGAPA HARPTS/GPPSOLGGGACQDGBCQADAPGICGKNAPPG GGPAGAGGDA/LPGRCPSAPWRAGSRPAASCPDWIPDGGAPA HARPTS/GPPSOLGGGACQDGBCQADAPGICGKNAPPGAGGILPGAGA GSPAGAGGADA/LPGRCSAPPGAGGSEDAPGAGGGAPPGAGGAGAAACGAUTTS COULVERCHTLANDAGSSAGAADAPGICGKNAPPSKEPBEGG FPOVPSAGEBAAVARAGGGAFTEAGAGGSCALARGPKYDEKAGGAA KSSPRALAPPDDJAAGGGARTAATTSCALTSGAGAACAACAACAACAACAACAACAACAACAACAACAACA	1			NVPANTAVHIHODI.CDADUCEMWA TODNIDDI TANAMDOMTODOG
SGRLSSHTYSIDGRMASRQSARPSINSIPERTMSVSDFPNYSR TSP  2 486 SSILSWMMSGLFASSHSKLPVTVGFSGVVKRLRIHGRPLAGE GSSPGSGGSGFPLSSSSGPLFADLGGATLPDVSLELEVTPLAVT GLIPHLGQARTPYLQLQVTERGVLRADDG GOSPGGSGGSPLSSSSGPLFADLGGATLPDVSLELEVTPLAVT GLIPHLGQARTPYLQLQVTERGVLRADDG THAGAATSTPRINSSKRRSSLPNUS  5727 21 221 RPILILKETRELPWATGYASVINAGKSTTINEDGASCEVLTVKKK AGAVTSTPRINSSKRRSSLPNUS  5728 2 877 GTRIGGFFPRGGABGESAGGLRAPGANAGGPGVOPRISSOT/VKK AGAVTSTPRINSSKRRSSLPNUS GR\PMAGGRPPRPVSGVLGSRVCOPLYSTSPAGFG\SGGLSPG GSPAGAGGDAG\LPGGCASSPFWLSLFURDLAPPTPHAGAPADPPAVE GR\PMAGGRPPRPVSGVLGSRVCOPLYSTSPAGFG\SGGLSPDAG GSPAGAGGDAG\LPGGCASSPFWLSLFURDLAPPTPHAGAPADPPAVE GR\PMAGGRPPRVSGVLGSRVCOPLYSTSPAGFG\SGGLSPDAG GSPAGAGGDAG\LPGGCASSPFWLSTTPTQADVURSPHTGFGGLML HEMPTS\GPFSQLGSGAGGDGGVADAPG\GCIN\GARDPPAVE GR\PMAGGRPPRVSGVLGSRVCOPLYSTSPAGFG\SGGLSPDAG EPPCVPEAGEEDAVATEGGFTYTPRLIIMDLKSSLSSLKERGGG\TYSTAG FOPDULKTGRTLINGGFTYTPRLIIMDLKSSLSSLKERGG\TYSTAG GLYANAGGREVUT\GGFTATTPRKLIIMDLKSSLSSLKERGG\TYSTAG GLYANAGGREVUT\GGFTATTPRKLIIT\MDLKSSLSSLKERGG\TYSTAG GLYANAGGREVATIGATIT\CHARTS\GGFTYTPRLIIMDLKSSLSSLKERGG\TYSTAG GTYMGGG\TUKNIBGGBAGRLAFFG\GGSVLKERY\GGSLLSDGVWRV KSINKGSSPLENTTPRKLIIT\MDLKSSLSSLKERGG\TYSTAG GTYMGGG\TUKNIBGGBAGRLAFFG\GGSVLKERY\GGSLLSDGVWRV KSINKGSSPLENT\GGGFTYTPRLIIMDLKSSLSSLKERGG\TYSTAG GTYMGGG\TUKNIBGGAGRLAFTG\GGTYTYTGS\TYSLGSSLGLR PEPPVSFYLHTDATLPFRG\STLATALTVTCS\TYSLCSSDG\TWY KSINKG\TYSLGSSBLLLTTPCT\STLATAGG\TYTTCS\TYSLGSSLGLR PEPPVSFYLHTDATLPFRG\STLATAGT\TYTCS\TYSLGGS\TWY WILL\ADMLSSTCCCR\TYTYTYT\TYSLG\TSTLATAGT\TYTCS\TYSLGGS\TY WITHLADMLST\TYSLGT\TYTT\TYSLT\TYTT\TYTT\TYT\TYT\TYT\TYT\TYT\TYT\TYT	1			CACCANCINI CODOCARDA OLDBONAL CALBERRA CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTR
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TRIMGUTPCILIPLEMOLIP PROSOCVITI/SEVGACIPOPERAG QGS POGSGEOPPLSSPSGPIDADLEGATLEDVOLLEEVRPLAVT GLIFHLOGARTPPYLLOGOTTERVEVLARADO GLIFHLOGARTPPYLLOGOTTERVEVLARADO S727 21 221 RFILLIKETRELEWARTGVASTIRAGESTHREDGASCEVLTVKKK AGAVTSTIRARSSKRESSLIPMOLREPPTERVEVLARADO FOR CHIRAGOFEPRIGRAMGGSAGGELGAPGAJAGGGPUQPRGSGJ/LPG RILLIKETRELEWARTGVASTIRAGESTHREDGASCEVLTVKKK AGAVTSTIRARSSKRESSLIPMOLREPPTERAGGAPDPPAVE GR\PMAGGRPPMPVSGVLGSRVCGPLYSTSPAGGF6/SGGLSPG GGPAGAGGAGA/LPGGCSJARPAGASGRASGPUPPERAGGAPDPPAVE GR\PMAGGRPPMPVSGVLGSRVCGPLYSTSPAGGF6/SGGLSPG GGPAGAGGAGA/LPGGCSJARPAGASGRASGPUPFGPQGLMI HENDTS/GFFSQLGBGABCGDEGVADAPCIQCKN/GAEDPPAED EPPCVPEAGAEDAVPAEBGFGTFSTQADOVHFGPCGGLMI HENDTS/GFFSQLGBGABCGDEGVADAPCIQCKN/GAEDPPAED EPPCVPEAGAEDAVPAEBGFGTFSTQADOVHFGPCGGLMI HENDTS/GFFSQLGBGABCGDEGVADAPCIQCKN/GAEDPPAED EPPCVPEAGAECHAPGFGFTSTQADOVHROSTGRAGTABKEPFGEL CPDVLWATGRTLINGGSTTPRLILAMDLKGSLSSLKEPGGLYDK GLDAATAMGGALTHHEELPVARPVLQDFLSGAGGATGABC CPDVLWATGRTLINGGSTTPRLILAMDLKGSLSSLKEPGGLYDK KSIPNCKGSSPLPTAATTEKPLIPTEASIRWADPLARVHLHPRSI CHICKYNHOLGSGRGALABAGGGSVLKPPKVGGASCSLOCHEV KSIPNCKGSSPLPTAATTEKPLIPTEASIRWADPLARVHLHPRSI CHICKYNHOLGSGRGALABAGGGAGAGAACALLDBYTGCSLOCHEV KSIPNCKGSSPLPTAATTEKPLIPTEASIRWADPLARVHLHPSSI CHICKYNHOLGSGRGAGARAAGCHUSSCHUNGCHUNGLEDHHPVELD PEPPVSFPVLHYDATLIPTUATHLARHDLKGGGGSSVLKPKYGGGGAGCSGCGGCGACA WARTHAADANATTERLARVHLAGAGATAATAADAPCHCSLOCHEV WHILADALLSCACKAVVYAGATALIPTUACSAYNICALDHPVELD PPPSLAGAGGRAGAACAGATAATAATAACAAAAAAAAAAAAAAAA	5706	<del> </del>		
GGSPGGGGGPLSSTSQFLEADLPGATLEDVGLEADUD    5727   21   221   RPILILKETRELPMAGYAETINAGKSTHNEDQASCEVLTVKK   AGAVTSTPHRISSKRRSSLNGE     5728   2   877   GTREGGFEPRERAMGGSAGGLEAPGAAAGGGPVQPRESGJARG   GARAGGFEPRERAMGSAGGLEAPGAAAGGGPVQPRESGJARG   GARAGGFEPRERAMGSAGGLEAPGAAAGGGPVQPRESGJARG   GARAGGFEPRERAMGSAGGALEAPGAAAGGGPVQPRESGJARG   GARAGGFEPREVENGGALEAPGAAAGGPVQPRESGJARG   GARAGGFEPREVENGGALEAPGAAAGGPVQPRESGJARG   GARAGGPPRPVGGALEAPGAAAGGPVAPERSGJARG   GARAGGPPRPVGGALEAPGAAAGGPVAPERSGJARG   GARAGGPPRPVGGALEAPGAAAGGPVAPERSGJARG   GARAGGPPRPVGGARGARGAAPGAAPGAAAGAAPAGAAACAAAAAAAAAAA	3/26	2	486	
ST27   21   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221		1	ł	TRMAGVTPCILGPLEAGLFFPGSGGVITL/ESVGAGIPGPSRAG
ST27   21   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221   221		1	ł	QGSPGGSGEGPPLSSPSQPLPADLPGATLPDVGLELEVRPLAVT
S727   21   221   RPILIKETRELPWATGYAEVINAGKSTHNEDGASCEVLTVKKK AGAUTST PRANSISKRRSLYNGS   2   877   GTRKGGFEPRGEARGSKGTLTAGAAAGGGOOGDAGAAGTST PARNSISKRRSLYNGS   GRANGGROPPRANSISKRRSLYNGS   GRANGGROPPRANSISKRRSLYNGS   GRANGGROPPRANSISKRRSLYNGS   GRANGGROPPRANSISKRRSLYNGS   GRANGGGOODDAGADGGOOGDAGAAGGGOOGDAGAAGGGOOGDAGAAGGGOOGDAGAAGGGOOGDAGAAGGGOOGDAGAAGGGOOGDAGAAGGGOOGDAGAAGGGOOGDAGAAGGGOOGDAGAAGGGOOGDAGAAGGGOOGDAGAAGGGOOGDAGAAGGGOOGDAGAAGGGOOGDAGAAGGGOOGDAGAAGGGOOGDAGAAGGGOOGDAGAAGGGOOGDAGAAGGGOOGDAGAAGGGOOGDAGAAGGGOOGDAGAAGGGOOGDAGAAGAAGGGOOGDAGAAGAAGGGOOGDAGAAGAAGGGOOGDAGAAGAAGGGOOGDAGAAGAAGAGGGOOGDAGAAGAAGAAGGGOOGDAGAAGAAGAAGAAGGGAAGAAGAAGAAGGGAAGAAGAA		1	}	GLIFHLGQARTPPYLQLQVTEKQVLLRADDG
5728 2 877 GTRRGGEPERRGRWESSAGGRAPGAAGGEVQPEGGG/LEC GTRRGGEPERRGRWESSAGGRAPGAAGGEVQPEGGG/LEC GTRRGGEPERRGRWESSAGGRAPGAAGGEVQPEGGGPLEDPEAVE GR\PMAGGEPPPMCSGUPGGRVCGPLYSTEPAGPG\SGGLSPSQ GGPAGAGDAG/LEGRCPESTEPTADOVREPERHALARGGA ERPQVPEAGEEDAVPAREGFGTFETCADOVREPERHALARGGA KGSPRALADPODLEAGGMSLAPFFFVAAVIESK GGREVLIGUGGFFAGGAGGEGGAAGGGCAACGAAGGACGAAGAGAAGAAGAAGAAGAAGA	5727	21	221	
S728   2   877   GTRNGGEPERGENMEGSAGGILAPGANGGGVQPPGSG7LEV   GR\PNAGGIPPHPUSGVLGSRVCGPLYSTSPAGPG/SGGLSPSQ   GR\PNAGGIPPHPUSGVLGSRVCGPLYSTSPAGPG/SGGLSPSQ   GR\PNAGGIPPHPUSGVLGSRVCGPLYSTSPAGPG/SGGLSPSQ   GGPAGAGGIDAG/LEGRCGPGSWDAD/GICCRN/GAEDPPAED   EPGVVERAGEEDAVPAEGFGSTETQADOVERPPERHLARGGA   STORLAND-DOLLARGANGALPPFPFVANTISNK   SSPRILADD-DOLLARGANGALPPFPFVANTISNK   SSPRILADD-DOLLARGANGALPPFPFVANTISNK   GRANGSPLILADD-DOLLARGANGALPPFPFVANTISNK   GRANGSPLILADD-DOLLARGANGALPPFPFVANTISNK   GRANGSPLILADD-DOLLARGANGALPPFPFVANTISNK   GRANGSPLILADD-DOLLARGANGALPPFPFVANTISNK   GRANGSPLILADD-GRANGALPPFPVANTISNK   GRANGSPLILADD-GRANGALPPFPFVANTISNK   GLANDALAMGGKLTTHKEEL-YEKNPY-QDELEDRIHTYVEE    COLVIGGFG/LOLHD-GFSGVAGRABALLD-GSSGGRUFPK   KSIPNCKGSSS-JLPTATTH-FULLPULASSISVLESGGLVRDK   GRANGSSLICH-THE GRANGALPH GOGSS-JLKEPK-VOBELEDRIHTYVEE    COLVIGGFG/LOLHD-GFSG-VGAGRABLLD-GSSGGRUFPKD-WIRT   GFYRRGEAGRNI-YRLIN-TA-FGL-WILA-SISVL-VGS-GGL-PR-PR-PR-PR-PR-PR-PR-PR-GRANGALP-GGGLT-PR-PR-PR-PR-PR-PR-PR-PR-PR-PR-PR-PR-PR-	1	1		
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GR\PMAGGRPPHPVSGVLGSRVCGPLYSTSPAGPG/SGGLSPSG GGPGAGGGDAG/LOFGCPSAPMAGSTPASCPOWINGDQUML HRNPTS/GPPSGIGEGARGGEGVADAPQIQCKN/GAEDPPAED EPPQVPEAGEDAVPAGEGFGTFETQADQVRERPEAHLAGGGA KOSPRIADPQDLEPAGCMSLAPPFPPVAAVIENK AGGREVLITLGIGHFAGFVGAHKWMQDAALGERTDKREPPEG CPDVLVSTGRTHAGGSTYTPRILIMD LKGSLSSLKEEGGLYKDK QLDAALAWGGKLTTHKEELYPKNPYLQDFLSARGVLSSDGWRV KSIPNGKGSSPLPATTYPKLIPTEN ERWSDFLEVHLHPRSI CMIGKYNHIGRAGRILAFGGGSSVLKEPKYQESLEDRLHFYVEE CDYLGGFQLLCDLHOGFSGVGAKAAELLQDFSGGSILTDK KSIPNGKGSSPLPATTYPKLLIPTEN ERWSDFLEVHLHPRSI CMIGKYNHIGRAGRILAFGGGSSVLKEPKYQESLEDRLHFYVEE CDYLGGFQLLCDLHOGFSGVGAKAAELLQDFSGGSILGK KSIPNGKGSSPLPATTYPKLLIPTEN ERWSDFLEVHLHPRSI CMIGKYNHIGRAGRILAFGGGSSVLKEPKYQESLEDRLHFYVEE CDYLGGFQLLCDLHOGFSGVGAKAAELLQDFSGGSILGK GPYHRGEAQRNIYHLLATARGSLVCPLSISGGILG FPPPVSFPYLHYDATLFFHCSALIPATQGSPUSSGGSGLGS MYHIL\ADMISSCGKKVVTAGAIIPPTHAPQGSIPDILMGFGGAT PWTPLSACGEPSGTRCFAGSVVVLRGIDRACHTSCJTFCTPPPSA LHACTTGGEILAQVLQQOPGWMSSILTFTCRYVPPYPHLFS SCSSPGMVLLDSSPKGAAVESVPVFG  KKFGAPARTCVCCGKLTVYPMERLLANGQVFHTSCFRCSYCNNK KJEGTYASLHGRIYCKPHPNQLFKSKGNYDEGFGHRPHKDLMAT KIETEGFWERPRNFENCGGPLFKSVGGCGCGCGCSNY*AQ GSSSREKGGQASMNPKIRVA  5731  122 443 RSHRGELIFKDSCYMKRPPRRFKKRGG/CALPQGCLFFKDVAL KJETKSGAGASMANDRIVARAVMLERNYRNLESVGLTSKOSWYMKK KPGRGRGKRRAGBFFLKVY GSSSREKGGGASMNPKRRNA KFGGRGRGKRRAGBFFFRVY SCHLARAFTAGARKFLLAPNI\N LLGTKSGABRATALALRCGGRKDQFGRLKXVGGIGVFLDKKNIA LLGTKSGABRATALALRCGGRKDQFGRLKXVGGIGVFLDKKNIA LLGTKSGABRATALALRCGGRKDQFGRLKXVGGIGVFLDKKNIA LLGTKSGABRATALALRCGGRKDQFGRLKXVGGIGVFLDKKNIA ALLDAA AQVYSMWYTKNIAMYRNIPSKNRGAYATFFIVPTVI CSLPLMNILLTALIYSOFRGYIMKSLQTSLFRRRLOTRAAFEVLS SMYGRGGAFPQAVGVRCPGILLQTLAVGLGLIFVLUESS GVSLLSABEFGULFFISLDLLTLTPANNLFVLI PAYSKMRAYATFFIVFTVI CSLPLMNILLTALIYSOFRGYIMKSLQTSLFRRRLOTRAAFEVLS SMYGRGGAFPQAVGVRCPGULLQTLAVGLJUNGKAMMEKNRS FDSILVP JEFTGKMDEVJSTVLEMPFREYGSFFLOSIALLTH TLVCTDCHTDAGGGRRNW/RLLSLMDMTMLMMLIVFRFLRIIP SMCPAGAYVATSVLGL VFFTVYTLEMLLAVFALGRGRYSTYSTENDELLTVULLDEIS TLVCTDCHTDAGGGRRNSFLINFYLMFINTLAGRTYNDLIVG VFFTVYTLEMLLAVFALGRGRYSTGALGRANDFVAGA RYFTGULFK,SSNMTGRUGRREISNFFYLMFINTLAGRTYNDLIVG VFFT	1	I -		NATRACINEGRADA COENT. CT. DINIT INDEPENDENT ACCESS.
GGPAGAGGDAG/LPGRCPSAPMRAGSRPAASCPPWTGFQGGLTHANNTS/GSPPSQLTGGEGGPGFTOCKN/CAGEDPPAED HRNPTS/GSPPSQLTGGEGAVPAEGGPGGTPETOADOVRERPEAHLAEGGA KGSPRLADPODLPAGOMSLAPPFPPVAAVIRSNK  5729 1 1525 AGGAREVUITLQTGHFRGFVGARKWROQDALGEATDSKEPPGEL CPDVLYKTGRTLHGGETTTPRLILMDLKGSLSELKEEGGLYKDK CLDAAL NAMGOKLTTHKELPKNPFYLDFASGVLKSENGGWRV KSIPNGKGSSPLPTATTPKPLLIPTEASIRWNSPLRWHLHDRSI CMIQKYMHDGARGHLAFGGGSSVLKEPKYQBELEDRLHFYVEE CDYLGGPOLLCDLHDGFSGVGAKAAELLQDEYSGRGITTMCLLP GFYHRGEAGRNIYRLHATAFGLVHLTAHSSLVCYBLGGSSIGLR PEPPVSFPYLHYDATLPHFASAILATHALDTVTCS\YRLCSSPVS MVHI\ADMESRGGKKVVTAGAIIPPPLAPGGSIPDSLMQFGGAT PWTPLSAGACEPSGRRCPAGSVVLKGIPGATSOLTPGTPPPSA LHACTTGEBILAOVIQQQDGWMSSSHLLITPCRVAPPYPHLFS SCSPPGWVLDGSPKGAAARSSVPVFG SCSPFGWVLDGSPKGAAARSSVPVFG KIETEGFMERRYNERGGSVCKKGVPDGFGRFPHKOLWAT KIETEGFMERRYNERGGFLKSCRGFTSPPSA LHACTTGEBILAOVIQQODGWSSSHLLITPCRVAPPYPHLFS SCSPFGWVLDGSPKGAAARSSVPVFG SCSPFGWVLDGSPKGAAARSSVPVFG GSSSRKGGQASWPKLRVA GSSSRKGGGASWPKLRVA SFRIGGLIPKDSCYMREPPEPKKRRGG/CALEGGCLFFKDVAI EFSLEENKCLNPAGRALYRAVMLENYRNLESVGLTSKDSWYMRX KPGGRGGKGRRGBFPLRYV  5731 122 443 EFSHEGELIPKDSCYMREPPEPFKKRRGG/CALEGGCLFFKDVAI EFSLEENKCLNPAGRALYRAVMLENYRNLESVGLTSKDSWYMRX KPGGRGGKGRRGBFPLRVY  5732 226 772 FPSRSCQSPRRKSRRRAHVTVTLVCGFTSFFSLFLYLCGCLRF PERTCSQLQQADWAPDFGFSSFVPSMGATATGRRFFLIAFNI\N LLGTKRGAMRALAMLGGCGRKCDGFGKLVQGIGWVLDGRNLA QVGSMWVTRKTAMVFANYDPRMKRRGGLHYVVIERDEKM\AS GVSTNILDFEVTALHTVYFETCREQELSLPVVGSQLVGLUPLLX ALLDAA AQVQSMWVTRKTAMVFANYDPRMKRRGGHTYVVIERDEKMA\AS FDEILVP\EFIGKMDEVJSRDPM  SCSPFSTSLLVLLTTANNLFVLIPAYSKNRAVAIFFIVFTVI GSLFLMNLLTALTYSQFTRGVMKRLGGFSCCDPGARRSVLS GSGLLSABEPGKLIPAGGRCDDGFGTSFRRLGTRAAFBVLS SWGSGGAFPQAGVVSKQDALLQVLQXDSHKQDSHLVAVERUS GSULLSABEPGKLFNLLAAMLUSTCFFULDADVLPAERDPTLGSILNC VFIVYYLLEMILAKVFALGLGCYLLYSPODGLTVVULNELS TLVCTDCHTQAGGGRANGFGLSCHPLDATVILDESING VFIVYTLLEMILAKVFALGLGCYLLYSPODGLTVVULNELS TLVCTDCHTQAGGGRANGFELSNFEYLMFVLLAGTNDLIVG YEVFWULTNYESSEELDLTLBFGYLMFVLAGATSVNDLIVG YEVFWULTNYESSEELDLTLBFGYLMFVLAGATSVNDLIVG YEVFWULTNYESSEELDLTLBFGYLMFYLDSTATATAGE RYSTMEDDQSPFYHYNTHYSTATSTLSMLVRIVSIFFIELACLWY LKLIT	1			
HENDTS/GPPSGIGEGAEQGBEGVADAPCIQCKN/GAEDPPAED EPPGVPBAGEDAVABEGGGGTETOADVEREPEAHLAGGA KGSPRILADPODLPAGGMSLAPPFPPVAAVIESNK  5729  1 1525 AGGREVUTQUIGHFAGFVGAHWENQQDALGRATDSKEPPGEL CPDVLYRTGRTHAGGETYTPRILIADLGSISLSEGGLYRDK GLDAAIAWGGKLTHKEELYPKNPYLQDFISABGVLSSIGWRW KSIPNGKGSSPLPHATTPKLLIPTASICVENSSILKEEGGLYRDK GLDAAIAWGGKLTHKEELYPKNPYLQDFISABGVLSSIGWRW KSIPNGKGSSPLPHATTPKLLIPTASICVENSSILKEEGGLYRDK GLOWANHIGEBGRIEAFGGESVLKEPKYQEELEBRIHFFYEE COMIQKYNHIGEBGGRIEAFGGESVLKEPKYQEELEBRIHFFYEE GPYMRGEAQRNIYRILMTAFGLUHLTAHSSLVCPLSLGGSIGLR PEPPVSFPVLHYDATLPHCSAILATALDTVTCS\YRICSSPVS MVHL\ADMLSFCGKKVUTAGAIIPPLAFGGSIPDSINGFGGAT BWTPLSACGEPSGTRCPAGSVVLRGIDRACHTSQLIPCTPPPSA LHACTTIGEBILAQVILQOQPGWMSSILHDFCKVAPPULLSF SCSPPGMVLDGSPKGAAVESVEVE  5730  1258  1713  KKFGAPARETUCEQGKVYPMERLLANQOVFHISCFRCSYCNNK LSIGTYASILHGRIYCKPHYNOLFKSKGNYDEGGRIPPKKDLWAT KKFGAPARETUCEQGKVYPMERLLANQOVFHISCFRCSYCNNK LSIGTYASILHGRIYCKPHYNOLFKSKGNYDEGGRIPPKKDLWAT KKFGAPARETUCEQGKVYPMERLLANGOVFHISCFRCSYCNNK LSIGTYASILHGRIYCKPHYNOLFKSKGNYDEGGGRIPPKKDLWAT KKFGAPARETUCEQGRYVPMERLANGOVFHISCFRCSYCNNK KKFGAPARETUCEQGRYVPMERLANGOVFHISCFRCSYCNNK KKFGAPARETUCEQGFRLPKSPKGRGFYCALPQGCLTFKDVAI EFSLEENKCLBPAGRALYRAVMLEBYNLESVOLTSKOSWYMKX KPGGRGKGRGRORMPFLRVY  5731  122  443  RSHRGELIPKDSCYMRKPPERFKKRRGG/CALPQGCLTFKDVAI EFSLEENKCLBPAGRALYRAVMLESVALTSKOSWYMKX KPGGRGKGRORMPFLRVY  KPGGRGKGRORMPFLRVY  FPSRCGGJGPRKSERRAHTVYLLVGGTSFSPSLPLYLCGCLRF  PERTCSGLQADANAPDFGFSSFVPSWGATATGARKFLIAPNI\N  LLGTKRAGHARIALMLEGGGRGCDGDGFTKANGOLANG  ACQUSYMWWYTKNAMYTRANFVRAYDFRKKRGGFTALKSAYM AQQUSYMWYTKNAMYTRANFVRAYDFRKKRGGFTALKSAYM AQQUSMWYTKNAMYTRANFVLTANDFVLITAYSKNRAYATFPTVFTV  GSLPLMNLLTALTYSOFRGYLMKSLQTSLFBRRLGTRALFFVLS  SMCGGAPPQAVGVRPQNLLQVILQVGLUSKKQAMMEKURS  GSVLLSABEPGKLFFRLIGRGVYKEPBFTERYGSFFLGSAGFLGE  HYFTYTLLHAMLAVALGLGRYTYSTERDELLTRALFFULLUSIS  TLVCTDCHTDAGGGRRDWYRLLSHFIGHTMLIMMLIVERSL  TLVCTDCHTDAGGGRRDWYRLLSHFIGHTMLIMMLIVERSL  TLVCTDCHTDAGGGRRDWYRLLSHFIGHTMLIMMLIVERSL  TLVCTDCHTDAGGGRRDWYRLLSHFIGHTMLIMMLIVERSL  TLVCTDCHTDAGGGRRDWYRLLSHFIGHTMLIMFULLESIS  TLVCTDCHTDAGGRRDWYRLSHFIGH		1		GCDAGAGGDAG (LDGDGDAGADADAGAGAGAGAGGLSPSQ
SPPQVPEAGEDAVPAEESPGGTTETQADQVERPPEAHLAEGGA   KOSPREADPOOLPAGQVISLAPPVAAVIESNUK   SOSPREADPOOLPAGQVISLAPPVAAVIESNUK   SAGAREVULTUJUHPRAGFYGGAHWANQQDAALGRATDSKEPPGEL   CPDVLYRTGRTLHQGETYTPRLILIMDLKSSLSLKEESGULROK QLDAALAWGKULTHKEELIYKNYPLQDFLSAEGVLRSDGVWRY   KSIPNGKGSSPLPTATTEKPLIPTEASIRVWBDFLRVULHPRSI   CMIQKVRHDCHSAEGVLSSDGVWRY   KSIPNGKGSSPLPTATTEKPLIPTEASIRVWBDFLRVUHLHPRSI   CMIQKVRHDCHSAGRIEAFRQGGESVLSHAPVQUELDRHHFYVEE   CDYLQGGPOLLCULHDGFSGVGAKAABELLQDRYSGRGITTMGLLP   GPYRTGRAGRANT YRILLINTA/SGLVHAHSSLVCPJLSLGGSLGLR   PEPPPVSFPYLHYDATLPPHCSAILATALDIVTCS YRILCSSPVS   WWHL\ADMLSPGSKCVVTRAGAITPFPLARGQSEPDSIMQFGGGT   PWTPLSSACGEPSGTKCPAGSVVLIGTBACHTSQLTPSTPPSSA   LHACTTGEBILAQYLQQQQPGVMSSSHLLITCRVAPPYPHLFS   SCSPFGMVLJGSPJKGAAVESVPVE   SCSPFGMVLJGSPJKGAAVESVPVE   SCSPFGMVLJGSPJKGAAVESVPVE   SCSPFGMVLJGSPJKGAAVESVPVE   SCSPFGMVLJGSPJKGAAVESVPVE   SCSPFGMVLJGSPJKGAAVESVPVE   SCSPFGMVLJGSPJKGAGAAVESVPVE   SCSSFRKGGQASWNPKLRVA   GSSSRKGGQASWNPKLRVA   SKHEGEFBRENKCLNPAGRALYRAMLENYRNLESVGLTSKDSWYMKX   KPGGRGKQRGGBPFLKVY   SEFSLEENKCLNPAGRALYRAMLENYRNLESVGLTSKDSWYMKX   KPGGRGKQRGGBPFLKVY   SEFSLEENKCLNPAGRALYRAMLENYRNLESVGLTSKDSWYMKX   KPGGRGKQRGGBPFLKVY   SPSSECQSPRKSRRRAHVTVTLVCGFTSFSFSLPLYLCGCLRF   PERTCSGLQQADMAPDGFSSFFPSWGATATARKFLIARNI \N LLATTKEQARMADAGCPGRLKKVQGIGWLJDEKNLA   CUSTNLIDBEVTALHTVYEETCREAQELSLPVVGSQLVGLVPLK   ALDJAA   ALDJAA   CUSTNLIDBEVTALHTVYEETCREAQELSLPVVGSQLVGLVPLK   ALDJAA   ALDJAA   ALDJAA   ALDJAA   AQVQYSMWVTRKNANYFANYDPMKREGLHLVVLERDEKYM\AS   FDEI\VP\EFFAGRADDLCSGMONGLELKCPTFAGFFTGVNDTGSFTIYRDES   MRTACSPDOLCSGMONGLELKCPTFAGFFTGVNDTGSFTIYRDES   MRTACSPDOLCSGMONGLELKCPTFAGFFTGVNDTGSFTIYRDES   SMCGGGAFPGAVKYNCHNLOLGKVLDAVLAFRADFFTLIGITNC   CSLFLMNLLTATIYSQFRGYLMSSLCTSLFRRIGTFAAFBVLS   SWGGGGAFPGAVKYNCHNLOLGKVLDAVLAFRADFFTLIGTT   SKMPAVASTVLGL   TUVCTDCHTGAGGRRNW/RELISLBCHMTRMLMMLIVERFERIIP   SMCPRAVASTVLGL   TUVCTDCHTGAGGRRNW/RELISLBCHMTRMLMMLIVERFERIIP   SMCPRAVASTVLGL   TUVCTDCHTGAGGRRNW/RLISLBCHMTRMLMMLIVERFERIIP   YRFFWQDGSPYNYNTHNTSTATSTSLSKLVRIVSIFIELACLWY   YPVFWVLINTEBEBLDLTLIGN	1	1		GGFAGAGGDAG/ LFGKCPSAPWRAGSRPAASCPDWIPGPQGLWL
S729   1   1525   AGGAREVULTU,GHPHAGYWGAMWAQDAALGEATDSKEPPEEL	1			HRNPTS/GPPSQIGEGAEQGDEGVADAPQIQCKN/GAEDPPAED
1 1525 AGGREVLITIQUEHPAGEVEGAHWANQODAJGRATDSKEPEGEL CDDILYPTGRETINGGETTYPELLITIMALKGSLSSLKEEGGLYEDX QLDAA IAWQOKLTTHKEELYPKNPYLQDFLSAEGGLYEDX QLDAA IAWQOKLTTHKEELYPKNPYLQDFLSAEGGLYEDX KSIPNGKGSSPLPTATTEKPLIFTEAS IRWEGDILHYFYVEE CDYLQGGGILCOLHDGFSGVGKRAAELLQDBYSGRGITHMGLLP GFYRRGEAGRAT YELLINTAFGLYHATSSLVCPLSIGGSLGK PEPPVSSFPYLHTDATLPPHCSAILATALDTVTCS YERLCSSPVS MYHLA,DAMLSPCSKKVVTAGAI IPPPLAPGQSLPDSLNGFGGAT PWTPLSACGEPSGTRCFAQSVVLKGGIDRACHTSQLTFETPPPSS LHACTTGEBILAQYLQQQPGVMSSSHLLITTCRVAPPYPHLFS SCSPPGMVLLDSPNGAAVESVPVEG  5730 1256 1713 KKFGAPARETCVECQKTVYPMERLLANQOVFHISCFRCSYCNNK LSIGGTVASLHGRITVASLHGRITVASKGINTAGTFGRCSYCNNK KSTGGFWERPENFENQGEPLKSPGGGCPGSNY*AQ GSSSREKGGQASWNPKLRVA  5731 122 443 RSHRGELIPKDSCTWRKPPERFKKRRGF/CALPGGCLTFKDVAI EFSLEENKCLNPAQRALYRAVMLENYRNLESVGLTSKDSWYMKK KFGGRGKRRGEWPFLRVY GSSSREKGGQASWNPKLRVA  5732 226 772 PPSRSCQSPRKSRRABAVTUTLVGGFTSFSSEDFLYCGGCLRF PERTCSOLQQADWAPDFGFSSFVPSWGATATGARKFLIAFNI\N LLGTKRQAHRIALBLREGGRKORQFGRLKKVQGIGWYLDEKNLA QUSTNILDBEVTALHTYPEETCREAQELSLEVVGSQLVGLUPLK ALLDAA ALLDAA ALLDAA ALLDAA ALLDAA ALLDAA ALLDAA AQVOYSMWYTRNANYFANYDPRMKFELGFFALNSAYM AQVOYSMWYTRNANYFANYDPRMKFELGFFALNSAYM AQVOYSMWTRNANYFANYDPRMKREGLHYVVIERDEKM\AS FDEI\VP\EFIGKMDEVISCDTSHFRRIGTRAAFEVLS SWGRGGGAFGQAVGKPOLLOKVQLOLDSSHKQAMMEKVRSY GSVLLSAEFGKLFNELDRSVVKEHPPRPEVQSPFLQSAQFLFG HYYFDYLGNLIALANLVSICVFLVILDADVLPAERDDFIIGINC VFIVYYLLEMLLKVFALGGRGVLDVVKOLDSSHKQAMMEKVRSY GSVLLSAEFGKLFNELDRSVVKEHPPRPEVQSPFLQSAQFLFG HYYFDYLGNLIALANLVSICVFLVILDADVLPAERDDFIIGINC VFIVYYLLEMLLKVFALGGRGVKPONLOLQUCKVOLDSSHKQAMMEVRSY GSVLLSAEFGKLFNELDRSVVKEHPPRPEVQSPFLQSAGPLFG HYYFDYLGNLIALANLVSICVFLVILDADVLPAERDDFIIGINC VFIVYYLLEMLLKVFALGGRGVKPONLOLQUCKVLDSSHKQAMMEVRSY GSVLLSAEFGKLFNELDRSVVKEHPPRPEVGSPFLGAGPTGRIT TÜVCTDCHTGAGGRRNW/RLLSLMMTRMLNMLIVVRFIERIIP SMEPBAVVASTVLGL VFIVYYLLEMLLKVFALGGRGVINFROLTSHTYNDINQ YPVFPWVITNYESEELDLTLPGNFROLTSKFJGLPGARRILL ATTGLLYK/SSNMTQRWGRREISNFFSYLMFLNTIAGRTYNDINQ YPVFPWVITNYESEELDLTLFGNFROLTSKPSTFGGLPGARRILL ATTGLLYK/SSNMTGGRGVGREISNFFSYLMFLNTIAGRTYNDING YPVFPWVITNYESEELDLTLFGNFROLTSKP	1			EPPQVPEAGEEDAVPAEEGPGGTPETQADQVRERPEAHLAEGGA
CPDVLYRTGRTLHGQGTYTPRLIAMDLKGSLSSLKERGGLYRDK QLDAAIAMQGKLTTHKEELYPKNPYLQPSLAGGGTSGYMRY KSIPNGKGSSPLPTATTPKPLTPTRASIRVMSDFLRVHLHPRSI CMIQKYNHDGEAGRLEAFGGGSVLKEPKYQEBLEDRLHFYVEE CDYLOGPOILCULHGFSGVGAKAAELLQDEYSGGGITHGLLFY GPYHRGEAQRNIYRLLNTAFGLYHLTAHSSLVCPLSIGGSLGLR PEPPVSFPYLHYDATLPPRCSAILATALDTVTCS\YRLCSSPVS WYHH\ADMLSFCKKVUTAGAILATALTUTCS\YRLCSSPVS BWTPLSACGEPSGTRCFAQSVVLRGIDRACHTSQLTFGTPPPSA LHACTTGEBILAQPLQOQDQFWGSSHLLLTPCRVAPPYPHLFS SCSPPGMVLDGSPKGAAVESVPVFG  5730  1256  1713  KKFQAPARETCVECQKTVYPMERLLANQQVFHISCFRCSYCNNK KKFQAPARETCVECQKTVYPMERLLANQQVFHISCFRCSYCNNK KIETEGFWERPRRFENCGRPLKSPGGEDCPSC*GGCPGSNY*AQ GSSSREGGGGAWPKLRVA  5731  122  443  RSHRGELIPKDSCYMEKPDFRFKKRRQG/CALPQGCLTFKDVAI EFSLEENKCLNPAQRALYRAWMLENVRILSSVGLTGSCBSYMRK KPGRGRKGRRGBWFPLRVY  FFSTSCQSPRRKSRRRAHTVTULVCGFTSFSFSLPLYLCGCLRF PERTCSQLQADAWAPDFGFSSFVPSWGATAGGARKFLIARNI\N LLGTKRQAHRIALNIRECGGKKDQFGRLXKVQGTGWVLDEKNLA QVSTNILDFEVTALHTVYBETCREAQELSLPVVGSQLVGLVPLK ALLDAA  ALLDAA  1 460  PALQEVNANALAMGKQYENDARTLFEFTSGVNDTESFITYRDES MRTACSPDGLCSDGNGLBLKCPFTSRPFMKRRLGFFALKSAYM AQVOYSMWVTRKNAWYFANYDPRMKREGLHYVVLERDEKYM\AS FDEILVP\SFIGKMEDVLSQPB  SMGGGASPQAVGNONLUQLVQLVGLVOSLSKKOMMEKVRSY GSULLSAEBFQKLFMFELDRSVVKEHPPRFBYQSPFLOSAQFLFG HYYFDYLGMLTALARLANJSICTYLLDADVLPAERDDFILGILNC VFIVYYLLEMLLKVFALGLRGYLSVFNHDEDRSTVKHNINNLIVFRFLRIIP SMKPRAVVASTVLCL  SMGGGGAFPGAVGRONLULDADVLPAERDDFILGILNC VFIVYYLLEMLLKVFALGLRGYLSVFNHDELDRSVVKEHPPRFBYGSPFLOSAQFLFG GSVLLSAEBFQKLFMFELDRSVVKEHPPRFBYGSPFLOSAQFLFG TLVCTDCHTGAGGGRRWK/RLLSLMDMTRKIMNLIVFRFLRIIP SMKPRAVVASTVLCL  5735  2 540  FFFCVARRFNFPDQATVKKANYSLPRVGGGTSCGLPQARRISL APPGLYK/SSMTOTGWQRRGISNFEYLMFLNTIAGRTYNDLNQ YPVFPWVLTNYESBELDLITLDFGRFRILSKPIAGRTYNDLNQ YPVFPWVLTNYESBELDLITLDFGRFRILSKPIAGRTYNDLNQ YPVFPWVLTNYESBELDLITLDFGRFRILSKPIAGRTYNDLNQ YPVFPWVLTNYESBELDLITLDFGRFRILSKPIAGRTYNDLNQ YPVFPWVLTNYESBELDLITLDFGRFRILSKPIAGRTYNDLNQ PRETTGRAFTYNDLNG RYTHEDDQSPPYHYNTHYSTATSTLSMLVRIVSIFIELACLWY LKLIT				KGSPRRLADPQDLPAGQMSLAPPFPPVAAVIRSNK
CPDVLYRTGRTLHGGTTYPRILIMDLKSSLSSLKEBGGLYRDK  QLDADAIAMQGKLTTHREELIPMYLQDFLSAEGQUISSDGWRV  KSIPNGKGSSPLPTATTPKPLIPTEASIRVWSDFLRVHLHPRSI  CMIQKYMHOEAGRLEAFGGGSVLKEPKYQBELEDRLHFYVEE  GPYRRGBQRNIYRLLNTAFGLWHLTAHSSLVCPLSIGSIGGLE  GPYRRGBQRNIYRLLNTAFGLWHLTAHSSLVCPLSIGSIGGLE  GPYRRGBQRNIYRLLNTAFGLWHLTAHSSLVCPLSIGSIGGLE  PEPPVSPYLHINDATLPBYCSAELLQDEYSGRGITTMGLLP  GPYRRGBAQRNIYRLLNTAFGLWHLTAHSSLVCPLSIGSIGGLE  WHHL\ADMLSFCCKKVVTAGAIIPPLAPQQSLPDSIMQFGGAT  PWTPLSACGEPSGTRCFAQSVVLRGIDRACHTSQLTFSTPPFSA  LHACTTGEBILAQYLQQQPGWSSSHLLLHTCXAPPYPHLFS  SCSPFGMVLDGSPKGAAVESVPVFG  SCSPFGMVLDGSPKGAAVESVPVFG  SCSPFGMVLDGSPKGAAVESVPVFG  SCSPFGMVLDGSPKGAAVESVPVFG  SCSPFGMVLDGSPKGAAVESVPVFG  SCSSREKGGQASWNFCLRVA  KKFTGFFREFRNFENCGRPLKSPGGBDCPSC*GGCPGSNY*AQ  GSSSREKGGQASWNFCLRVA  SSSREKGGQASWNFCLRVA  FSHRGELIPKDSCYMEKPPRRFKKRRGC/CALPGGCLTFKDVAI  EFSLEENKCLINAPARALLENYRNLESVGLTSKDSWYMRK  KPGGGGGKQRGDWFPLRVY  FPSRSGQSPFRKSRRRAHVTVTLVCGFTSFSFSLPLYLCGCLRF  PERTCSQLQQADWAPDFGPSSFVPSWGATATGARKFLIABNI IN  LLGTKRQAHRIALINLREGGRGKDQFGRLKKVQGIGWLDEKNLA  QVSTNILDBEVTALHTVYEETCREAQELSLPVVGSQLVGLVPLK  ALLDAA  1 460 PALQEVNANALAWGKQYENDARTLFEFTSGVNDTESPTIYRDES  MRTACSPDGLGSDGNGLBLKCPFTSRFFMKRRGGFFAIKSNYM  AQVQYSMWVTRKNAWYFANYDPRWKRBGLHYVVIERDEKYM\AS  FDEILVP\SFIGKMEDVLSRDW  SWGBGGAFPQAVGVKPQNLLQVLQKVQLDSSKKQAMMEKVRSY  GSVLLSABEFGKLFNFELDRSVVKEHPPRFYQSPFLQSAGFLFG  HYYFDYLGNLITALARLUSICTYLLDAVSKRRAYAIFFTVFTVI  GSLFLMNLLTAIIYSQFRGYMKKSLQTSLFRRRLGTFAALFULS  SWGBGGAFPQAVGVKPQNLLQULQKVQLDSSKQAMMEKVRSY  GSVLLSABEFGKLFNFELDRSVVKEHPPRFYQSPFLQSAGFLFG  HYYFDYLGNLITALARLUSICTYLLDAVSKRRAYAIFFTUFTIID  SKKPPAVVASTVLUCL  SKEPPAVVASTVLUCL  FTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL  APPRQLYKY/SNMTGRWGRREISNFEVLMFLWTLAGRTYNDLNQ  YPVFPWULTNYESBELDLTLPGNFRDLSKPIGGTSCGLPQARRISL  APPRGLYKY/SSMTMGRWGRREISNFEVLMFLWTLAGRTYNDLNQ  YPVFPWULTNYESBELDLTLPGNFRDLSKPIGGTSCGLPQARRISL  RYSTKEDDQSPPYHYNTHYSTATSTLSKUVIVSIFIELACLWY  LKLIT	5729	1	1525	AGGAREVLTLQLGHFAGFVGAHWWNQQDAALGRATDSKEPPGEL
QLDANIAWQGKLTTHKEELYPKNPYLOPISABEGYLSSDGVWRV KSIPNGKGSSEPLPTATTPKPLIPTBASTRVMSDFLRVHLHPRSI CMIQKYNHDGEAGRLEAFGQESVLKEPKYQEBLEDKLHFYVEE CDYLQGFQILCDLHDOFSGVGKAAELLQDEYSGRGIITMGLLE GFYTMEGAQRNI TYKLINTAFGLIVHTAMSSLVCJESIGGSLGLE PEPPVSFPYLHYDATLPFHCSAILATALDTVTCS\YELGSPVS MYHLA\ADMLSFGCKKVVTAGAIIPPLAGQSLPDSIMQFGGAT PWTPLSACGEPSGTRCFAQSVVVLRGIDRACHTSQLTFGTPPFSA LHACTTGEBILAQYLQQQQFGVMSSHLLLTPCRVAPPYPHLFS SCSPFGWVLDGSVKGAVESVPVFG  5730 1256 1713 KKFQAPARETCVBCQKTVYPMBRLLANQQVFHISCFRCSYCNK LSLGTYASLHGRIYYCKPHFNQLFKK KGNYDEGFGHRPHKDLWAT KIETEGFWERPRRFENGCRPLKSVGGCCTSCYGCGGSNY*AQ GSSSREKGGASWNPKLRVA FSHRGELIPEMSCYMKKPPRPFKKRGG/CALPGGCLTFKDVAI EFSLEENKCLNPAQRALYRAVMLENYRNLESVGLTSKDSWYMK KPGRGRGKRRQEWFPLRYY FSRSCQSPRKKSRRAHVTVLVCGFTSFSFSLPLYLCGCLRF PERTCSGLQADWAPDFGFSSFVPSWGATATGARKFLLAPNI\W LLGTKRCAHRILANLEGGGRGKDQFGLKXVQGIGWYLDEKNLA QVSTNLLDFEVTALHTVJEETCRRQCLSLFVVGSQLVGLVDLK ALLDAA  5733 1 460 PALQEVNANALAWGKQYENDARTLFEFTSGVNDTESPITYRDES MRTACSPDGLCSDGRGUBLKCPFTSRPFMKRRLGGFEAIKSAYM AQVQYSMWVTRNAWYFANYDPRMKRRLGGFEAIKSAYM AQVQYSMWVTRNAWYFANYDPRMKRRLGGFEAIKSAYM AQVQYSMWVTRNAWYFANYDPRMKRRLGGFFAIKSAYM AQVQYSMWVTRNAWYFANYDPRMKRLGGFFAIKSAYM AQVQYSMWVTRNAWYFANYDPRMKRLGGFFAIKSAYM AQVQYSMWVTRNAWYFANYDPRMKRLGGFFAIKSAYM AQVQYSMWVTRNAWYFANYDPRMKRLGGFFAIKSAYM AQVQYSMWVTRNAWYFANYDPRMKRLGGFFAIKSAYM AQVQYSMWVTRNAWYFANYDPRMRRDLGHTVVTUFTDEI SSPSLTSLLVLLTTANNLFVLIPAYSKNRAYATFFTVFTVI GSLFLMNLLTAITYSQFRGYLMKSLQATSLFRRLGGTFAAFEVLS SMCGGAPPQAVGVKPQNLLQVLQKVQLDSSHKQAMMEKVRSY GSVLLSAESFGKLFNELDRSVVKEHPPREYGSPFLGSAGFLIG HYYFDYLGNLITALARLAUSICCTLYJLDADVLPARFDDFILGINC VFTVYYLLEMLLKVPALGLRGYLSYPSNVEGGLTTVALLVLEIS TLVCTDCHTQAGGRRNW/RLLSLMDMTRNAMLIVFRFLIIP SMKPPAVVASTVLGL SMKPPAVVASTVLGL FTFCVARRFRFPDDATVKKAAYSLPRVGGGTSCGLPQARRISL ATPGLIXY/SSMMTROWGREEISRFSVLMPLNTLAGRTYNDLNQ YPVFPWULTNYESELDLTLPGNFRDLSKPIGHTGATTYNDLNQ YPVFPWULTNYESELDLTLPGNFRDLSKPIGGTSCGLPQARRISL ATPGLIXY/SSMMTROWGREEISRFSVLMPLNTLAGRTYNDLNQ YPVFPWULTNYESELDLTLPGNFRDLSKPIGGTSCGLPQARRISL ATPGLIXY/SSMMTROMGRORFEISRFSVLMPLNTLAGRTYNDLNQ YPVFPWULTNYESELDLTLPGNFRDLSKPIGGTSCGLPGATCHAALRICHY	1		i	CPDVLYRTGRTLHGQETYTPRLILMDLKGSLSSLKEEGGLYRDK
KSIPNGKGSPLPTATTPKPLLPTEASIRVMSDFLRVHLHPRSI  CMIGKYNHDGEAGRLEAFGGGESVLKEPKYQEELEDRLHFYVEE CDYLQGPQILCDLHDGFSGVGAKAAELLQDEYSGRGIITMGLLP GFYRRGEAGRNIYRLLNTAFGLVHLTAHSSLVCPLSIGSIGLK PEPPVSFYLHINDATLPFRGSALTATALDTVTCS\YRLGSPVS MYHL\ADMLSFCGKKVVTAGAIIPPPLAPGQSLPDSIMQFGGAT PWTPLSACGEPSGTRCFAQSVVLRGIDRACHTSQLTPGTPPPSA LHACTTGEEILAQYLQQQQPGWSSSHLLLTPCRVAPPYPHLFS SCSPPGMVLDGSPKGAAVESVPVFG SCSPPGMVLDGSPKGAAVESVPVFG KKFQAPARETCVECQKTVYPMERLLANQQVFHISCFRCSYCNNK LSLGTTASLHGRIYCCPHTNOLFKKGNYDEGFGHRPHKDLWAT KISTEGFWERPRRFENCGRPLKSPGGEDCPSC*GGCPGSNY*AQ GSSSREGGGABNPKLRVA STRIEGFWERPRRFENCGRPLKSPGGEDCPSC*GGCPGSNY*AQ GSSSREGGGABNPKLRVA FSFLEENKCLNPAQRALVRAVMLENYRLLESVGLTSKDSWYMRK KPGRGRGKQRRGWFPLRVY PERTCSQLQADMAPDFGPSFVPSWGATATGARKFLIAPNI\N LLGTKRQAHRIALNLREGGRCKDCPGRLKKVQGIGWLDEKNLA QUSTNLLDERVTALHTVYEETCREAQELSLPVUGSQLVGLVPLK ALLDAA  5733 1 460 PALQEVNANALAMGKQYENDARTLFEFTSGVNDTESPIIYRDES MRRACSPDSLCSDGNGLBLKCPFTSGFMRRRGGFBALKSAYM AQQVSMWVTRRNAWYFANVPDRWKREGLHYVVIERDEKYM\AS FDEI\VP\SPIGKMDEVLSRPPM  5734 3 968 RNSPESLTSLLVLTTANNLFVLIPAYSKNRAYATFFTVFTVI GSLFLMNLLTATIYSQFRGYLMKSLQTSLFRRRLGTRAFFVLS SMYGRGGAPPQAVGVKPQNLLQVLQKVQLDSSKKQAMMEKVRSY GSVLLSABEFQXLFNELDRSVVKHPPPRPEYQSPFLQSAQFLFG HYYFDYLGNLITALANLVSICVFLUDADVLPARRDDFILGILNC VFTVYYLLEMLLKVFALGLRGYLSYPSNVFOGLLTVVLLVLEIS SMYGRGGRPPQAVGVKPQNLLQVLQKVQLDSSKKQAMMEKVRSY GSVLLSABEFQXLFNELDRSVVKHPPPRPEYQSPFLQSAQFLFG HYYFDYLGNLITALANLVSICVFLUDADVLPARRDDFILGILNC VFTVYYLLEMLLKVFALGLRGYLSYPSNVFOGLLTVVLLVLEIS SMYEMAVVASTVLGL  5735 2 540 FFTECVARAFNFPDQATVKKAYSLPRVGGGTSCGLPQARRISL ATFRQLYK/SSNMTYGNORFEIS SNFEVLMFLNTIAGRTYNDLNQ YPVFPPWULTNYESBELDLTLPGNFRDLSKPJGGTSCGLPQARRISL ATFRQLYK/SSNMTYGNORFEIS SNFEVLMFLNTIAGRTYNDLNQ YPVFPPWULTNYESBELDLTLPGNFRDLSKPJGGTSCGLPQARRISL ATFRQLYK/SSNMTYGNORFEIS SNFEVLMFLNTIAGRTYNDLNQ YPVFPPWULTNYESBELDLTLPGNFRDLSKPJGGTSCGLPQARRISL ATFRQLYK/SSNMTYGNORFEIS SNFEVLMFLNTIAGRTYNDLNQ YPVFPPWULTNYESBELDLTLPGNFRDLSKPJGGTSCGLPQARRISL ATFRQLYK/SSNMTYGNORFEIS SNFEVLMFLNTIAGRTYNDLNQ YPVFPPWULTNYESBELDLTLPGNFRDLSKPJGGTSCGLPGARTYNGEN RYTWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELAC				QLDAAIAWQGKLTTHKEELYPKNPYLODFLSAEGVI.SSDGVWRV
CMIGKYNHOGEAGRLERFGGGESVLKEPKYQBELEDRLHFYVEE CDYLGGFGILCDLHDGFSGVAKAAELLQDEYSGRGITMGLLP GPYHRGEAQRNIYRLLNTAFGLVHLTAHSSLVCPLSIGGSLGLR PEPPVSFPYLHYDATLPFHCSÄLIAFLDTVTCS\YRLCSSPVS WYHH\ADMLSFGGKKVVTAGGITPFHDFGGGAT PWTPLSAGGEPSGTRCTPAGSVULRGIDRACHTSQLTPGTPPPSA LHACTTGEBILAQYLQQQQPGVMSSSHLLTPCRVAPPYPHLPS SCSPPGMVLDGSKGAAVESVPVFG  5730  1258  1713  KKFGAPARETCVSCOKRVYYPMERLLANQOVFHISCFRCSYCNNK KLGLGTYASLIGRIYCKCHFMQLFKSKGNYDEGFGHRRHONWAT KIETEGFWERPRNFENGGRPLKSPGGEDCPSC*GGCPGSNY*AQ GSSSREKGGQASWNPKLRVA  5731  122  443  RSHRGELIPKDSCYMRKPFRFFKKRRGG/CALFQGCLTFKDVAI EFSLEENKCLNPAQRALYRAVMLENYRNLESVGLTSKDSWYMKK KPGRGRGKQRGWPPLRVY FPSRSCQSPRRKSRRRAHTVVTLVCGFTSFSFSLPLYLCGCLRF PERTCSGLQQADWAPDFGPSSFVPSWGATATGARKFLIAFNI NU LLGTKRGAHRIANLRECGGRKOQFGRLXKVGCIGWYLDEKNLA QVSTNLLDFEVTALHTVYBETCREAQELSLPVVGSQLVGLVPLK ALLDAA AQVQSMWVTRKANNYFANYFMRKEGLHYVVIERDEKNLA QVSTNLLDFEVTALHTVYBETCREAQELSLPVVGSQLVGLVPLK ALLDAA AQVQSMWVTRKANNYFANYFMRKEGLHYVVIERDEKNLA AQVQSMWVTRKANNYFANYFMRKEGLHYVVIERDEKYM\AS FDEI\VP\EFIGKMDEVLSRDPM  5734  3  968  RCNSPSSLTSLLVLLTTANNLFVLIDAVSKNRAYATFFTVFTVI GSLFLNNLLITAITYSGFGFYLMKSLGTSLFFRRLGTRAAFEVLS SMYGGGAPPQAVGVKQNLLQVLQXVQLDSSHKQAMMEKVRSY GSVLLSAEEFQKLFNELDRSVVKEHPRREYGGFFSLGSAGFLFG HYYFDYLGMLIALANLIVSCTGVULDADVLPAERDDFTIGILNC VFIVYYLLBMLLKVFALGLRGYLSVFSNVFDGLLTVVLLVLEIS TLVCTDCHTOAGGRRNW/RLLSLUMMTRMLNMILVFRFLRIIP SMKPMAVVASTVLGL  5735  2  540  FFTPCVARAFNFPDQATVKKAAYSLEPVGGTSCGLPQARRISL ATPRQLYK/SSMTOTROGRETSNEFVLMFLMTLAGRTYNDLNQ YPVFPWLTNYESEELDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWEDDQSPYYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT		į l		KSIPNGKGSSPLPTATTPKPLTPTEASTRVWSDET.PVWT.HDPGT
CDYLOGFQILCDLHDGFSGVGAKABELLQDEYSGRGITHGLLE GPYRRGEAQNI YRLLMTAFGLUFUTATASSLVCPLSIGGSLGLR PEPPVSFPYLHYDATLPFHCSAILATALDTVTCS\YRLCSSPVS MVHL\ADMLSFCGKKVVTAGAIIPFDJAPQGSLPDSIMQFGGAI PWTPLSAGGEPSGTGCFAGSVULRGIDRACHTSOLTFGTPPFSA LHACTTGEBILAQYLQQQQPGVMSSSHLLLTPCRVAPPYPHLFS SCSPPGMVLDGSPKGAAVESVPVFG LHACTTGEBILAQYLQQQPGVMSSSHLLLTPCRVAPPYPHLFS SCSPPGMVLDGSPKGAAVESVPVFG KKFQAPARETCVECQKTVYPMERLLANQQVFHISCFRCSYCNK LSLGTYASLHGRIYCKPHFMQLFKSKGNYDEGFGHRPHKDLWAT KIETEGFWERPRNFENCGRPLKSPGGEDCPSC*GGCPGSNY*AQ GSSSREKGGGASNNPKLRVA  5731 122 443 RSHRGELIPKDSCYMRKPPFRFFKKRRG/CALFQGCLTFKDVAI EFSLEEMKCLNPAQRALYRAMLENYRNLESVGLTSKDSWYMK KPGRGRGKQRRQEWFFLRVY  5732 226 772 PFSRSCGSPRRKSRRRAHVIVTUVCGFTSFSSLPLYLCGCLRF PERTCSCJCQADMADPDGFSSFVPSWGATATGARKELLARNI\M LLGTKEQAHRIALNLREQGRGKDQPGRLKKVQGIGWYLDEKNLA QUSTNLLDEEVTALHTVYEETCREAQELSLPVVGSQLVGLVPLK ALLDAA  5733 1 460 PALQEVMANALAWGKQYENDARTLFEFTSGVNDTESPIIYRDES MRTACSPDGLCSDGNGLELKCPFTSFFFFFKWFNAS FDEI\VP\EFIGKMDEVLSRDPM RCMSPESLTSLLVLTTANNLFVLIPAYSKNRAYAIFFIVFTVI GSLFLMNLLTAIIYSQFRGYLMKSLQTSLFRRRLGTRAAFEVLS SMYGGGAFPQAVGVKPDNLLQVLOKVQLDSSHKQAMMEKVRSY GSVLLSAEEFGKLFFELDRSVLFHPDESTYMFLIGTINC VFIVYYLLEMLLKVPALGLRGYLSVFSNVFDGLLTVVLLVLEIS SMYGGGAFPQAVGVKPRPLEVKHPVREPSCPSFPLFIGTINC VFIVYYLLEMLLKVPALGLRGYLSVFSNVFDGLLTVVLLVLEIS TL\VCTDCHTGAGGRRWW/RLSLBMDTRMLINVLIVEIS SMYPMAVVASTVLGL 5735 2 540 FFTECVARAFNFPDQATVKKAAYSLEVVGGTSCGLPQARRISL ATPRQLYK/SSMYTGNGCREISNFEVLMFLNTLAGRTYNDLNQ YPVFFPVLINYESBELDLTLPGNPRDLSKPIGALNPKRAVFYAE RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT		ŀ		CMIOKANHDGEAGBI EVEGOGESAL KEDKAOBEL EDDA HEALIER
GFYHRGEAQRNI YRLINTAFGLVHLTAHSSLVCPLSLGGSLGLR PEPPVSFPYLHYDATLPPHCASALLATALDTVTCS\YRLCSSPVS MVHL\ADMLSRCGKKVVTAGAIIPPPLAPGQSLPDSIMOFGGAT PWTPLSAGGEPSGTRCFAQSVVLRGIDRACHTSQLTPGTPPPSA LHACTTGEBILAQVI_QQQPGWMSSSHLLLTPCRVAPPYPHLFS SCSPPGMVLDGSPKGAAVESVPVFG  5730  1258  1713  KKFQAPARETCVECQKTVYPMERLLANQQVFHISCFRCSYCNNK LSLGTYASLHGRIYCKPHYPOLFKSKGNYDEGFGHRPHKDLWAT KIETEGFWERPRNFENGGRPLKSPGGEDCPSC*GGCPGSNY*AQ GSSSREKGGQASWMPKLRVA  5731  122  443  RSHRGELIPKDSCYMKRVDPFRFKKRRQG/CALPQGCLTFKDVAI EFSLEEWKCLNPAQRALYRAVMLENYRNLESVGLTSKDSWYMK KPGRGRKQRRQEWFPLRVY  5732  226  772  PPSRSCQSPRKSKRRAHVTVTLVCGFTSFSFSLPLYLCGCLRF PERTCSQLQQADWAPDFGFSSFVPSWGATATGARKFLIAFNI\N LLGTKEQAHRIALNLREGGRCKDQFGRLKKVQGIGWYLDEKKIA QUSTNLLDFSRYALHTVYEETCREAQELSLPVVGSQLVGLVPLK ALLDAA  5733  1  460  PALQEVNANLAWGKQYENDARTLFEFTSGVNDTESPIIYRDES MRRACSPDGLCSDONGLELKCPFTSRDFMKFRLGGFEAIKSAYM AQVQYSMWVTKKNAMYFANYDPRMKREGLHYVVIERDEKYM\AS FDEI\VP\EFIGKMDEVLSRDP GSSLLSAESFQKLFNELDRSVVKEHPPRPEXGSFFLOSAQFLFG GSVLLSAESFQKLFNELDRSVVKEHPPRPEXGSFFLOSAQFLFG GSVLLSAESFQKLFNELDRSVVKEHPPRPEXGSFFLOSAQFLFG HYYFDYLGNLIATALNLVSICYFLVLDADVLPAERDDFILGILNC VFIVYYLLEMLLKVFALGLRGYLSYPSNVFGGLTVVLILVLEIS TL\VCTDCHTQAGGRRNW/ALLSLWDMTRMLNMLIVPFFLRIIP SMKPMAVVASTVLGL  5735  2  540  FFTPCVARAFNFPDQAVVKRAAYSLPRVGGGTSCGLPQARRISL ATTRQLYK/SSNMTQRWQRREISNFEVLMFLNTIAGRTYNDLNQ YPVFFWVLINNYESBELDLTLPGMFRDLSKPIGAINPKRAVFYAE RYETWEDDQSPPYNYNTHYSTATSTLSWLVRIVSIFIELACLWY	1			CDVLOGEOILCDLUDGEGGGGAKAAELLODEVGGDGITEWGTID
PEPPVSFYLHYDATLPFHCSÄILATALDTVTCS\VRLCSSPUS MVHL\ADMLSFGKKKUVTAGAIIPPPLAPGQSLPDSIMQFGGAT PWTPLSAGGEPSGTRCFAQSVVLRGIDRACHTSQLTPGTPPPSA LHACTTGEBILAQVLQQQQFGWMSSHLLLTPCRVAPPYPHLFS SCSPPGWVLDGSPKGAAVLGQQQFGWMSSHLLLTPCRVAPPYPHLFS  F730 1256 1713 KKFQAPARETCVECQKTVYPMERLLANQQVFHISCFRCSYCNNK LSIGTYASLHGRIYCKPHFNQLFKSKGNYDEGFGRPHKDLWAT KIETEGFWERPRNFENGGFPLKSKGNYDEGFGRPHKDLWAT KIETEGFWERPRNFENGGFPLKSKGRYDEGFGRPHKDLWAT KIETEGFWERPRNFENGGFPLKSPGGEDCPSC*SGCPGSNY*AQ GSSSREKGGQASWNPKLRVA  FST31 122 443 RSHRGELIPKDSCYMRKPFRFRKRQC/CALPQGCLTFKDVAI EFSLEEMKCLNPAQRALYRAVMLENYRLESVGLTSKDSWYMRK KPGRGRGKQRRQEWFPLRVY  FPRSCQSPRRKSRRAHVTUTLVCGFTSFSFSLPLYLCGCLRF PERTCSQLQQADWAPDFGFSSFVPSWGATATGARFFLIAFNI\N LLGTKEQAHRIALALREGGRGKDQPGRLKXVQGIGWYLDEKALA QVSTNLLDFEVTALHTVYEFTCREAQELSLPVVSQLVGLVPLK ALLDAA  ALLDAA  FALQEVMANALAWGKQYENDARTLFFFTSGVNDTESPIIYRDES MRTACSPBGLIGCDGNGIGLKCPFTSRDFWKRRLGGFEAIKSAYM AQVQYSMWVTRKNAWYFANYDPRMKREGLHVVUERDEKYM\AS FDEI\VP\EFIGKMDEVLSRDFW GSULSABEFGRUKJFNELDSKVYKHPPRPEPCQSPFLQSAQFLFG GSULSABEFGRUKJFNELDSKYKHPLPREPCQSPFLQSAQFLFG GSULSABEFGRUKJFNELDGRYVKHPPRPEPCQSPFLQSAQFLFG GSULSABEFGRUKJFNELDGRGYLSYFSNVFGGLITVVLLVLEIS TL\VCTDCHTQAGGRRWYALSLEMDMTRMLMMLIVFFRLIIP SMKPMAVVASTVLGL  FFTPCVARAFNTEGD  FFTPCVARAFNTEGD ATTRQLYK/SSNNTQRNQRREISNFEVLMFLNTITAGRTYNDLNQ YPVFFPWLITNYESBELDLTLPGMFROLSKPIGALNPKRAVFYAE RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKKLT	1			CDYUDGENODNIVDI I NIIN POLITIK INNIGOT KON ON
WHIL\ADMISFCSKKVUTAGAII PPPLAPGGSLPDSLMQFGGAT   PWTPLSACGEPSGTRCFAQSVVLRGIDRACHTSQLTFGTPPFSA   LHACTTGEEILAQYLQQQPGVMSSSHLLLTPCRVPPPHLFS   SCSPPGMVLDGSPKGRAVESVPVPG   SCSPPGMVLDGSPKGRAVESVPVPG   SCSPPGMVLDGSPKGRAVESVPVPG   KKFQAPARETCVECQKTVYPMERLLANQQVFHISCFRCSYCNNK   LSLGTYASLHGRIYCKPHFNQLFKSKGNYDEGFGRPHKDLMAT   KIETEGFWERPRNFENCGRPLKSPGGEDCPSC*GGCPGSNY*AQ   GSSSREKGGQASWNPKLRVA   GSSSREKGGQASWNPKLRVA   SFRIRGELIPKDSCYWRKPPFRFKKRRGG/CALPQGCLTFKDVAI   EFSLEEWKCLMPAQRALYRAVMLENYRNLESVGLTSKDSWYMRK   KPGRGRGKQRRQEWFPLRVY   FPSRSCQSPRRKSRRAHVTVTLVCGFTSFSFSLPLYLCGCLRF   PERTCSQLQQADWAPDFGPSSFVDSWGATATGARKFLLAFNI\N   LLGTKEQAHRIALNLREQGRGKDQPGRLKKVQGIGWYLDEKNLA   QUSTNLLDFBVTALHTVYSETCREAQELSLPVVGSQLVGLVPLK   ALLDAA   ALDDAA   PALQEVNANALAWGKQYENDARTLFFFTSGVNDTSFIIYRDES   MRTACSPGLCSDGNGLBLKCFFTSGVFMKFRLGGFEAIKSAYM   AQVQYSMWVTRKNANYFANYDPRMKREGLHYVVIERDEKYM\AS   FDEI\VP\EFIGKMDEVLSRDPM   SMMCHGGAFPQAVGVKPQNLLQVLQKVQLDSSHKQAMMEKVRSY   GSVLLSAEBFQKLFNELDRSVVKEHPPREFYQSFFLQSAOFLFG   HYYFDYLGNLLALANLVSICVFLVLDADVLPARRDFILGILMC   VFIVYYLLEMLLKVFALGLRGYLSYFSNVFDGLLTVVLLVLEIS   TLVCTTCCHTQAGGRRWW/RLLSLMDMTRMLMMLIVPRFLRIIP   SMMPMAVASTVLGL   SMMPMAVASTVLGL   SMMPMAVASTVLGL   SMMPMAVASTVLGL   ATTRQLYK/SSNNTQRWGREISNEEYLMFLNTLAGRTYNDLINQ   YPVFPWVLTNYEGBELDLTLPONFROLSKPIGALNPRAVFYAE   RYSTWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   LKILT   L	l .			
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KIETEGFWERPRNFENCGRPLKSPGGEDCPSC*GGCPGSNY*AQ GSSSREKGGQASWMPKLRVA RSHRGELIPKDSCYMRKPPRPRKKRRQG/CALPQGCLTFKDVAI EFSLEEWKCLNPAQRALYRAVMLENYRNLESVGLTSKDSWYMRK KPGRGRGKQRQEWFPLRVY PFSRSCQSPRRKSRRAHTVTLVCGFTSFSFSLPLYLCGCLRF PERTCSQLQQADMAPDFGPSSFVPSWGATATGARKFLIAPHI\N LLGTKEQAHRIALNLREQGRGKDQPGRLKKVQGIGWYLDEKNLA QUSTNLLDFEVTALHTVYEETCREAQELSLPVVGSQLVGLVPLK ALLDAA  5733 1 460 PALQEVNANALAWGKQYENDARTLFEFTSGVNDTESPIIYRDES MRTACSPDGLCSDGNGLELKCPFTSRDFMKFRLGGFEAIKSAYM AQVQYSMWVTRKNAMYFANYDPRMKREGLHYVVIERDEKYM\AS FDEI\VP\EFIGKNDEVLSRDPM  5734 3 968 RCNSPESLTSLLVLLTTANNLFVLIPAYSKNRAVAIFFTVFTVI GSLFLMNLLTAIIYSQFRGYLMKSLQTSLFRRRLGTRAAFEVLS SMWGEGGAFPQAVGVKPQNLLQVLQKVQLDSSHKQAMMEKVRSY GSVLLSABEFQKLFNELDRSVVKEHPPRPEYQSPFLQSAQFLFG HYYFDYLGNLIALANLVSICVFLVLDADVLPAERDDFILGILNC VFIVYYLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS TL\VCTDCHTQAGGRRW/RLLSLWDMTRMLNMLIVFRFLRIIP SKMPMAVVASTVLGL  5735 2 540 FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ YPVFFWULTNYESEELDLTLPGNFRDLSKPIGGLNPKRAVFYAE RYSTWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT	1			LSLGTYASLHGRIYCKPHFNQLFKSKGNYDEGFGHRPHKDLWAT
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KPGRGRGKQRRQEWFFLRVY  5732  226  772  PPSRSCQSPRRKSRRRAHVTUTLVCGFTSFSFSLPLYLCGCLRF PERTCSQLQQADWAPDFGPSSFVPSWGATATGARKFLIAFNI\N LLGTKEQAHRIALNIREQGRGKDQPGRLKKVQGIGWYLDEKNLA QVSTNLLDFEVTALHTVYBETCREAQELSLPVVGSQLVGLVPLK ALLDAA  1  460  PALQEVNANALAWGKQYENDARTLFEFTSGVNDTESPIIYRDES MRTACSPDGLCSDGNGLELKCPFTSRDFMKFRLGGFEAIKSAYM AQVQYSMWVTRKNAWYFANYDPRMKREGLHYVVIERDEKYM\AS FDEI\VP\EFIGKMDEVLSRDPM  5734  3  968  RCNSPESLTSLLVLLTTANNLFVLIPAYSKNRAYAIFFIVFTVI GSLFLMNLLTAIIYSQFRGYLMKSLQTSLFRRRLGTRAAFEVLS SMYGEGGAFFQAVGVKPQNLLQVLQKVQLDSSHKQAMMEKVRSY GSVLLSAEEFQKLFNELDRSVVKEHPPRPEYQSPFLQSAQFLFG HYYFDYLGNLIALANLVSICVFLVLDADVLPAERDDFILGILNC VFIVYYLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS TL\VCTDCHTQAGGRRNW/RLLSLWDMTRMLNMLIVFRFLRIIP SMKPMAVVASTVLGL  5735  2  540  FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ YPVFPWVLTNYESBELDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWBDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT	1 !			EFSI-FEWKCI.NDAODAT.VUAUMI ENVONI ECUOI DOVOCIIVANY
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AQVQYSMWUTKINANYFANYDPRMKREGLHYVVIERDEKYM\AS FDEI\VP\EFIGKMDEVLSRDPM  RCNSPESLTSLLVLLTTANNLFVLIPAYSKNRAYAIFFIVFTVI GSLFLMNLLTAIIYSQFRGYLMKSLQTSLFRRRLGTRAAFEVLS SMVGEGGAFPQAVGVKPQNLLQVLQKVQLDSSHKQAMMEKVRSY GSVLLSAEBFÇKLFNELDRSVVKEHPPRPEYQSPFLQSAQFLFG HYYFDYLGNLIALANLVSICVFLVLDADVLPAERDDFILGILNC VFIVYYLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS TT\VCTDCHTQAGGRRWW/RLLSLWDMTRMLNMLIVFRFLRIIP SMKPMAVVASTVLGL  5735 2 540 FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTLAGRTYNDLNQ YPVFPWVLTNYESBELDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWBDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT		İ		MRTACSPDGLCSDGNGLELKCPFTSRDFMKFRLGGFEAIKSAYM
FDEI\VP\EFIGKMDEVLSRDPM  5734  3 968  RCNSPESLTSLLVLLTTANNLFVLIPAYSKNRAYAIFFIVFTVI GSLFLMNLLTAIIYQÇFRGYLMKSLQTSLFRRRLGTRAAFEVLS SMVGEGGAFPQAVGVKPQNLLQVLQKVQLDSSHKQAMMEKVRSY GSVLLSAEEFQKLFNELDRSVVKEHPPRPEYQSPFLQSAQFLFG HYYFDYLGNLIALANLWSICVFLVLDADVLPAERDDFILGILNC VFIVYYLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS TL\VCTDCHTQAGGRRNW/RLLSLWDMTRMLNMLIVFRFLRIIP SMKPMAVVASTVLGL  5735  2 540  FFTPCVARAFNFPQATVKKAAYSLFRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTLAGRTYNDLNQ YPVFPWVLTNYESBELDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWBDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT		ŀ		AQVQYSMWVTRKNANYFANYDPRMKREGLHYVVIERDEKYM\AS
5734  3  968  RCNSPESLTSLLVLLTTANNLFVLIPAYSKNRAYAIFFIVFTVI GSLFIMNLLTAIIYSQFRGYLMKSLQTSLFRRRLGTRAAFEVLS SMVGEGGAFPQAVGVKPQNLLQVLQXVQLDSSHKQAMMEKVRSY GSVLLSAEEFQKLFNELDRSVVKEHPPRPEYQSPFLQSAQFLFG HYYFDYLGNLIALANLVSICVFLVLLDADVLPAERDDFILGILNC VFIVYYLLEMLLKVFALGLRGYLSYESNVFDGLLTVVLLVLEIS TL\VCTDCHTQAGGRRNW/RLLSLWDMTRMLNMLIVFRFLRIIP SMKPMAVVASTVLGL  5735  2  540  FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEVLMFLNTIAGRTYNDLNQ YPVFPWVLTNYESEELDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT	1			FDEI\VP\EFIGKMDEVLSRDPM
GSLFLMNLLTAIIYSQFRGYLMKSLQTSLFRRRLGTRAAFEVLS SMVGBGAFPQAVGVKPQNLLQVLQKVQLDSSHKQAMMEKVRSY GSVLLSAEEFQKLFNELDRSVVKEHPPRPEYQSPFLQSAQFLFG HYYFDYLGNLIALANLVSICVFLVLDADVLPAERDDFILGILNC VFIVYYLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS TL\VCTDCHTQAGGRRWW/RLLSLWDMTRMLNMLIVFRFLRIIP SMKPMAVVASTVLGL  5735 2 540 FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ YPVFPWVLTNYESBELDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWBDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT	5734	3	968	
SMVGEGGAFPQAVGKPQNLLQVLQKVQLDSSHKQAMMEKVRSY GSVLLSAEEFQKLFNELDRSVVKEHPPRPEYQSPFLQSAQFLFG HYYFDYLGNLIALANLVSICVFLVLDADVLPAERDDFILGILNC VFIVYYLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS TL\VCTDCHTQAGGRRW/RLLSLWDMTRMLNMLIVFRFLRIIP SMKPMAVVASTVLGL  5735 2 540 FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ YPVFPWVLTNYESEELDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT		ŀ		GSLFLMNLLTAI IYSOFRGYLMKSLOTSLEDDDI GTDA A FEET C
GSVLLSAEEFÇKLFNELDRSVVKEHPPRPEYQSPFLQSAQFLFG HYYFDYLGNLIALANLVSICVFLVLDADVLPAERDDFILGILNC VFIVYYLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS TTL\VCTDCHTQAGGRRNW/RLLSLWDMTRMLNMLIVFRFLRIIP SMKPMAVVASTVLGL  5735 2 540 FFTPCVARAFNFPDQATVKKAAYSLFRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ YPVFPWVLTNYESBELDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWBDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT				SMVGRGGAPPOAUGUKPONIT.OUT OPTIOT DOCUMOANTER
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TL\VCTDCHTQAGGRRNW/RLLSLWDMTRMLNMLIVFRFLRIIP SMKPMAVVASTVLGL  5735  2 540 FFTPCVARAFNFPDQATVKKAAYSLFRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTLAGRTYNDLNQ YPVFPWVLTNYESBELDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWBDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT				TITLD I DONE TAMEN SICVE LV LDADV LPAERDDFILGILNC
SMKPMAVVASTVLGL  5735 2 540 FFTPCVARRFNFPDQATVKKANYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ YPVFPWVLTNYESBELDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWBDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT			1	VF1V11DLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS
5735 2 540 FFTPCVARAFNFPDQATVKKANYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ YPVFPWVLTNYESBELDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWBDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT				
ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ YPVFPWVLTNYESBELDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWBDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT				
ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ YPVFPWVLTNYESBELDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWBDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT	5735	2	540	FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPOARRISI.
YPVFPWVLTNYESEELDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWBDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT		1		ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDING
RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT		1		YPVFPWVLTNYESEELDLTLPGNFRDLSKPIGALNPKRAVEVAE
LKILT		!	j	RYETWEDDOSPPYHYNTHYSTATSTISWINGTUSTETELACTOR
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GTAPSTANSGISPQQVAVIHCKGHQKENTAVAHSNQKADSAAQV	5736	1	382	
				A MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO MANAGO

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
j	corresponding	to first	
į.	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	Sequence	Codon, /=possible nucleotide deletion,
	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		\=possible nucleotide insertion)
		1	TARLSVTPPNLLPTVSFPQPDLPDNPVYSTTTEKLASDLRANKN
5737	290	1041	QES**ILPDSGIFIP*T*TSYLQSTTHLRRAKLPQLLRR
		1041	KACLHLLSSFLTSNFLFNPLLPDSLYSVEARSQRANLGPCRRKR
	1		LQTLMRLAAGFQYSSHKDPSLSAKEKHTDYHNEARGPWPGWVG*
	1	l	RTADGSCGRGPDGAHHPGPKSSSWRASRLLPGLGGSHHLDAYVG
1	1		RDLECGTPAPLQLEIPPQPRGHPAPIPTGQAGPRDSGPGASP*V
1			ETRPLTDGRR*PGVRPVGWTPAHPAGTLRPRGAVEPSVSACGKW
5738	8	460	APSPTSQGCCEGRCDAVPKHRAWRTPLCSQ
		400	DTLSLNCTLPETLPMTPSF*LSFL*FPGLARAKSIPTKTYSNEV
1	i i		VTLWYRPPDILLGSTDYSTQIDMW*GQVEVWQGPCGKGGGLVTT
Ì	ł		ATQPAAFLFTVPSLPRGVGCIFYEMATGRPLFPGSTVEEQLHFI
5739	1	1222	FRILSEEAWALCAVETHR
	-	1622	SFORRGIRWNVHTLHPHPRAVWAGIGRGHGS*ALLGRARAPALC
	ļ		PPTLLEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEV
ĺ	ĺ		SAEVDGPVPGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKI
	ł l		LQCQGFYQLCGVHQEDVIYLALPLYHMSGSLLGIVGCMGIGATV
1			VLKSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPPSKAERG
			HKVRLAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINY
			TGQRGAVGRASWLYKHIFPFSLIRYDVTTGEFIRDPQGHCMATS
1			PGEPGLLVAPVSQQSPFLGYAGGPELAQGKLLKDVFRPGDVFFN TRDLLVCDDQGFLRFHDRTGDPFRWKGENVATTEVAEVFEALDF
1 . 1			LQEVNVYGVTV
5740	265	231	PAYWLKVPTLCLESKTDLREKASHVSAQLQGEVRGLAGALWM*A
i I	i		YVYERVYN*NISRMVHALEQKRHPAGLSSSMALQLNPCLGMLMA
L			LQSELHKLYDEETQSWVSGSACGGYP
5741	1	650	PRKTMRRGVLMTLLQQSAMTLPLWIGKPGDRPPPLCGAIPASGD
	İ		YVARPGDKVAARVKAVDGDEQWILAEVVSYSHATNKYEVDDIDE
1 1	į		EGKERHTLSRRRVIPLPQWKANPETDPEALFQKEQLVLALYPQT
1 1			TCFYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV
I			ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK
5742	2	362	TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG
1 1	1		TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK
55.5			TALYWAVEKGNATMVRDILQCNPDTEICTKDG
5743	2	415	GKTPEGIDAIEEIEIDLEETEREISPQENGLEEVKPLGEMQTDL
ľ	ļ		KATGREISPREKTPEVIDATEEIDKDLEETGRREISPEENGDER
	1		VKPVDEMETDLKTTGREGSSREKTREVIDAAEVIETDLEETERE
			ISPQE
5744	3	703	TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA
1	l	i	VFTTANTCLSLTPSTLPEEATGLLTPEPSKEGPILTAESETVI.D
1			SDSWSSAESTSADTVLLTSKESKVWDLPSTSHVSMWKTSDSVSS
ļ			POPGASDTAVPEONKTTKTGOMDGIPMSMKNEMPISOLLMITAD
i			SIGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV
5745			QHGREDEDGLFTL
3/43	1400	599	GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM
	ł		KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIOTYPRSCNIPOT
1			VENRLPQWLPAHDSRLRLDSLSYCOFTRDCFSEKPVPLNFNOOF
- 1	[	1	YICGSHGVEHRVYKHFSSDNSTSTHOASHKOIHOKRKRHPERGP
	1		EKSEEERSKHKRKKSCEEIDLDKHKSIORKKTEVEIETVHVSTE
į	1		KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDOSI
5746	3		LGF
5.40	3	821	SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES
	l		RAGERREPCPVCGKRERENSILALHLRTHOPERPRSPAARLLIE
j	İ	ļ	LEERALLREARLGRARSSGGMOATPATEGLARPOAPSSARDCD
ł	ļ	1	YCKGKFRTSAERERHLHILHRPNKCGLCSFGSSOBEELLHHSLT
1			AHGAPERPLAATSAAPPPQPQPQPPPPQPEPRSVPQPEPRPQPEP
1		ļ	EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA
5747			SFDHACPV
3/4/	2	1328	DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG
- 1		I	PSPRGKGYSSNYRRSPERPTGDLRERIKNKRODVDTEPOKRNTE
			ESSSPVRKESSRGRHREKEDIKITKERTPESEEENVEWETNRDD

SEO	Predicted	Predicted end	Amino agid
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	to first	L=Leucine, M=Methionine, N=Asparagine,
- 1	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1		residue of	S=Serine, T=Threonine, V=Valine,
į.	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
L.	sequence		\=possible nucleotide insertion)
		<del></del>	SDNGDINYDYVHELSLEMKRQKIQRELMKLEQENMEKREEIIIK
	Į.		KEVSPEVVRSKLSPSPSLRKSSKSPKRKSSPKSSSASKKDRKTS
}	}	į	AUCCDI I DOODUGUTUOGUUUGADEEAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
1			AVSSPLLDQQRNSKTNQSKKKGPRTPSPPPPPIPEDIALGKKYKE
i		i	KYKVKDRIEEKTRDGKDRGRDFERQREKRDKPRSTSPAGQHHSP
1		ì	ISSRHHSSSSQSGSSIQRHSPSPRRKRTPSPSYQRTLTPPLRRS
1	1		ASPYPSHSLSSPQRKQSPPRHRSPMREKGRHDHERTSQSHDRRH
ľ		1	ERREDTRGKRDREKDSREEREYEQDQSSSRDHRDDREPRDGRDR
<u> </u>			RE
5748	934	473	SEGPQVFYKGLAPTLIAIFPYAGLQFSCYSSLKHLYKWAIPAEG
	i		KKNENLQNLLCGSGAGVISKTLTYPLDLFKKRLQVGGFEHARAA
1	1	{	FGQVRRYKGLMDCAKQVLQKEGALGFFKGLSPSLLKAALSTGFM
		1	FFSYEFFCNVFHCMNRTASQR
5749	552	1	
3,23	332	1	GFPVDPRVRGSTLSLAERPKGMIRSGSFRDPTDDVHGSVLSLAS
1			SASSTYSSAEERMQSEQIRKLRRELESSQEKVATLTSQLSANAN
1	ì		LVAAFEQSLVNMTSRLRHLAETAEEKDTELLDLRETIDFLKKKN
1			SEAQAVIQGALNASETTPKELRIKRQNSSDSISSLNSITSHSSI
			GSSKDADA
5750	22	866	IFISICLWNAHLCFLLLPKDCIDQVMKLQNLFVDDSGRYLAIQF
			IILEWAYVFLYYYEYRKAKDQLDIAKDISQLQIDLTGALGKRTRF
į			QENYVAQLILDVRREGDVLSNCEFTPAPTPQEHLTKNLELNDDT
Į.	}		ILNDIKLADCEQFQMPDLCAEEIAIILGICTNFQKNNPVHTLTE
	1		VELLAFTSCLLSQPKFWAIQTSALILRTKLEKGSTRRVERAMRQ
			TONE ADDREDVERSUIT EDI VIEWOGOVEDIVEN TODOS SER TEN
	İ		TQALADQFEDKTTSVLERLKIFYCCQVPPHWAIQRQLASLLFEL GCTSSALQIFEKLEMWE
5751	3	751	
3.31		/51	SCGSALRAWRCGAAALATFPAPALPGLMYRALYAFRSAEPNALA
			FAAGETFLVLERSSAHWWLAARARSGETGYVPPAYLRRLQGLEQ
	ļ <u></u>		DVLQAIDRAIEAVHNTAMRDGGKYSLEQRGVLQKLIHHRKETLS
1	i		RRGPSASSVAVMTSSTSDHHLDAAAARQPNGVCRAGFERQHSLP
	l i		SSEHLGADGGLFQIPLPSSQIPPQPRRAAPTTPPPPPVKRRDREA
			LMASGSGGHNTMPSGGNSVSSGSSVSSCI
5752	3	471	GPVCGVGLSVAWAGPWRGPVHSVGGGGRAALHGAELPCLSGAAT
1	i i		VEREMELRHKNEMLRVETEARARAKAERENADIIREQIRLKASE
	1		HRQTVLESIRTAGT_FGEGFRAFVTDRDKVTATVNIFIKQGWQV
1	, ,		AERQHVGASWSPRSCPCRLCTAL
5753	34	483	DDSXAIPGGVQAPFGAVRNIYTPRTGHRIRKLDQIQSGGNYVAG
		403	COENERGY DATA DEGREE OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PRO
			GQEAFKKLNYLDIGEIKKRPMEVVNTEVKPVIHSRINVSARFRK
			PLQEPCTIFLIANGDLINPASRLLIPRKTLNQWDHVLQMVTEKI
5754	14		TLRSGAVHRLYTLEGRLV
3/34	14	331	TLVHVVEFAGEHAEAIASREQEVLQGWKELLSACEDARLHVSST
į į	İ		ADALRFHSQVRDLLSWMDGIASQIGAADKPRCPSSLLGLPASPW
<b></b>			WPTPATPSPLTAPFSME
5755	3	888	LGDQFYKEAIEHCRSYNSRLCAERSVRLPFLDSQTGVAQNNCYI
1	İ		WMEKRHRGPGLAPGOLYTYPARCWRKKRRLHPPEDPKLRIJETK
j †			PEVELPLKKDGFTSESTTLEALLRGEGVEKKVDAREEESIQEIQ
1	ļ.		RVLENDENVEEGNEEEDLEEDIPKRKNRTRGRARGSAGGRRRHD
1 1			AASQEDHDKPYVCDICGKRYKNRPGLSYHYAHTHLASEEGDEAQ
] ]	ŀ	j	BORTES CRIMINITATION POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POWER POW
}			DQETRSPPNHRNENHRPQKGPDGTVIPNNYCDFCLGGSNMNKKS
5756	<del></del>		GRPEELVSCADCGRSAHLGGEGRKEKEAAA
1 2,26	3	621	SSKLQALFAHPLYNVPEEPPLLGAEDSLLASQEALRYYRRKVAR
1 1			WNRRHKMYREQMNLTSLDPPLQLRLEASWVQFHLGINRHGLYSR
1	1		SSPVVSKLLQDMRHFPTISADYSQDEKALLGACDCTQIVKPSGV
	1	ļ	HLKLVLRFSDFGKAMFKPMRQQRDEETPVDFFYFIDFQRHNAEI
		f	AAFHLDRILDFRRVPPTVGRIVNVTKEIL
5757	3	473	YKDALLLPDNHRQVVFENGTLKLTDVQKGMDEGEYLCSVLIQPQ
; I	1	f	LSISQSVHVAVKVPPLIQPFEFPPASIGQLLYIPCVVSSGDMPI
]	į		RITWRKDGQVIISGSGVTIESKEFMSSLQISSVSLKHNGNYTCI
		i	
5758	1	474	ASNAAATVSRERQLIVRVPPRFVV
	-	**/4	FRRGAGAERGEHREGERGAAGMGEFKVHRVRFFNYVPSGIRCVA
]	İ		YNNOSNRLAVSRTDGTVEIYNLSANYFQEKFFPGHESRATEALC
L			WAEGQRLFSAGLNGEIMEYDLQALNIKYAMDAFGGPIWSMAASP

SEQ	Predicted	Decade - 1   1	
ID	beginning	Predicted end	
NO:	nucleotide	location	(A=Alanine, C=Cvsteine, D=Aspartic Acid r_
1	location	corresponding	Glucamic Acid, F=Phenylalanine G-Glucine
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
I	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
· ·	residue of.	amino acid	S=Serine, T=Threonine, V=Valine,
- }	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, +=Stop
J	sequence	Joguerise	Codon, /=possible nucleotide deletion,
		<del></del>	\=possible nucleotide insertion)
5759	2	1240	SGSQLLVGCEDGSVKLFQITPDKIPV
	_	1270	GNAAFAGQGVVYETFHMSDLPSYTTNGTVHVVVNNQIGFTTDPR
ł	1		MARSSPYPTDVARVVNAPIFHVNADDPEAVIYVCSVAAEWRNTF
	1		NKDVGADLVCYRRRGHNEMDEPMFTQPLMYKQIHRQVPVLKKYA
1	i .		DEPHOGRANDOCEPHONE
1			DSPWPGFFNVDGEPKSMTCPATGIPEDMLTHIGSVASSVPLEDF KIHTGLSRILRGRADMTKNRTVDWALAEYMAFGSLLKEGIHVRL
			NGQDVERGTFSHREHVLHDQEVDRRTCVPMNHLWPDQAPYTVCN
	i		SSLSEYGVLGFELGYAMASPNALVLWEAQFGDFHNTAQCIIDQF
1		ļ	ISTGQAKWVRHNGIVLLLPHGMEGMGPEHSSARPERFLQMSNDD
1			SDAYPAFTKDFEVSQL
576C	1	1221	VRDITSDSLSLSWTVPEGQFDHFLVQFKNGDGQPKAVRVPGHED
1			GVTISGLEPDHKYKMNLYGFHGGQRVGPVSAVGLTAPGKDEEMA
1	1		PASTEPPTPEPPIKPRLEELTVTDATPDSLSLSWTVPEGQFDHF
			LVQYKNGDGQPKATRVPGHEDRVTISGLEPDNKYKMNLYGFHGG
1	į į		CRVGPVSAIGVTAAEEETPTPTEPSMEAPEPPEEPLLGELTVTG
1	1		SSPDSLSLSWTVPQGRFDSFTVQYKDRDGRPQVVRVGGEESEVT
l	i i		VGGLEPGRKYKMHLYGLHEGRRVGPVSTVGVTAPQEDVDETPSP
ł	j j		TEPGTEAPEPPEEPLLGELTVTGSSPDSLSLSWTVPQGRFDSFT
1	]		VQYKDRDGRPQAVRVGGQESKVTVRGLEPGRKYKMHLYGLHEGR
			RLGPVSAIGVT
5761	3	1275	SCDMAEAAALVWIRGPGFGCKAVRCASGRCTVRDFIHRHCQDQN
	ļ ,		VPVENFFVKCNGALINTSDTVQHGAVYSLEPRLCGGKGGFGSML
			RALGAQIEKTINREACROLSGRRLRDVNHEKAMAEWVKQQAERE
]			AEKEQKRLERLQRKLVEPKHCFTSPDYQQQCHEMAERLEDSVLK
1	1		GMQAASSKMVSAEISENRKRQWPTKSQTDRGASAGKRRCFWLGM
	İ		EGLETAEGSNSESSDDDSEEAPSTSGMGFHAPKIGSNGVEMAAK
1			FPSGSQRARVVNTDHGSPEOLOIPVTDSGRHTLEDSCAFLGESK
			EHMESRMVTETEETQEKKAESKEPIREEPTGAGLNKDKETERPT
1 [			DGERVAEVAPEERENVAVAKLQESQPGNAVIDKETIDLLAFTSV
5762			AELELLGLEKLKCELMALGLKCGGTLO
3,62	2	344	GSTGQTPLHSQGGGGGGGGGRRRTPRGMPKEKYEPPDPRRMYTI
1			MSSEEAANGKKSHWAELEISGKVRSLSASLWSLTHLTALHLSDN
5763	3		SLSRIPSDIAKLHNLVYLDLSSNKIR
3,63	3	129	LDKDTGLIMLIARLDYELIQRFTLTIIARDGGGEETTGRVRINV
i .	1		LDVNDNVPTFQKDAYVGALRENEPSVTOLVRLRATDEDSDRNNO
i i	1		ITYSIVSASAFGSYFDISLYEGYGVISVSRPLDYEOISNGLTVI.
5764	19	444	TVMAMDAGN
		441	VCARACGEMRQLLRPIDRQRYDENEDLSDVEEIVSVRGFSLEEK
		ļ	LRSQLYQGDFVHAMEGKDFNYEYVQREALRVPLIFREKDGLGIK
1	1		MPDPDFTVRDVKLLVGSRRLVDVMDVNTQKGTEMSMSQFVRYYE
5765	3	825	TPEAQRDKL
1	-	023	QKILRLNNSHQPPTSSSNSKDCGGPASSGAGATAALADGLKFAS
	1	l	VQASAPQGNSHKETSKSKVKRSKTSKDANKSLPSAALYGIPEIS
}			STGKRQEVQGRPGEATGMNSALGQSVSSGGSGNPNSNSTSTSTS
ļ		1	AATAGAGSCGKSKEEKPGKSQSSRGAKRDKDAGKSRKDKHDLLQ GHONGSGSOA PSCGLI YGEGA YGYGGGA ONTUGGGSOA
1	Ī	1	GHQNGSGSQAPSGGHLYGFGAKSNGGGASPFHCGGTGSGSVAAA
			GEVSKSAPDSGLMGNSMLVKKEEEEEESHRRIKKLKTEKVDPLF TVPAPPPHV
5766	1608	663	SGLFSVDPASSQAMBLSDVTLTEGVGNEVMVVAGVVVLTLALVL
	1		AWLSTYVADSGSNQLLGAIVSAGDTSVLHLGHVDHLVAGQGNPE
l	ļ		PTELPHPSEGNDEKAEEAGEGRGDSTGEAGAGGGVEPSLEHLLD
1	ĺ		IOGLDKROAGAGGGCDDADLDGDCTGEAGAGGGVEPSLEHLLD
1		•	IQGLPKRQAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLND
1	Í	}	TEELAVARPEDTVGALKSKYFFGQESQMKLIYQGRLLQDPARTI.
}		1	RSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG
			SLMVPVFVVLLGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLV FGMYGR
5767	2		NFRATPRPPTRPELRTGTEVILWYLDWRALMKRKRMKANIKLVG
			SGFPLPSSDLDDSLTEEIDEKIGFRNDANFDWQNVADFRDAGGS
		1.	LTEVKVEEEBRDPQSPEFEIEEEEEMLSSVIPDSRRENELPDFP
			ZOL DI BIBGEBERBSVI PUSKRENEBPDFP

SEO	Predicted	1 50 37 5 3	
ID	beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
I NO:		location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
İ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
į	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence	-	\=possible nucleotide insertion)
			HIDEFFTLNSTPSRSAYDEPHLLVNIEKQKLELEKRRLDIEAER
1	1		TOWERED OF THE DATE OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PART
1	İ	•	LQVEKERLQIEKERLRHLDMEHERLQLEKERLQIEREKLRLQIV
į	j		NSEKPSLENELGQGEKSMLQPQDIETEKLKLERERLQLEKDRLQ
5768	<del></del>		FLKFESEKLQIEKERLQVEKDRLRIQKEGHLQ
5/68	3	476	SSRSRLSVSVSPPPPGIVELGPPFAWEFCSRLGSAVTSQRAGPA
			AAMVAKDYPFYLTVKRANCSLELPPASGPAKDAEEPSNKRVKPL
			SRVTSLANLIPPVKATPLKRFSQTLQRSISFRSESRPDILAPRP
1	ł	i	WSRNAAPSSTKRRDSKLWSETFDVC
5769	38	667	TKTKKGVKEKATDQSVKAFAEHCPELQYVGFMGCSVTSKGVIHL
		1	TKLRNLSSLDLRHITELDNETAMEIVKRCKNLISLNLCLNWIIN
1	1	!	DECUENTA VEGOVE YOU WE AND TAKE TO VERCENTED IN THE TOTAL OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF T
	l	Į	DRCVEVIAKEGQNLKELYLVSCKITDYALIAIGRYSMTIETVDV
1	1		GWCKEITDQGATLIAQSSKSLRYLGLMRCDKVNEVTVEQLVQQY
	ļ- <u>-</u>		PHITFSTVLQDCKRTLERAYQMGWTPNMSAASS
5770	1	484	DSRRYDVKTRKWSFLLEEHSKLIAKVRCLPQVQLDPLPTTLTLA
			FASQLKKTSLSLTPDVPEADLSEVDPKLVSNLMPFORAGVNFAI
1	]		AKGGRLLLADDMGLGKTIQAICIAAFYRKEWPLLVVVPSSVRFT
	<u> </u>		WEQAFLRWLPSLSPDCINVVVTGKDRLTA
5771	168	741	GLLPSACLRARSWREASEGPSSRACSNGSQDTFEACYSGTSTPS
			FHGSHCSGSDHSSLGLEQLQDYMVTLRSKLGPLEIQQPAMLLRE
			YRLGLPIQDYCTGLLKLYGDRRKFLLLGMRPFIPDQDIGYFEGF
			LEGVGIREGGILTDSFGRIKRSMSSTSASAVRSYDGAAQRPEAQ
1			AFHRLLADITHDIE
5772	148	383	
3.72	110	383	EFNLALVSPSHPQIKAEDDQPLPGVLLSLSGGLFRSNLLTQDNG
5773			ILTFSNLVTCSAIYHLPVFPEREPGCSMRDLRVA
3//3	2	723	PRVRSKHNFCFMEMNTRLQVEHPVTEMITGTDLVEWQLRIAAGE
			KIPLSQEEITLQGHAFEARIYAEDPSNNFMPVAGPLVHLSTPRA
1			DPSTRIETGVRQGDEVSVHYDPMIAKLVVWAADRQAALTKLRYS
1	!		LRQYNIVGLHTNIDFLLNLSGHPEFEAGNVHTDFIPQHHKQLLL
			SRKAAAKESLCQAALGLILKEKAMTDTFTLQAHDQFSPFSSSSG
			RRLNISYTRNMTLKDGKNSK
5774	· 2	592	FVEBENIRVVRCGGSELNFRRAVFSADSKYIFCVSGDFVKVYST
1 1			VTBECVHILHGHRNLVTGIQLNPNNHLQLYSCSLDGTIKLWDYI
1	1		DGILIKTFIVGCKLHALFTLAQAEDSVFVIVNKEXPDIFQLVSV
			NI DAGGOGENERADE I CHILL DATA CONTROL TO THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTRO
] ]	i		KLPKSSSQEVEAKELSFVLDYINQSPKCIAFGNEGVYVAAVREF
5775			YLSVYFFKKETTSRVTLSSS
"''"	3	538	SSGCCDPAAPSSLAEAATMPVSKCPKKSESLWKGWDRKAQRNGL
1			RSQVYAVNGDYYVGEWKDNVKHGKGTQVWKKKGAIYEGDWKFGK
1 1			RDGYGTLSLPDQQTGKCRRVYSGWWKGDKKSGYGIQFFGPKEYY
	ł		EGDWCGSQRSGWGRMYYSNGDIYEGQWENDKPNGEGMLRLSQNP
	[		RP
5776	2	484	RLPQDCVCQNLSESLGTLCPSKGLLFVPPDIDRRTVELRLGGNF
1 1	i		IIHISRQDFANMTGLVDLTLSRNTISHIQPFSFLDLESLRSLHL
1	ļ		DSNRLPSLGEDTLRGLVNLQHLIVNNNQLGGIADEAFEDFLLTL
	ľ		PDIDI CVINI GODANGI DODANGA
5777	2	040	EDLDLSYNNLHGPAVGLRGDANVQPSTS
"'''	4	949	GQDPEPGQDLFQPEREVDPSWGRGREPRLGKLRFQNDHLSVLKQ
1 !			VKKLEQALKDGSAGLDPQLPGTCYSPHCPPDKAEAGSTLPENLG
į l			GGSGSEVSQRVHPSDLEGREPTPELVEDRKGSCRRPWDRSLENV
}	}		YRGSEGSPTKPFINPLPKPRRTFKHAGEGDKDGKPGIGFRKEKR
		ĺ	NLPPLPSLPPPPLPSSPPPSSVNRRLWTGRQKSSADHRKSYEFE
1 1			DLLQSSSESSRVDWYAQTKLGLTRTLSEENVYEDILDPPMKENP
Į ,	1	İ	YEDIELHGRCLGKKCVLNFPASPTSSIPDTLTKQSLSKPAFFRQ
			NSERRNV
5778	1	1210	
	-	1010	QRRQSVSRLLLPVFLLEPPAEPGLEPPPEEEGGEPAGVAEEPGS
]	1		GGPCWLQLEEVPGPGPLGGGGPLRSPSSYSSDELSPGEPLTSPP
1		. 1	WAPLGAPERPEHLLNRVLERLAGGATRDSAASDILLDDIVLTHS
ŀ	1		LFLPTEKFLQELHQYFVRAGGMEGPEGLGRKQACLAMLLHFLDT
	1	1	YQGLLQEEEGAGHIIKDLYLLIMKDESLYQGLREDTLRLHQLVE
1	ĺ	I	TVELKIPEENQPPSKQVKPLFRHFRRIDSCLQTRVAFRGSDEIF
		f	CRVYMPDHSYVTIRSRLSASVQDILGSVTEKLQYSEEPAGREDS
			LILVAVSSSGEKVLLQPTEDCVFTALGINSHLFACTRDSYEALV

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
j	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence	-	\=possible nucleotide insertion)
			PLPEEIQVSPGDTEIHRVEPEDVANHLTAFHWELPRCVHELEFV
			DAALHOE
5779	138	1671	EAVQVLIKHSADVNARDKNWQTPLHVAAANKAVKCAEVIIPLLS
			SVNVSDRGGRTALHHAALNGHVEMVNLLLAKGANINAFDKKDRR
İ	1		ALHWAAYMGHLDVVALLINHGAEVTCKDKKGYTPLHAAASNGQI
1	1		NVVKHLLNLGVEIDEINVYGNTALHIACYNGQDAVVNELIDYGA
- [	1		NVNQPNNNGFTPLHFAAASTHGALCLELLVNNGADVNIQSKDGK
1		1	SPLHMTAVHGRFTRSQTLIONGGEIDCVDKDGNTPLHVAAPVGU
}		Į.	ELLINTLITSGADTAKCGIHSMFPLHLAALNAHSDCCKKLLSSG
1	1		QKYSIVSLFSNEHVLSAGFEIDTPDKFGRTCLHAAAAGGNVECI
ł	1		KLLQSSGADFHKKDKCGRTPLHYAAANCHFHCIETIJTTGANUN
İ			ETDDWGRTALHYAAASDMDRNKTILGNAHDNSEELERARELKEK
			EATLCLEFLLQNDANPSIRDKEGYNSIHYAAAYGHROCLELLLE
F 7 7 7			RTNSGFEESDSGATKSPLHLAVSEMP
5780	154	624	QPFRVITCLPFKGPDYRLYKSEPELTTVAEVDESMGERKSEDUS
	1		EIETSVVKGSHFPVGVVPPRAKSPTPESSTIASYVTI.RKTYKMM
			DLRTERPRSAVEQLCLAESTRPRMTVEEOMERIRRHCOACLPEY
5781			KKGLNVIGASDQSPLQSPSNLRDNP
2,01	19	941	RGSLGGHPWRPPMRAASQGCLPVSFVTGPHQERAYGGRGPGGAF
i	1 1		PAPPVSGTCPPDLIYAPTPEKAEGGSOKNHOPPDGEPAAUDDGP
			QAPCRAGPTRKVAVAPRPPSCP*GPE\PGEEPRRPLDPSDPLGO
1			VQPHFTSQDAKSAEDEAPSRHLGKHOPRSAOVGSPI.DAT.OGDVT
			QHSIHTVTCKSPRQKEDRSPKPPOAPKHPERHGPOS\OADBDLD
1	1		VAPSRTCGGC*TWDPALLVSP/POGDSTPELPAP\OOPTGGPSP
			CRQALPPQG*RQQPRQRPR/PTGASRSHPAKAKGCOGPPKIRNY
5782	5176		NIMD
1 3.52	37.76	1237	DRSMMSMAADSYTDSYTDTYTEAYMVPDLPPEEPPTMPPLPPEE
]			PPMTPPLPPEEPPEGPALPTEQSALTAENTWPTEVPSLPSEESV
i i			SQPEPPVSQSEISEPSAVPTDYSVSASDPSVLVSEAAVTVPEPP
			PEPESSITLTPVESAVVAREHEVVPERPVTCMVSETPAMSAEPT
			VLASEPPVMSETAETFDSMRASGHVASEVSTSLLVPAVTTPVLA
			ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL
	i		EPSVVTVPEPPVVAEPDYVTI PVPVVSALEPSVPVLEPAVSVLQ
			PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVALESTPM
[ ]			ILESSIMSSHVMKGINLSSGDONLAPEIGMORIALHSGERPHAE EHLKGDFYESEHGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE
}	í		IGEEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALEPD
l [	1		ATG\TSKGIEFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP
	i		SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ
	1		TLAALI\SLXESSGGEKEVPPPS*REHLPDSGFSANIEDINEAD
	l	i	LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVQNLYSSPVV
l			\SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKMKMDDKG
			EKEKKRDSSLRSRSKRSKSSEHKSRKLTSESDSDADVDSGV6V6
İ			HRS\QTRSRSRS/RDRRRRSSRSRSKSRGRRSVSKEKPKPSDVU
1	i	·	RSKSRERKRKRSSSRDNRKTVRARSRTPSRRSRSHTPSPDPDGD
	i		SVGRRRSFSISPSRRSRTPSRRSRTPSRRSRTPSRPS
			RTPSRRSRTPSRRRRSRSVVRRRSFSISPVRLRRSRTPI.RRBRS
- 1	İ		RSPIRRKRSRSSERGRSPKRLTDLDKAOLLEIAKANAAAMCAKA
	1	1	GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKOIAOSKE
Į.	1		DDDVIVNKPHVSDEEEEEPPFYHHPFKLSEPKPIFFNINTAAA
- 1		ı	PTPPKSQVTLTKEFPVSSGSOHRKKEADSVYGEWVPVEKNGEEN
ļ	J	i	KDDDNVFSSNLPSEPVDISTAMSERALAOKRISENAFDI.Famem
į	İ		LNRAQERIDAWAQLNSIPGQFTGSTGVOVLTGEGLANTGAGAWI
1			KKDQFLRAAPVTGGMGAVLMRKMGWREGEGLGKNKEGNKEDILM
[			DFKTDRKGLVAVGERAQKRSGNFSAAMKDLSGKHPVSALMETON
	}	į.	KRRWQPPEFLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR
5783	1692		Y
3,03	1693	698	DSGLRVAFTMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFM
		1 1	QKLGFGTGVNVYLMKRSPRGLSHSPWAVKKINPICNDHVPSVVO
- 1		[ ]	KRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEVGGFKGI
			NDLIEE/PI*SQ/PKILFQQP/LILKVALNMARGLKYLHQEKKL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ŀ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
.	residue of	amino acid	W=Tryptophan, Y=Tyrpsine, X=Unknown *-Stop
ŀ	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
			LHGDIKSSNVVIKGDFETIKICDVGVSLPLDENMTVTDPEACVI
}	1	ļ	GTEPWKPKEAVEENGVITDKADIFAFGLTLWEMMTLSIPHINLS
Ì		j	NDDDDEDKTFDESDFDDEAYYAALGTRPPINMEELDESYQKVIE
-			LFSVCTNEDPKDRPSAAHIVEALETDV
5784	2669	1388	PRVRPRVRTDHNYYISRIYGPSDSASRDLWVNIDQMEKDKVKIH
1			GILSNTHRQAARVNLSFDFPFYGHFLREITVATGGFIYTGEVVH
1			RMLTATQYIAPLMANFDPSVSRNSTVRYFDNGTALVVOWDHUHI.
Ī		ĺ	QDNYNLGSFTFQATLLMDGRIIFGYKBIPVLVTQISSTNHPVKV
			GLSDAFVVVHRIQQIPNVRRRTIYEYHRVELQMSKITNISAVEM
			TPLPTCLQFNRCGPCVSSQIGFNCSWCSKLQRCSSGFDRHRQDW
1	ł		VDSGCPEESKEKMCENTEPVET\FLEPPQP*ERQPPSSGS*LPP
1			E/DAVTSQFPTSLPTEDDTKIALHLKDNGASTDDSAAEKKGGTL
ł			HAGLIVGILILVLIVATAILVTVYMYHHPTSAASIFFIERRFSR
5785	2659	1388	WPAMKFRRGSGHPAYAEVEPVGEKEGFIVSEQC
		1300	PRVRPRVRTDHNYYISRIYGPSDSASRDLWVNIDQMEKDKVKIH GILSNTHRQAARVNLSPDFPFYGHFLREITVATGGFIYTGEVVH
1			RMLTATQYIAPLMANFDPSVSRNSTVRYFDNGTALVVQWDHVHL
1			QDNYNLGSFTFQATLLMDGRIIFGYKEIPVLVTQISSTNHPVKV
ŀ			GLSDAFVVVHRIQQIPNVRRRTIYEYHRVELQMSKITNISAVEM
ļ			TPLPTCLQFNRCGPCVSSQIGFNCSWCSKLQRCSSGFDRHRQDW
-			VDSGCPEESKEKMCENTEPVET\FLEPPQP*ERQPPSSGS*LPP
i			E/DAVTSQFPTSLPTEDDTKIALHLKDNGASTDDSAARKKGGTI.
1			HAGLIVGILILVLIVATAILVTVYMYHHPTSAASIFFIERRPSR
5786	2532		WPAMKFRRGSGHPAYAEVEPVGEKEGFIVSEOC
1 3,00	2534	1674	SYKLPAAERRASSCSQPPTPTRRRWPAPGRTSRGHRPOM*SGTP
1			APRPPARSTVSPASPLPKPRAGRCGSRPRSACSTFRPC*SLN*M
1	1		S*H*KRNLSQRSSSMSRRPLSCARPHR**RQGLTVAARLPTWAK
	1		SPPLACSFCQAAQKSQSLSSGRSTR*PERMSFRP\SPPGNPAIP
1			SLAPSSRP/PKGRPQCTWIPSRWPASPTAPPTTT*APTSSPGST GRSMMTCPTRWTATPWSARASSRPRNWPTP*WRPSGRLSTV*RA
<u> </u>	1		TGGSTATAPPKRFPRNWNPMMAE
5787	2	1460	MASAASVTSLADEVNCP\ICQGTLKEAGSLSNCG/HKNFCRACL
1			T\RYCEIP\GPD\LEESP\TCP\LCKEPFRP\GSFRPNWQLANV
1			VENIERLQLVSTLGLGEEDVCQEHGEKIYFFCEDDEMOLCVVCR
			EAGEHATHTMRFLEDAA\APYREOIHKCLKCLIKERERIORIOS
		j	RENKRMQVLLTQVSTKRQQVISEFAHLRKFLEEOOSILLAOLES
			QDGDILRQRDEFDLLVAGEICRFSALIEELEEKNERPARRLLTD
		1	IRSTLIRCETRKCRKPVAVSPELGORIRDFPOOALPLOREMKMF
1	}		LEKLCFELDYEPAHISLDPQTSHPKLLLSEDHQRAQFSYKWQNS
1 1		ŀ	PDNPQRFDRATCVLAHTGITGGRHTWVVSIDLAHGGSCTVGVVS
1 1			EDVQRKGELRLRPEEGVWAVRLAWGFVSALGSFP\TRLTLKEQP
,	1		ROVRVSLDYEVGWVTFTNAVTREPIYTFTASFTRKVIPFFGLWG RGSSFSLSS
5788	2	6860	EHSVSGRSSAYGDATAEGHPAGPGSVSSSTGAISTTTGHQEGDG
			SEGEGEGETEGDVHTSNRLHMVRLMLLERLLQTLPQLRNVGGVR
1 1	1		AIPYMQVILMLTTDLDGEDEKDKGALDNLLSQLIAELGMDKKDV
]		ì	SKKNERSALNEVHLVVMRLLSVFMSRTKSGSKSSICESSSLISS
j		i	ATAAALLSSGAVDYCLHVLKSLLEYWKSQQNDEEPVATSQLLKP
1 1		}	HTTSSPPDMSPFFLRQYVKGHAADVPEAYTQLLTEMVLRLPYQI
1 1		í	KKITDTNSRIPPPVFDHSWFYFLSEYLMIQOTPFVRROVRKLLL.
]			FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEGGIFLRASVVTA
ļ !			SPQSALQYDTLISLMEHLKACAEIAAQRTINWQKFCIKDDSVLY
			FLLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSAS
	Ì		SSPAPVAASSGQATTQSKSSTKKSKKEEKEKEKDGETSGSOEDO
]	ŀ	] :	LCTALVNQLNKFADKETLIQFLRCFLLESNSSSVRWQAHCLTLH
	ļ	j	IYRNSSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK
	1	1	TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF
	1		DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI
		);	GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA
		1;	RWHKAKKVQLTPGQTEVKIDLPLPIVASNLMIEFADFYENYQAS IETLQCPRCSASVPANPGVCGNCGENVYQCHKCRSINYDEKDFF

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
j	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
1			LCNACGFCKYARFDFMLYAKPCCAVDPIENEEDRKKAVSNINTL
-	1		LDKADRVYHQLMGHRPQLENLLCKVNEAAPEKPQDDSGTAGGIS
1.	1		STSASVNRYILQLAQEYCGDCKNSFDELSKIIOKVFASRKELLE
ļ	İ		YDLQQREAATKSSRTSVQPTFTASQYRALSVLGCGHTSSTKCYG
ŀ	1		CASAVTEHCITLLRALATNPALRHILVSQGLIRELFDYNLRRGA
	İ		AAMREEVRQLMCLLTRDNPEATQQMNDLIIGKVSTALKGHWANP
			DLASSLQYEMLLLTDSISKEDSCWELRLRCALSLFLMAVNIKTP
	[		VVVENITLMCLRILQKLIKPPAPTSKKNKDVPVEALTTVKPYCN
İ			EIHAQAQLWLKRDPKASYDAWKKCLPIRGIDGNGKAPSKSELRH
		•	LYLTEKYVWRWKQFLSRRGKRTSPLDLKLGHNNWLRQVLFTPAT
1			QAARQAACTIVEALATIPSRKQQVLDLLTSYLDELSIAGECAAE
1			YLALYQKLITSAHWKVYLAARGVLPYVGNLITKEIARLLALEEA
1			TLSTDLQQGYALKSLTGLLSSFVEVESIKRHFKSRLVGTVLNGY
1	]		LCLRKLVVQRTKLIDETQDMLLEMLEDMTTGTESETKAFMAVCI
į			ETAKRYNLDDYRTPVFIFERLCSIIYPEENEVTEFFVTLEKDPQ
}	ļ		QEDFLQGRMPGNPYSSNEPGIGPLMRDIKNKICQDCDLVALLED
	l i		DSGMELLVNNKIISLDLPVAEVYKKVWCTTNEGEPMRIVYRMRG
1 .	i l		LLGDATEEFIESLDSTTDEEEDEEEVYKMAGVMAQCGGLECMLN
			RLAGIRDFKQGRHLLTVLLKLFSYCVKVKVNRQQLVKLEMNTLN
1	]		VMLGTLNLALVAEQESKDSGGAAVAEQVLSIMEI\IQAEPNVEP
			LSEDKGNLLLTGDKDQLVMLLDQINSTFVRSNPSVLCGLLRIIP
			YLSFGEVEKMQILVERFKPYCNFDKYDEDHSGDDKVFL\DCFCK
	l i		IAAGIK\NNSNGHQL\KDL\ILQKGITQNALD\YMKKHIP/SAA
1	]		RIWDADI\WKSFCLRPALPFILRLLRGLAIQHPGTQVLIGTDSI PNLHKLEQVS\SDEGIGTLA\ENL\LESLREHPDVNKKIDA\AR
1			RETRAEKKRMAMAMRQKALGTLG\MTTNEKGQVVD/TRTALLEA
1			DWEELIEEP\GLTCCICREGYKFQPTKVLGIYTFTKRVVLGGVW
			ENKPRETSRATSTVSHFNIVHYDC\HLA\AVSLARGREEWESAA
1	ļ		LQNANTKCNGLLPVWGPHVPESAPATCLARHNTYLQECTGQREP
1			TYQLNIHDIKLLFLRFAMEQSFSADTGGGGRESNIHLIPYIIHT
1	_		GLYVLNTTRATSREEKNLQGFLEQPKEKWVESAFEVDGPYYFTV
ł			LALHILPPEQWRATRVEILRRLLVTSQARAVAPGGATRLTDKAV
			KDYSAYRSSLLFWALVDLIYNMFKKVPTSNTEGGWSCSLARYIR
			HNDMPIYEAADKALKTFQEEFMPVETFSEFLDVAGLLSEITDPE
			SFLKOLLNSVP .
5789	1	2407	LPLHAVEKTGRPGQPALKMPGKLRSDAGLESDTAMKKGETLRKQ
ł		1	TEEKEKKEKPKSDKTEEIAEEEETVFPKAKQVKKKAEPSEVDMN
		1	SPKSKKAKK\KEEPSQNDISPKTKSLRKKKEPIEKKVVSSKTKK
i I			VTKNEEPSEEEIDAPKPKKMKKEKEMNGETREKSPKLKNGFPHP
1			EPDCNPSEAASEESNSEIEQEIPVEQKEG\AFSNFPISEETIKL
1	1		LKGRGVTFLFPIQAKTFHHVYSGKDLIAQARTGTGKTFSFAIPL
1	İ		IEKLHG\ELQDRKRGRAPQVLVLAPTRELANQVSKDFSDITKKL
j ]		j	SVACFYGGTPYGGQFERMRNGIDILVGTPGRIKDHIQNGKLDLT
1 }	ĺ		KLNHVVLDEVDQMLDMGFADQVEEILSVAYKKDSEDNPQTLLFS
1 1			ATCPHWVFNVAKKYMKSTYEQVDLIGKKTQKTAITVEHLAIKCH
i I			WTQRAAVIGDVIRVYSGHQGRTIIFCETKKEAQELSQNSAIKQD
	1		AQSLHGDIPQKQREITLKGFRNGSFGVLVATNVAARGLDIPEVD
1			LVIQSSPPKDVESYIHRSGRTGRAGRTGVCICFYQHKEEYQLVQ
1	1	f	VEQKAGIKFKRIGVPSATEIIKASSKDAIRLLDSVPPTAISHFK QSAEKLIEEKGAVEALAAALAHISGATSVDQRSLINSNVGFVTM
1			ILQCSIEMPNISYAWKELKEQLGEEIDSKVKGMVFLKGKLGVCF
1 1	ļ	1	DVPTASVTEIQEKWHDSRRWQLSVATEQPELEGPREGYGGFRGQ
, ,		1	REGSRGFRGQRDGNRRFRGQREGSRGPRGQRSGGGNKSNRSQNK
[ ]		1	GQKRSFSKAFGO
5790	3786		ARRQRDPLQALRRRNQELKQQVDSLLSESQLKEALEPNKRQHIY
			QRCIQLKQAIDENKNALQKLSKADESAPVANYNQRKEEEHTLLD
		[	KLTQQLQGLAVTISRENITEVGAPTEEEEESESEDSEDSGGEEE
	i	Į.	DAEEEEEKEENESHKWSTGEEYIAVGDFTAQQVGDLTPKKGEI
		1	LLVIEKKPDGWWIAKDAKGNEGLVPRTYLEPYSEEEEGQESSEE
İ	Í	1	GSEEDVEAVDETADGAEVK\QRTDPHWSAVQKAISEAGIFCLVN
			HVSFCYLIVLMRNRMETVEDINGSETGFRAWNVQSRGRIFLVSK
			TOTAL TANK

SEQ	Predicted	Predicted end	1 12-1
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
- 1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ŀ	amino acid	residue of	Serine, TeThreonine, VeValine
- 1	residue of	amino acid	W=Tryptophan, Y=Tvrosine, Y=Unknown +-ch
	amino acid	sequence	Couon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
1	1		PVLQQINTVDVLTTMGAIPAGFRPSTLSQLLFEGNOFPANVEY
1		İ	FEDAPSQUAFROLDMWDATEGTIRSRPSRTST.TLTT.WGCVMTDY D
- [			GMSIQVLSRHVRLCLFDGNKVLSNTHTVDATWODKVDVTMTDG
			QVIRILIPCLLDGDCFIRSNSASPDLGII.FEI.GTSVTDMSTGDDG
1	1		BLSCGWVFLKLFDASGVPIPAKTVELFLMCCTDVPVCLEtmpor
1	1		SRRAHGSVFYQIMTMRRQPQLLVKLRSLNRRSRNVLSLLPETLI
			GNMCSIHLLIFYRQILGDVLLKDRMSLQSTDLISHPMLATFPML
1	1		LEOPDVMDALRSSWAGQES\TLKRSEKR\PKEFLKVPRFLLVYH
			\GCVLPLL/HTPTRLPPFRWAEEETETARWKVITDFLKQNQENQ GALQALLSPDGVHEPFDLSEQTYDFLGEMRKNAV
5791	3	1636	LRVAEFAGTSR/IGAGLIQPLHRAPARDHGLLRGGAAPALSVSH
	1		GN/GKQL/AMSSQGSDDEQIKRENIRSLTMSGHVGFESLFDQLV
j	l		MRSIQQGFCFNILCVGETGIGKSTLIDTLFNTNFEDYESSHFCP
1		1	NVALKAQTYELQESNVQLKLTIVNTVGFGDOINKFRQVOJIVDV
Į.			1DAQFEAYLQEELKIKRSLFTYHDSRIHVCI.VFTSDTGUGI VTV
İ			DUBINKNEDSKVYIIPVIAKADTVSKTELOVEKTVIMSELUONO
i i		1	VQ11QFPTDDDTIAKVNAAMNGOLPFAVVGSMDEVKVGNYMIVA
1		ł	KUIPWGVVQVENERHCDFVKLREMLICTNMEDI.DEOTUTDUVET
1			YRRCKLEEMGFTDVGPENKPVSVQETYEAKRHEFHGERQRKEEE
			MKQMFVQRVKEKEAILKEAERELQAKFEHLKRLHQEBRMKLEBK
İ			RRLLEEEIIAFSKKKATSEIFHSQSFLATGSNLRKDKDRKNSQF
L			FVKQKVPEHRRSSSQANFIKKKLEVCFDFAVICFITSIFGEQPQ LLIFMEKYFQVQGQYISQSE
5792	2263	653	AAAAPSPAWWCGVFVVYVVHTCWVMYGIVYTRPCSGDASCIQPY
		İ	LARRPKLQL\RHSFTTTRSHLGAENNIDLVLNVEDFDVESKFER
1		•	I VNVSVPKKTRNNGTLYAYIFLHHAGVI, PWHDGKOVHI, VGDI TUD
l	j .		IMVPRPEEINLLIGESDTOOTFADKKDTGAIDEDUCTION TO THE
1			NVMADNEVEDGSSLPADVHRYMKMIOLGKTVHYLDTLETDOLON
1	Į.		RVADDIVINKSTTEDPLTVSYDKVSLGRIDEUTHMODALTVCT OO
i	<b>!</b>		FGFSERDADEVKGIFVDTNLYFLALTFFVAAFHLLFDFLABVND
<u> </u>			1 13FWARKASMIGMSTKAVLWRCFSTVVTFLFLLDFOTGLLUTUD
ĺ			AGVGAAIELWKVKKALKMTIFWRGLMPEFQFGTYSESERKTEEY
			DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV
1			YAFGFLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE
			EKATRAPHTD
5793	2263	653	AAAAPSPAWWCGVFVVYVVHTCWVMYGIVYTRPCSGDASCIQPY
			LARREKLQL\RHSFTTTRSHLGAENNIDI.VI.NVEDEDVECKEED
			I TANASA PEKTENNGTLYAYI FLHHAGVI PWHDGKOVEL VEDI TET
	ì		IMVPRPEEINLLTGESDTOOTEANKKOTSALDEDVOUWDDDIAL
			NVMADNEVEDGSSLPADVHRYMKMIOLGKTVHVI.DIL.ETDOLEN
			RVKDLHVINKSTTELPLTVSYDKVSLGRLRFWIHMODAVVST.OO
	]		FOFSEKDADEVKGIFVDTNLYFLALTFFVAAFHIJFDETAFVND
·			ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLFLLDEQTSLLVLVP
ł	1	;	AGVGAAIELWKVKKALKMTIFWRGLMPEFQFGTYSESERKTEEY
			DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFUNGV YAFGFLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF
ľ	1		IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE
5794			EKATRAPHTD
3,34	1	5016	MGPRLSVWLLLLPAALLLHEEHSRAAAKGGCAGSGCGKCDCHGV
1	1	ł	AGUKGERGLPGLQGVIGFPGMOGPEGPOGPPGOKGDTGEPGI DC
	ĺ	į	TKGTRGPPGASGYPGNPGLPG1PGODGPPGPPGTPGCNGTVGPP
		]	GPLGPPGLPGFAGNPGPPGLPGMKGDPGEILGHVPGMII.VCCPC
		1	FPGIPGIPGPPGLPGLOGPVGPPGFTGPPGPPGPPGPPGPMGPMGM
1		i	GLSFUGPKGDKGDQGVSGPPGVPGOAOVOEKGDFATKGEKGOKG
ļ			EMGFQGMPGVGEKGEPGKPGPRGKPGKDGDKGEKGSPGERGERG
1		J	YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT
[		i	PGPRGEPGPKGFPGLPGQPGPPGLPVPGQAGAPGFPGERGEKGD
	1	1.	RGFPGTSLPGPSGRDGLFGPPGSPGPPGQPGYTNGIVECQPGPP GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGPQG
			PPGEIGPPGQPGAKGDRGLPGRDGVAGVPGPQGTPGLIGQPGAK

SEQ	Predicted	Dwadi - bad and	
ID	beginning	Predicted end nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
i	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	L=Leucine, M=Methioninc, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Upknown *-Ston
1	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
	ĺ		GEPGEFYFDLRLKGDKGDPGFPGOPGMPGRAGSBGBDGUPGT DG
1		1	PKGSPGSVGLKGERGPPGGVGPPGSRGDTGPDGPGQCPAGDTG
- (			DKGQAGFPGGPGSPGLPGPKGRPGKTVDI.DCDDGAPGI.DCCDG
J			PGPQGDRGFPGTPGR\PGL\PGEKGAVG\OPGTGEPGPPGPVCTI
1	1	1	DGLPGDMGPPGTPGRPGFNGLPGNPGVQGQKGEPGVGLPGLKGL
	1		PGLPGIPGTPGEKGSIGVPGVPGEHGAIGPPGLQGIRGEPGPPG
1			LPGSVGSPGVPGIGPPGARGPPGGQGPPGLSGPPGIKGEKGFPG
		1	FPGLDMPGPKGDKGAQGLPGITGQSGLPGLPGQQGAPGIPGFPG
1		İ	SKGEMGVMGTPGQPGSPGPWGAPGLPGEKGD\HGFFGSSGPRGD PGLKGDKGDVGLPGKPGSMDKVYMGSMKGQKGDQGEKGQIGPIG
1		!	EKGSRGDPGTPGVPGKDGQAGQPGQPGPKGDPGISGTPGAPGLP
		1 '	GPKGSVGGMGLPGTPGEKGVPGIPGPGGSPGLPGDKGAKGEKGQ
1			AGPPGIGIPGLRGEKGDQGIAGFPGSPGEKGEKGSIGIPGMPGS
			PGLKGSPGSVGYPGSPGLPGEKGDKGLPGLDGTPGVKGEAGLDG
1			TPGPTGPAGQKGEPGSDGIPGSAGEKGEPGT.PGPGEPGPDGP
			DKGSKGEVGFPGLAGSPGIPGSKGEOGFMGPPGPOGOPGLAGSP
	1		GHATEGPKGDRGPQGQPGLPGLPGLPGTDGVKGDKGND
1			GWPGAPGVPGPKGDPGFOGMPGIGGSPGTTGSKGDMGDDGVPGF
1	[		QGPKGLPGLQGIKGDOGDOGVPGAKGI,PGPDGPDGPVDTTVCPD
			GLPGPEGPPGLKGLOGLPGPKGOOGVTGTNGTPGPDGTPGPDGN
1	!		PGQKGEMGPAGPTGPRGFPGPPGPDGLPGSMGPPGTPSVDHGFL
1			VTRHSQTIDDPQCPSGTKILYHGYSLLYVQGNERAHGQDLGTAG
1			SCLRKFSTMPFLFCNINNVCNFASRNDYSYWLSTPEPMPMSMAP ITGFNIRPFISRCAVCEAPAMVMAVHSQTIQIPPCPSGWSSLWI
			GYSFVMHTSAGAEGSGQALASPGSCLEEFRSAPFIECHGRGTCN
i			YYANAYSFWLATIERSEMFKKPTPSTLKAGELRTHVSRCQVCMR
			RT
5795	1192	61	STRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHE
1			PLAKIILESNOFRDFFKYVELSTFDIASDAFATEKDII.TDUKUT.
1	i		VADPLEQNYDTIFEDYEKLLOSENYVTKROSIKTIGELILDDUM
			FAIMTKYISKPENLKLMMNLLRDKSPNIOFEAFHVPKVFVASDU
í i			KTQPIVEILLKNQPKLIEFLSSFOKERTDDEOFADEKNVLTKOT
5796	2	1078	RDLKKTAP*RALRDSKR
		2070	GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF
i I			FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP
1 1			GIDIGDVSERRALRKSLKCKNFOWYLDHVYPEMRRYNNTVAYGE
1 ' 1	i		LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL
	i		GALGTITLLPDTRCLVDNSKSRLPOLLDCDKVKSSLVKDWMPTO
į į	Ì		NGAIMNKGTGRCLEVENRGLACIDLILRSCTGORWTTKNGTV+D
	ļ		EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG
5797			QRRDPG
3/3/	2	891	PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE
	į		VAQVENQLLKMKVESSOEANAEVMREMTKKLVSOVERKLOPPOP
	1		KHSAEKEALLEETNSFLKAIERANKKMOAAEISLEEKDODIGET
- 1		1	DRLIERMEKERHQLQLQLLEHETEMSGELTDSDKERYOOLEEAS
1	į	1	ASLRERIRHLNDMVHCQQKKVKOMVEEIESLKKKLOOKOLLTLO
İ	1	İ	LLEKISFLEGENNELQSRLDYLTETOAKTEVETRETGVGCDLLD
5798	644	115	SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT
ļ		-1.3	KILGSRWKSMSNQEKQPYYEEQARLSKIHLEKYPNYKYKPRPKR
İ		ĺ	TCIVDGKKLRIGEYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG
		j	VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT
5799	2679	1435	DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL
	İ		TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL
1	f		DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP
. 1			PASAGAGNLLVDVFDGPAAQPSLGPTPEEAFLSPGPEDIGPPIP
		1	EADBLLNKFVCKNNGVLFENOLLOIGVKSEFRONLGRMVI.FYCN
1		l.	KTSVQFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQQVI.
		1	NIECLRDFLTPPLLSVRFRYGGAPOALTLKLPVTINKFFORTEM
			AAQDFFQRWKQLSLPQQBAQKIFKANHPMDAEVTKAKLLGFGSA

SEQ	Predicted	Predicted end	
XD	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	•	\=possible nucleotide insertion)
	<del>                                     </del>	<del></del>	LLDNVDPNPENFVGAGIIQTKALQVGCLLRLEPNAQAQMYRLTL
			RTSKEPVSRHLCELLAQOF
5800	2679	1435	LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL
			TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL
			DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP
	İ		PASAGAGNLLVDVFDGPAAQPSLGPTPREAFLSPGPEDIGPPIP
1	}		EADELLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN
1			KTSVQFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQQVL
1		:	NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM
1			AAQDFFQRWKQLSLPQQEAQKIFKANHPMDAEVTKAKLLGFGSA
1.			LLDNVDPNPENFVGAGIIQTKALQVGCLLRLEPNAQAQMYRLTL
			RTSKEPVSRHLCELLAQQF
5801	3	1413	FPRLYHLIPDGEITSIKINRVDPSESLSIRLVGGSETPLVHIII
			QHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLLRQP
ļ	•		CQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEE
1			QLGIKLVRKVDEPGVFIFNVLDGGVAYRHGQLEENDRVLAINGH
			DLRYGSPESAAHLIQASERRVHLVVSRQVRQRSPDIFQEAGWNS
]			NGSWSPGPGERSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVA
			GGASHREWDLPIYVISVEPGGVISRDGRIKTGDILLNVDGVELT
1			EVSRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNH
			NMAPPSDWSPSWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIVG
			GYEEYNGNKPFFIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSG
5802	3		MIHACLARLLKELKGRITLTIVSWPGTFL
3002	, ,	290	CFSLYQIMERIMDLPTLLRHAFREMFSVGGLFWMFRIRIILCLM
1			GAFFYLISPLDFVPEALFGILGFLDDFFVIFLLLIYISIMYREV
5803	2234	1299	ITQRLTR
	~~~~	1299	EAQFGTTAEIYAYREEQDFGIEIVKVKAIGRQRFKVLELRTQSD GIQQAKVQILPECVLPSTMSAVQLESLNKCQIPPSKPVSREDQC
			SYKWWQKYQKRKFHCANLTSWPRWLYSLYDAETLMDRIKKQLRE
			WDENLKDDSLPSNPIDFSYRVAACLPIDDVLRIQLLKIGSAIQR
			LRCELDIMNKCTSLCCKQCQETEITTKNEIFSLSLCGPMAAYVN
1 1			PHGYVHETLTVYKACNLNLIGRPSTEHSWFPGYAWTVAQCKICA
i i	ı		SHIGWKFTATKKDMSPQKFWGLTRSALLPTIPDTEDEISPDKVI
}			PCF .
5804	2	1707	EMEKQRQEEQRKRTEEERKRRIEQDMLEKRKTQRELAKRAEQIE
1 1	İ		DINNTGTESASEEGDDSLLITVVPVKSYKTSGKMKKNFEDLEKE
	· ·		REEKERIKYEEDKRIRYEEQRPSLKEAKCLSLVMDDEIESEAKK
			ESLSPGKLKLTFEELERQRQENRKKQAEEEARKRLEEEKRAPEE
i l			ARRQMVNEDEENQDTAKIFKGYRPGKLKLSFEEMERQRREDEKR
! !			KAEEEARRRIEEEKKAFAEARRNMVVDDDSPEMYKTISQEFLTP
į l		i	GKLEINFEELLKQKMEEEKRRTEEERKHKLEMEKQEFEQLRQEM
į l	ì		GEBEEENETFGLSREYEELIKLKRSGSIQAKNLKSKFEKIGQLS
1 1			EKEIQKKIEEERARRAIDLEIKEREAENFHEEDDVDVRPARKS
i i		ĺ	EAPFTHKVNMKARFEQMAKAREEEEQRRIBEQKLLRMQFEQREI
l l			DAALQKKREEEEEEGS IMNGSTAEDEEQTRSGAPWFKKPLKNT
	}		SVVDSEPVRFTVKVTGEPKPEITWWFEGEILQDGEDYQYIERGR
5805	3	776	TYCLYLPETFPEDGGEYMCKAVNNKGSAASTCILTIESKN
	-	,,,	YISDTLGQVYKSKIRWWIEENGGNGNISVDDLIALLDLAEHASS
			AFKESQQQSEDREYEVKERLYPKSKRRYDTYNIAGYQGEIEVGL
1		İ	YTIQILQLIPFFDNKNELSKRYMVNFVSGSSDIPGDPNNEYKLA
[			LKNYIPYLTKLKFSLKKSFDFFDEYFVLLKPRNNIKQNEBAKTR
	1	1	RKVAGYFKKYVDIFCLLEESQNNTGLGSKFSEPLQVERCRRNLV ALKADKFSGLLEYLIKSQEDAISTMKCIVNEYTFLLK
5806	1257	877	
		١	AVFTFHNHGRTANLYSLHSWLGITTVFLFACORFLGFAVFLLPW ASMWLRSLLKPIHVFFGAAILSLSIASVISGINEKLFFSLKNTT
<u> </u>	[	[	RPYHSLPSEAVFANSTGMLVVAFGLLVLYILLASSWKRP
5807	2267	1302	RFSKKTFRRPMAVDIQPACLGLYCGKTLLFKNGSTEIYGECGVC
	==:		PRGQRTNAQKYCQPCTESPELYDWLYLGFMAMLPLVLHWFFIEW
			YSGKKSSSALFQHITALFECSMAAIITLLVSDPVGVLYIRSCRV
			LMLSDWYTMLYNPSPDYVTTVHCTHEAVYPLYTIVFIYYAFCLV
			THE CHA

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SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
- 1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
- 1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ŀ	sequence	sequence	Codon, /=possible nucleotide deletion,
	bequence		\=possible nucleotide insertion)
i	1		LMMLLRPLLVKKIACGLGKSDRFKSIYAALYFFPILTVLQAVGG
1	}	}	GLLYYAFPYIILVLSLVTLAVYMSASBIENCYDLLVRKKRLIVL
]	1	]	FSHWLLHAYGIISISRVDKLEQDLPLLALVPTPALFYLFTAKFT
5808			EPSRILSEGANGH
3000	2	433	SLPDSGVVEYLSNGGVADNHKDFGELRYNECLMNFSCNGKNGSS
	j		EGRITHGFQLKSAYENNLMPYTNYTFDFKGVIDYIFYSKTHMNV
1			LGVLGPLDPQWLVENNITGCPHPHIPSDHFSLLTQLELHPPLLP
		L	LVNGVHLPNRR
5809	464	2422	ILVPGFQGILHPGVYCALQSQHQAQELVADIDECEVSGLCRHGG
1	1	1	RCVNTHGSFECYCMDGYLPRNGPEPFHPTTDATSCTEIDCGTPP
		Í	EVPDGYIIGNYTSSLGSQVRYACREGFFSVPEDTVSSCTGLGTW
İ			ESPKLHCQEINCGNPPEMRHAILVGNHSSRLGGVARYVCQEGFE
	1		SPGGKITSVCTEKGTWRESTLTCTEILTKINDVSLFNDTCVRWQ
	ľ		INSRRINPKISYVISIKGQRLDPMESVREETVNLTTDSRTPEVC
1			LALYPGTNYTVNISTAPPRRSMPAVIGFQTAEVDLLEDDGSFNI
1	İ		SIFNETCLKLNRRSRKVGSEHMYQFTVLGQRWYLANFSHATSFN
ł			FTTREQVPVVCLDLYPTTDYTVNVTLLRSPKRHSVQITIATPPA
1	<b>{</b>		VKQTISNISGFNETCLRWRSIKTADMEEMYLFHIWGQRWYQKEF
1			AQEMTFNISSSRDPEVCLDLRPGTNYNVSLRALSSELPVVISL
1	<b>!</b>		TTQITEPPLPEVEFFTVHRGPLPRLRLRKAKEKNGPISSYQVLV
	•		LPLALQSTFSCDSEGASSFFSNASDADGYVAAELLAKDVPDDAM
			BI DICODI, VVCDVVNA DI VDCCDVCT II DICODI.
			EIPIGDRLYYGEYYNAPLKRGSDYCIILRITSEWNKVRRHSCAV WAQVKDSSLMLLQMAGVGLGSLAVVIILTFLSFSAV
5810	3	1641	VUDCTURDUDING TO TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE T
	-	1041	KVFGTHKDHEVSTLDTAISAVKVQLAEFLENLQEKSLRIEAFVS
1	i		BIESFFNTIEENCSKNEKRLEEQNEEMMKKVLAQYDEKAQSFER
			VKKKKMEFLHEQMVHFLQSMDTAKDTLETIVREAEELDEAVFLT
			SFEEINERLLSAMESTASLEKMPAAFSLFEHYDDSSARSDOMLK
			QVAVPQPPRLEPQEPNSATSTTIAVYWSMNKEDVIDSFQVYCME
1 1			EPODDQEVNELVEEYRLTVKESYCIFEDLEPDRCYQVWVMAVNF
1			TGCSLPSERAIFRTAPSTPVIRAEDCTVCWNTATIRWRPTTPEA
1 1		1	TETYTLEYCRQHSPEGEGLRSPSGIKGLQLKVNLQPNDNYFFYV
	Į.		RAINAFGTSEQSEAALISTRGTRFLLLRETAHPALHISSSGTVI
1 1	i.		SFGERRRLTEIPSVLGEELPSCGQHYWETTVTDCPAYRLGICSS
1 1	†		SAVQAGALGQGETSWYMHCSEPQRYTFFYSGIVSDVHVTERPAR
i l	1		VGILLDYNNQRLIFINAESEQLLFIIRHRFNEGVHPAFALEKPG
5811	1918	851	KCTLHLGIRPPDSVRHK
1 1		951	AAALADPLPEDKWSAEKRRPLKSSLGYEITFSLLNPDPKSHDVY
		ļ	WDIEGAVRRYVQPFLNALGAAGNFSVDSQILYYAMLGVNPRFDS
1 1	!		ASSSYYLDMHSLPHVINPVESRLGSSAASLYPVLNFLLYVPELA
			HSPLYIQDKDGAPVATNAFHSPRWGGIMVYNVDSKTYNASVLPV
1			RVEVDMVRVMEVFLAQLRLLFGIAQPQLPFKCLLSGPTSEGLMT
1 1			WELDRLLWARSVENLATATTTLTSLAQLLGKISNIVIKDDVASE
1 1			VYKAVAAVQKSAEELASGHLASAFVASQEAVTSSELAFFDPSLL
1		1	HLLYFPDDQKFAIYIPLFLPMAVPILLSLVKIFLETRKSWRKPE
5812	5204		KTD
	3204	2744	GGRQRCQRGRSCGAREBEVEPGTARPPPAASAMDASLEKIADPT
1	1	1	LAEMGKNLKEAVKMLEDSQRRTEEENGKKLISGDIPGPLQGSGQ
1 1	}		DMVSILQLVQNLMHGDEDEEPQSPRIQNIGEQGHMALLGHSLGA
1	ļ	İ	YISTLDKEKLRKLTTRILSDTTLWLCRIFRYENGCAYFHREERE
1 1			GLAKICRLAIHSRYEDFVVDGFNVLYNKKPVIYLSAAARDGLGO
1 1	1		YLCNQLGLPFPCLCRVPCNTVFGSQHOMDVAFLEKLIKDDIERG
1			RLPLLLVANAGTAAVGHTDKIGRLKELCEQYGIWLHVEGVNLAT
			LALGYVSSSVLAAAKCDSMTMTPGPWLGLPAVPAVTLYKHDDPA
1			LTLVAGLTSNKPTDKLRALPLWLSLQYLGLDGFVERIKHACQLS
į [		ſ	QRLQESLKKVNYIKILVEDELSSPVVVFRFFQELPGSDPVFKAV
			PVPNMTPSGVGRERHSCDALNRWLGEQLKQLVPASGLTVMDLEA
		}	EGTCLRFSPLMTAAVLGTRGEDVDQLVACIESKLPVLCCTLQLR
		1	EEFKQEVEATAGLLYVDDPNWSGIGVVRYEHANDDKSSLKSYPO
] {			GENIHAGLLKKLNELESDLTFKIGPEYKSMKSCLYVGMASDNVH
	ļ		AAELVETIAATAREIEDNSRLLENMTEVVRKGIQEAQVELOKAS
			EERLLEEGVLRQIPVVGSVLNWFSPVQALQKGRTFNLTAGSLES
			Sarrant and A A A Manager and a Manager and

000			
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning	nucleotide	A=Alanine, C=Cysteine, D=Aspartic Acid F-
NO:	nucleotide	location	Giutamic Acid, F=Phenvlalanine, G=Glycine
	location	corresponding	H=H1stidine, I=Isoleucine, K=Lysine
ı	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine
	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine.
1	residue of	residue of	S=Serine, T=Threonine, V=Valine.
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion
<b></b>	sequence		\=possible nucleotide insertion)
ł			TEPIYVYKAQGAGVTLPPTPSGSRTKQRLPGQKPFKRSLRGSDA
	1	1	LSETSSVSHIEDLEKVERLSSGPEQITLEASSTEGHPGARSPOH
5813	2936		TDQTEAFQKGVPHPEDDHSQVEGPESLR
3013	2936	699	HRDGVSGSLERPLTDRSRTGAFAQQRGKMATAGGGSGADPGSRG
1		l	LLRLLSFCVLLAGLCRGNSVERKIYIPLNKTAPCVRLLNATEGE
		į	GCQSSISGDTGVIHVVEKEEDLOWVLTDGPNPPYMVILLEGRUET
!	1		RDLMEKLKGRTSRIAGLAVSLTKPSPASGFSPSVOCPNDGFGVV
1	1		SNSYGPEFAHCREIQWNSLGNGLAYEDFSFPIFILEDFNFTKUI
ı	l .		KQCYQDHNLSQNGSAPTFPLCAMQLFSHMAWLSFSTAT\CMRRS
	1		SIQSTFSINPKIVCDPLSDYNVWSMLKPINTTGTI,KPDDPXXXX
	<b>i</b>		ATRLDSRSFFWNV\APGAESAVASFVTQLAAAEALQKAPDVTTL
1	1		PRNVMFVFFQGETFDYIGSSRMVYDMEKGKFPVOLENVDS#VET.
1			GQVALRTSLELWMHTDPVSQKNESVRNQVEDLLATLEKSGAGVP
			AVILERPNQSQPLPPSSLQRFLRARNISGVVLADHSGAFHNKVV
1			QSIYDTAENINVSYPEWLEPLKE/ETWNFG+QDTAKALADVATV
	l l		LGRALYELAGGTNFSDTVQADPQTVTRLLYG\FLIKANNSWFQS
			ILQGRDLRSYLG*RGLFQH\YIAV\SSPTNTIYV/VLQYALANL
			TGTVVNLTREQCQDPSKVPSENKDLYEYSWVQGPLHSNETDRLP
1			RCVRSTARLARALSPAFELSQWSSTEYSTWTESRWKDIRARIFL
1 1			IASKELELITLTVGFGILIFSLIVTYCINAKADVLFIAPREPGA
5814	8500	432	VSY
	0500	432	ALKCRPRRVLAILVGPVQPDRMAEEGAVAVCVRVRPLNSREESL
			GETAQVYWKTHNNVIYPVDGSKSFNFDRVLHGNETPKNVYEA\I
			AAPIIDSAIQGYNGTIFA\YGQT\ASGKTYTMMGSEDHLGVIPQ
1 1	İ		GQFHGHFSQKI*EVFLDREFLLRVSYMEIYNBTITDLLCGTQKM
			KPLIIREDVNRNVYVADLTEEVVYTSEMALKWITKGEKSRHYGE
	1		TKMNQRSSRSHTIFRMILESREKGEPSNCEGSVKVSHLNLVDLA
! i			GSERAAQTGAAGVRLKEGCNINRSLFILGQVIKKLSDGQVGGFI
ſ			NYRDSKLTRILONSLGGNPKTRIICTITPVSFDETLTALQFAST
			AKYMKNTPYVNEVSTDEALLKRYRKEIMDLKKQLEEVSLRTRAQ
			AMEKDQLAQLLEEKDLLQKVQNEKIENLTRMLVTSSSLTLQQ3L KAKRKRRVTWCLGKINKMKNSNYADQFNIPTNITTKTHKLSINL
1	i i		LREIDESVCSESDVFSNTLDTLSEIEWNPATKLLNQENIESELN
	1		SLRADYDNLVLDYEQLRTEKEEMELKLKEKNDLDEFEALERKTK
1			KDQBMQLIHEISNLKNLVKHREVYNQDLENELSSKVELLREKED
	1		QIKKLQBYIDSQKLENIKMDLSYSLBSIEDPKQMKQTLFDAETV
- 1			ALDAKRESAFLRSENLELKEKMKELATTYKQMENDIQLYQSQLE
1	f		AKKKMQVDLEKELQSAFNEITKLTSLIDGKVPKDLLCNLELEGK
1			ITDLQKELNKEVEENEALREEVILLSELKSLPSEVERLRKEIQD
	İ		KSEELHIITSEKDKLFSEVVHKESRVOGLLEEIGKTKDDLATTO
	ĺ		SNYKSTDQEFQNFKTLHMDFEOKYKMVLEENERMNOETVNLSKE
ľ		1	AQKFDSSLGALKTELSYKTQELOEKTREVOERLNEMEOLKROLE
1			NRDSPLQTVEREKTLITEKLOOTLERVKTI.TORKDDI.KOLORGI
	Í		QIERDQLKSDIHDTVNMNIDTOEOLRNALESIKOHOETTNTIKS
1	j	l	KISEBUSRNLHMBENTGETKDEFOOKMUGIDKKODI.EAKNTOTI
į.		ł	TADVKDNEI I EQQRKI FSLIQEKNELOOMLESVI AEKEOLKTDI.
[			KENIEMTIENQEELRLLGDELKKOOEIVAOEKNHAIKKEGEIGD
j		]	TCDRLAEVEEKLKBKSQQLQEKQQOLLNVOEEMSEMOKKTNETE
	1	1	NLKNELKNKELTLEHMETERLELAOKLNENVEEVKSTTKEDKVI
1		ĺ	KELQKSFETERDHLRGYIREIEATGLOTKEELKIAHIHI.KEHOF
1		1	TIDELRRSVSEKTAQIINTQDLEKSHTKLOEEIPVLHEEOELLD
1	}	i	NVKKVSETQETMNELELLTEQSTTKDSTTLARIEMERLELNEKE
}	<b> </b>	1	QESQEEIKSLTKERDNLKTIKBALEVKHDQLKEHIRETLAKIQE
1			SQSKQEQSLNMKEKDNETTKIVSEMEOFKPKDSALLRTETEMIC
ŀ	1		LSKRLQESHDEMKSVAKEKDDLORLOEVLOSESDOLKENTKETV
		1.	AKHLETEEELKVAHCCLKEOEETINELRVNISEKETEISTIOVO
			LEAINDKLQNKIQEIYEKEEQLNIKQISEVQEKVNELKQFKEHR
1			KAKDSALQSIESKMLELTNRLOESOERIOIMIKEKEEMKRVORA
ł		1 3	LQIERDQLKENTKEIVAKMKESOEKEYOFLKMTAVNETOEKMOR
- 1	1	1	IEHLKEQFETQKLNLENIETENIRLTOILHENLEEMRSVTKERD
			DLRSVEETLKVERDQLKENLRETITRDLEKQEELKIVHMHLKEH

SEQ	Predicted	Predicted end	Amino acid coment
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
- }	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Ì	amino acid	sequence	Codon, /-possible nucleotide deletion,
	sequence	.]	\=possible nucleotide insertion)
			QETIDKLRGIVSEKTNEISNMQKDLEHSNDALKAQDLKIQEELR
-			IAHMHLKEQQETIDKLRGIVSEKTDKLSNMQKDLENSNAKLQEK
1			IQELKANEHQLITLKKOVNETQKKVSEMEQLKKQIKDQSLTLSK
	Ī		LEIENLNLAQKLHENLZEMKSVMKERDNLRRVEETLKLERDQLK
1			ESLQETKARDLEIQQELKTARMLSKEHKETVDKLREKISEKTIQ
	1		ISDIQKDLDKSKDELQKKIQELQKKELQLLRVKEDVNMSHKKIN
	i	ĺ	EMEQLKKQFEPNYLCKCEMDNFQLTKKLHESLEEIRIVAKERDE
		}	LRRIKESLKMERDQFIATLREMIARDRONHOVKPEKRLLSDGOO
1	1		HLMESLREKCSRIKELLKRYSEMDDHYECLNRLSLDLEKETEFH
-	Ì		RIMKKLKYVLSYVTKIKEEQHECINKFEMDFIDEVBKOKELLTK
	1		IQHLQQDCDVPSRBLRDLKLNQNMDLHIBEILKDFSESEFPSIK
1	1		TEFQQVLSNRKEMTQFLEEWLNTRFDIEKLKNGIOKENDRICOV
	-		NNFFNNRIIAIMNESTEFEERSATISKEWEODLKSLKEKNEKTE
			KNYQTLKTSLASGAQVNPTTODNKNPHVTSRATOLTTEKTRELE
1			NSLHEAKESAMHKESKIIKMQKELEVTNDIIAKLOAKVHESNKC
1			LEKTKETIQVLQDKVALGAKPYKEEIEDLKMKLGKIDLEKMKNA
1			KEFEKEISATKATVEYQKEVIRLLRENLRRSQQAQDTSVISEHT
1	]		DPQPSNKPLTCGGGSGIVQNTKALILKSEHIRLEKEISKLKQQN
j			EQLIKQKNELLSNNQHLSNEVKTWKERTLKREAHKQVTCENSPK
1			SPKVTGTASKKKQITPSQCKERNLQDPVPKESPKSCFFDSRSKS
	1		LPSPHPVRYFDNSSLGLCPEVQNAGAESVDSQP\GPWARLFQGK DVP\ECKTO
5815	23	1460	SELVMWTVQNRESIGLLSFPVMITMVCCAHSTNEPSNMSYVKET
	1		VDRLLKGYDIRLRPDFGGPPVDVGMRIDVASIDMVSEVNMDYTL
1			TMYFQQSWKDKRLSYSGIPLNLTLDNRVADQLWVPDTYFLNDKK
1	ļ		SFVHGVTVKNRMIRLHPDGTVLYGLRITTTAACMMDLRRYPLDE
1			QNCTLEIESYGYTTDDIEFYWNGGEGAVTGVNKIELFQFSIVDY
Į.			KMVSKKVEFTTGAYPRLSLSFRLKRNIGYFILQTYMPSTLITIL
i	İ		SWVSFWINYDASAARVALGITTVLTMTTISTHLRETLPKIPYVK
J ·	1		AIDIYLMGCFVFVFLALLEYAFVNYIFFGKGPOKKGASKODOSA
i i			NEKNKLEMNKVQVDAHGNILLSTLEIRNETSGSEVLTSVSDPKA
1	]		TMYSYDSASIQYRKPLSSRE\A*GRAPDRHGVPSKGRTRRRAS\
5816	963		QLKVKIPDLTDVNSIDKWSRMFFPITFSLFNVVYWLYYVH
1 2010	861	191	TSSRSRAAAQEGDAETPGSVERRGRRAGAEDGMSQAPGAQPSPP
1			TVYHERQRLELCAVHALNNVLQQOLFSQEAADRICKRLAPDSRL
•	[		NPHRSLLGTGNYDVNVIMAALQGLGLAAVWWDRRRPLSOLALDO
1 1			VLGLILNLPSPVSLGLLSLPLRRRHLRWPCARL/VTVSYYNLDS
			K\LRAPEGPGGLRTE\*GPFLAAALAQGLCEVLLVVTKEVEEKG
5817	851	118	SWLRTD
		***	RLFRGPGANRGRSCRGCSGGREPSGGALPKRHCPC*PPSPPAAD
1			VMSNTTVPNAPQANSDSMVGYVLGPFFLITLVGVVVAVVMYVQX
į l	1		KKRVDRLRHHLLPMYSYDPAEELHEAEQELLSDMGDPKVV\QAG RVATSTSGCHCWMSRRDLTPLPHPSEPGVLDCLGPCHLLPLLSP
j		į	GSPCWVLGLHFSLHPPSAASASHALTITSLPPGLLPFVGVELTA
			HPQALMGRGFPSGMAAAGRHLCFL
5818	3	3918	QALRDKLWIFLVQSFYAVRHTESWKLMSTDDQQKIQAAAFDKGD
	ĺ		DRRIGKKPIFSSSQQRKQVSDSGDIKIKSWRGNNKKECWSYLST
į [			NKKMKSDGLGASGHSSSTNRNSINKTLKQDDVKEKDGTKIASKI
	1	1	TKELKTGGKNVSGKPKTVTKSKTENGDKARLENMSPRQVVERSA
		i	TAAAAATGQKNLLNGKGVRNQEGOISGARPKVLTGNLNVOAKAK
1. 1		1	PLKKATGKDSPCLSIAGPSSRSTDSSMEFSISTECLDEPKENGS
		1	TEEEKPSGHKLSFCDSPGQMMKNSVDSVKNSTVAIKSRPVSRVT
			NGTSNKKSIHEQDTNVNNSVLKKVSGKGCSEPVPOAILKKRGTS
		İ	NGCTAAQQRTKSTPSNLTKTQGSQGESPNSVKSSVSSROSDENV
			AKLDHNTTTEKQAPKRKMVKQVHTALPKVNAKIVAMPKNLNOSK
	1	,	KGETLNNKDSKQKMPPGQVISKTQPSSQRPLKHETSTVOKSMFH
			DVRDMNKDSVSEQKPHKPLINLASEISDAEALOSSCRP\DPOK
ł	1	i	PLNDQEKEKLALECQNISKLDKSLKHELESKOICLDKSETKFPN
ł	1	;	HKETDDCDAANICCHSVGSDNVNSKFYSTTALKYMVSNPNENSI.
1		Į.	NSNPVCDLDSTSAGQIHLISDRENQVGRKDTNKQSSIKCVEDVS
	<u>-</u>		LCNPERTNGTLNSAQEDKKSKVPVEGLTIPSKLSDESAMDEDKH

SEQ	Predicted	Predicted end	Amino poid formers
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
İ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
İ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Ston
	amino acid	sequence	Codon, /=possible nucleotice deletion
L	sequence		\=possible nucleotide insertion)
1	1 .		ATADSDVSSKCFSGQLSEKNSPKNMETSESPESHETPETPFVGH
ľ			WNLSTGVLHQRESPESDTGSATTSSDDIKPRSEDYDAGGSODDD
1			GSNDRGISKCGTMLCHDFLGRSSSDTSTPEELKIYDSNLRIEVK
		į	MKKQSSNDLFQVNSTSDDEIPRKRPEIWSRSAIVHSRERENIPR
			GSVQFAQEIDQVSSSADETEDERSEAENVAENFSISNPAPQQFQ
1			GIINLAFEDATENECREFSANKKFKRSVLLSVDECEELGSDEGE
ļ.			VHTPFQASVDSFSPSDVFDGISHEHHGRTCYSRFSRESEDNILE CKQNKGNSVCKNESTVLDLSSIDSSRKNKQSVSATEKKNTIDVL
1	ļ		SSRSRQLLREDKKVNNGSNVENDIQQRSKFLDSDVKSQERPCHL
1			DLHQREPNSDIPKNSSTKSLDSFRSQVLPQEGPVKESHSTTTEK
}	}		ANIALSAGDIDDCDTLAQTRMYDHRPSKTLSPIYEMDVIEAFEQ
			KVESETHVTDMDF*DDQHFAKQDWTLLKQLLSEQDSNLDVTNSV
1	<u> </u>		PEDLSLAQYLINQTLLLARDSSKPQGITHIDTLNRWSELTSPLD
			SSASITMASFSSEDCSPQGEWTILELETQH
5819	1	5557	AAAGLLGALHLVMTLVVAAARAEKEAFVQSESIIEVLRFDDGGL
	ŀ		LQTETTLGLSSYQQKSISLYRGNCRPIRFEPPMLDFHEOPVGMP
	<u> </u>		KMEKVYLHNPSSE*TITLVSIFATTSHFHASFFONRKILPGGNT
l i			SFDVS/VFLARVVGNVENTLFINTSNHGVFTY\OVFGVGVPNPY
			RLRPFLGARVTVNSSFSPIINIHNPHSEPLQVVEMYSSGGDLHL
<b>i</b> 1	1		ELPTGQQGGTRKLWEIPPYETKGVMRASFSSREADNHTAFIRIK
			TNASDSTEFIILPVEVEVTTAPGIYSSTEMLDFGTLRTQDLPKV
J i			LNLHLLNSGTKDVPITSVRPTPQ\NDAITVHFKPITLKAS\ESK
}	i		YTKVASISFDASKAKKPSQFSGKITVKAKEKSYSKLEIPYQAEV LDGYLGFDHAATLFHIRDSPADPVERPIYLTNTFSFAILIHDVL
1			LPEEAKTMFKVHNFSKPVLILPNESGYIFTLLFMPSTSSMHIDN
			NILLITNASKFHLPVRVYTGFLDYFVLPPKIEERFIDFGVLSAT
]			EASNILFAIINSNPIELAIKSWHIIGDG\LSIELVAVDRGNRTT
1 1			IISSLPECEKSSSSDQSSVTLASGYF\AVFRVKLTAKKL\EGIH
1			DGAIQITTDYEILTIPVK\AVIAVGSLTCSPKHVVLPPSFPGKI
		.	VHQSLNIMNSFSQKVKIQQIRSLSEDVRFYYKRLRGNKEDLEPG
1		, and the second	KKSKIANIYFDPGLQCGDHCYVGLPFLSKSEPKVOPGVAMOEDM
1 1			WDADWDLHQSLFKGWTGIKENSGHRLSAIFEVNTDLOKNIISKI
			TABLSWPSILSSPRHLKFPLTNTNCSS\EEEITLENP/SQDVPV
		ļ	YVQFIPLALYSNPSVFVDKLVSRFNLSKVAKIDLRTLEFQVFRN
l i			SAHPLQSSTGFMEG\LSPHLILNLILKPGEKKSVKVK\FTPVHN
	j		RTVSSLIIVRNNLTVMDAVMVQGQGTTENLRVAGKLPGPGSSLR FKITEALLKDCTDSLKLREPNFTLKRTFKVENTGQLQIHIETIE
1		Ī	ISGYSCEGYGFKVVNCQEFTLSANASRDIIILFTPDFTASRVIR
1		1	ELKFITTSGSEFVFILNASLPYHMLATCAEALPRPNWELALYII
	i	1	ISGIMSALFLLVIGTA\YLEAQGIWBP\FRRRLS\FEASNPPFD
i l		j	VGRPFDLRRIVGISSEGNLNTLSCDPGHSRGFCGAGGSSSRPSA
1 1		ì	GSHKQ*GPSGHPHSSHSNRNSADVDDVRAYNSGRTSSMTSAOAA
1 1		1	SSQPANKTRPLVLDSNTGAQGHSAGRKSKGAKOSOHGSOHHAHS
1 1	1		PLEQHPQPPLPPPVPQPQEPQPERLSPAPLAHPSHPERASSARH
1	1		SSEDSDITSLIEAMDKDFDHHDSPALEVFTEQPPSPLPKSKGKG
1 1			KPLQRKVKPPKKQEEKEKKGKGKPQEDELKDSLADDDSSSTTTE
1 1	j		TSNPDTEPLLKEDTEKQKGKQAMPEKHESEMSQVKQKSKKLLNI KKEIPTDVKPSSLELPYTPPLESKQRRNLPSKIPLPTAMTSGSK
1	İ		SRNAQKTKGTSKLVDNRPPALAKFLPNSQELGNTSSSEGEKDSP
	1	1	PPEWDSVPVHKPGSSTDSLYKLSLQTLNADIFLKQRQTSPTPAS
}		İ	PSPPAAPCPFVARGSYSSIVNSSSSSDPKIKQPNGSKHKLTKAA
į į	İ	ļ	SLPGKNGNPTFAAVTAGYDKSPGGNGFAKVSSNKTGFSSSLGIS
	ļ	ŀ	HAPVDSDGSDSSGLWSPVSNPSSPDFTPLNSFSAFGNSFNLTGE
			VFSKLGLSRSCNQASQRSWNEFNSGPSYLWESPATDPSPSWPAS
		Į.	SGSPTHTATSVLGNTSGLWSTTPFSSSIWSSNLSSALPFTTPAN
[ ]		'	TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSPTIGR
ECO			RSSDPWSNSHFPHEN
5820	310	1270	RVSLSGPVSLGVLLCARSSTMGKRDNRVAYMNPIAMARSRGPIQ
ļ		1	SSGPTIQ\VI*IDQGLPGKK*KSN*KRKRK/DSKALAEFEEKMN
i		] :	ENWKKELEKHREKLLSGSESSSKKRQRKKKEKKKSW*\DSSSS\
	L		SSSSDSSSSSSDSEDEDKKQGKRRKKKNRSHKSSESSMSETES
			379

WO 01/53312

SEQ	Predicted	Predicted end	L Domina
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	E-Histidine, I-Isoleucine, K-Lysine,
- 1	corresponding	to first	L-Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Ì	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			DSKDSLKKKKKSKDGTEKEKDIKGLSKKRKMYSEDKPLSSESLS
	1	1	ESEYIEEVRAKKKKSSEEREKATEKTKKKKKKKKKKKKKKKKAA
		l	SSSPDSP*H*EKSGFPYKESAMSEEISTVKTTTYLLKCMNFLVF
L			GIIPGLFSSHSDATV
5821	179	915	KWRNQSWRWPKPGTNWMLSCSVCWRRVTWTGSVWMRKLGKHPQT
ł	Ì		PT/IKDCSIAATGKRPSARFPHQRRKKRREMDDGLAEGGPQRSN
ł			TYVIKLFDRSVDLAQFSENTPLYPICRAWMRNSPSVRERECSPS
1	1		SPLPPLPEDEEG\SEVTNSKSR*CVQACPPTHTPGGQPKNACR\
}	İ		SRIPSPLAALRMQGTP*RWSPFEPEPSPSTLIYRNMQRWKRIRQ
<u> </u>			RWKEASHRNQLRYSESMKILREMYERQ
5822	464	4379	QTLKEMPIVMARDLEETASSSEDEEVISQEDHPCIMWTGGCRRI
i			PVLVFHADAILTKDNNIRVIGERYHLSYKIVRTDSRLVRSILTA
			HGFHEVHPSSTDYNLMWTGSHLKPFLLRTLSEAQKVNHFPRSYE
			LTRKDRLYKNIIRMQHTHGFKAFHILPQTFLLPAEYAEFCNSYS
			KDRGPWIVKPVASSRGRG\VYLINNPNQISLEENILVSRYINNP
<b>!</b>			LLIDDFKFDVRLYVLVTSYDPLVIYLYEEGLARFATVRYDQGAK
i			NIRNOFMHLTNYSVNKKSGDYVSCDDPEVEDYGNKWSMSAMLRY
1 1			LKQEGRDTTALMAHVEDLIIKTIISAELAIATACKTFVPHRSSC
]			FELYGFDVLIDSTLKPWLLEVNLSPSLACDAPLDLKIKASMISD
1 1			MFTVVGFVCQDPAQRASTRPIYPTFESSRRNPFQKPQRCRPLSA
			SDAEMKNLVGSAREKGPGKLGGSVLGLSMERIKVLRRVKRENDD
<u> </u>			RGGFIRIFPTSETWEIYGSYLEHKTSMNYMLATRIFODDMTADG
			APELKI*SLNSKAKLHAALYERKLLSLEVEKERERSSET.DAMDD
			KYPVITQPAEMNVKTETESEEEEEVALDNEDEROEASOFRSAGE
	1	ļ	LRENQAKYTPSLTALVENTPKENSMKVREWNNKGGHCCKLETOR
			LEPKFNLMQILQDNGNLSKMOARIAFSAYLOHVOT\RIMKDSGC
1 1			QTFSASWAAKEDEQMELVVRFLKRASNNLOHSLRMVT.PSPPT.At.
1	l.		LERTRILAHQLGDFIIVYNKETEOMAEKKSKKKVEEEEEDGVNM
1 1	j		ENFORFIRQASEAELEEVLTFYTOKNKSASVFLGTHSKTCKNNN
1 1			NYSDSGAKGDHPETIMEEVKIKPPKOOOTTETHSDKI.SDETTEN
[ ]	i	1	EKEAKLVYSNSSSGPTATLOKIPNTHLSSVTTSDI.SPGDCHHSS
1	ĺ	Í	LSQIPSAIPSMPHQPTILLNTVSASASPCI,HPGAONIPSPTCI,p
1 1	J		RCRSGSHTIGPFSSFQSAAHIYSOKLSRPSSAKAGSCYLNKHHS
1 1	į.		GIAKTQKEGEDASLYSKRYNQSMVTAELORLAEKQAARQVSDSS
1 1			HINLLTQQVTNLNLATGIINRSSASAPPTLRPTTSPSGDTWSTO
1 1	ĺ	Í	SDPQAPENHSSSPGSRSLOTGGFAWEGEVENNVYSOATGWROU
1 1	1		KYHPTAGSYQLQFALQQLEQQKLQSROLLDOSRARHQATEGSOT
l i	i		LPNSNLWTMNNGAGCRISSATASGOKPTTLPOKVVPPPSSCASI.
1 1	1		VPKPPPNHEQVLRRATSQKASKGSSAEGOLNGLOSSLNPAAFUD
5823	42		ITSSTDPAHTKIMNHKHTEKQPVHHSWVHD
	42	2293	LLTALSMEGGGGRDEPSACRAGDVNMDDPKKEDILLLADEKFDF
1 1		1	DLSLSSSSANEDDEVFFGPFGHKERCIAASLELNNPVPFOPPI.D
	1		TSESPFAWSPLAGEKFVEVYKEAHLLALHIESSSRNQAAQAAKP
			EDPRSQGVERFIQESKF\KINLFEKEKEMKKSPTSLKRETYYLS
1 1			DSPLLGPPVGEPRLLASSPALPSSGAQARLTRAPGPPHSAHALP
]			RESCTAHAASQAATQRKPGTKLLLPRAASVRGRGIPGAAEKPKK
	1	1:	EIPASPSRTKIPABKESHRDVLPDKPAPGAVNVPAAGSHLGQGK
1		ļ ·	RAIPVP\NKLGLKKTLLKAPGSYSN\LQRKSSSGA\VWSGASSA
			CTPOPVAKAKSSEFASIPAN*LPGLCPNISKS\GRMGPAMLRPA
	İ	1:	L\PAGPVG\ASSWQAKRVDVSELAAEQLTAPP\SASPTQPQTPE
			GGG\QWLNSSCAWSESSQLNKTRSIRRRDSCLNSKTKVMPTPTN
ŀ	İ	1;	OFKIPKFSIGDS\PDSSTPKLSRAQRPQSCTSVGRVTVHSTPVR
		1 :	RSSGPAPQSLLSAWRVSALPTPASRRCSGLPPMTPKTMPRAVGS
1	İ	1;	PL\CVPARRRSSEPRKNSAMRTEPTRESNRKTDSR\LVDVSPDR
1		1;	GSPPSRVPQALNFSPEESDSTFSKSTATEVAREEAKPGGDAAPS
	j	1 2	EALLVDIKLEPLAVTPDAASQPLIDLPLIDFCDTPEAHVAVGSE
l	ì	15	SRPLIDLMTNTPDMNKNVAKPSPVVGQLIDLSSPLIQLSPEADK
5824	42		ENVDSPLLKF
			LITALSMEGGGGRDEPSACRAGDVNMDDPKKEDILLLADEKFDF
1		1	DLSLSSSSANEDDEVFFGPFGHKERCIAASLELNNPVPEQPPLP
			Sespfawsplagekfvevykeahllalhiesssrnqaaqaakp

SEC	Predicted	Predicted end	Drive
ID	beginning	nucleotide	
NO:	1000000000	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asnaragine
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
	amino acid residue of	residue of	S=Serine, T=Threonine, V=Valine
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, Y=Inknown +-05
	sequence	sequence	Codon, /=possible nucleoride deletion
<b>——</b>	Ocquence		\=possible nucleotide insertion)
İ			EDPRSQGVERFIQESKF\KINLFEKEKEMKKSPTSLKRETYYLS
1		j	DSPLLGPPVGEPRLLASSPALPSSGAQARLTRAPGPPHSAHALP
-			RESCTAHAASQAATQRKPGTKLLLPRAASVRGRGIPGAAEKPKK
	1		EIPASPSRTKIPAEKESHRDVLPDKPAPGAVNVPAAGSHLGQGK
			RAIPVP\NKLGLKKTLLKAPGSYSN\LQRKSSSGA\VWSGASSA CTPQPVAKAKSSEFASIPAN*LPGLCPNISKS\GRMGPAMLRPA
	1		L\PAGFVG\ASSWQAKRVDVSELAAEQLTAPP\SASPTQPQTPE
			GGG\QWLNSSCAWSESSQLNKTRSIRRRDSCLNSKTKVMFTPTN
- 1	l l		QFKIPKFSIGDS\PDSSTPKLSRAQRPQSCTSVGRVTVHSTPVR
1			ASSOCIATED SAURVSALPTPASRRCSGL PDMTDKTMDD AVCC
1			PU (CVPACCRSSEPRKNSAMRTEPTRESNEKTDSP) LUDUSDDD
			USPPSKVPQALNESPEESDSTFSKSTATEVARREAKDCCDANDO
			BALLVUIKLEPLAVTPDAASOPLIDLPLIDECOTDEAUTANCE
ł		}	SKPLIDLMINTPDMNKNVAKPSPVVGQLIDLSSPLIOLSPEADK
5825	<del></del>	4210	ENVOSPLEKE
	_	4210	FLQIESASPAPFSSGFLAAHPHSPGGSLATKGRSRLSAPGMLHL
1	1		SAAPPAPPPEVTATARPCLCSVGRRGDGGKMAAAGALERSFVEL
			SGAERERPRHFREFTVCSIGTANAVAGAVKYSESAGGFYYVESG
			KLFSVTRNRFIHWKTSGDTLELMEESLDINLLNNAIRLKFONCS
ł			VLPGGVYVSETQNRVIILMLTNQTVHRLLLPHPSRMYRSELVVD SQMQSIFTDIGKVDFTDPCNYQLIPAVPGISPNSTASTAWLSSD
ļ			GEALFALPCASGGIFVLKLPPYDIPGMVSVVELKQSSVMQRLLT
1	1		GWMPTAIRGDQSPSDRPLSLAVHCVEHDAFIFALCQDHKLRMWS
	1		I LEOMCLMVADMLEYVPVKKDLRLTAGTGHKI,DI,AVEDIMGI VI
1	1		GIF \MHAPKRGQFCIFOLVSTESNRYSIDHISSI.FTGOFTT TOP
[			ADISTDIWALWHDAENOTVVKYINFFHNVACOWNDUEMODI DEE
ĺ			EIVIKUUQUPREMYLOSLFTPGOFTNEAI,CKAI,OTECPCTEDAIT
			DISWSELKKEVTLAVENELOGSVTEYEFSOFFFDNLOGFFWOVE
1			IACCLQIQEALSHPLALHLNPHTNMVCLLKKGVLSET.TDccrtxD
	1		HLYLLPYENLLTEDETTISDDVDIARDVICLIKCLRLIEESVTV
	1		DMSVIMEMSCYNLQSPEKAABQILEDMITIDVENVMEDICSKLQ
			EIRNPIHAIGLLIREMDYETEVEMEKGFNDAQPLNIRMNLTQLY GSNTAGYIVCRGVHKIASTRFLICRDLLILQQLLMRLGDAVIWG
	1 1		TGQLFQAQQDLLHRTAPLLLSYYLIKWGSECLATDVPLDTLESN
			LQHLSVLELTDSGALMANRFVSSPQTIVELFFQEVARKHIISHL
		į	FSQFKAPLSQTGLNWPEMITAITSYLLOLLWDSNDGCT PI PCIM
	1 .	.	GNCQIVQLQDYIQLLHPWCOVNVGSCRFMI.GRCVTAFTGFGOVAT
	1 1		ECFCQAASEVGKEEFLDRLIRSENCETUSTEDIAVVDVAR DIE 1
	1	1	VIGLPELVIQLATSAITEASDDW\KSOATI\PTCTEKUUT\DIG
	ĺ		VENEZAXGSL*PQIPDSSROLDCLROLVIVOLCEDEOLODT VERBO
	İ		YVNLHNEVVGIIESRARAVDLMTHNYYELLYAFHIYRHNYRKAG
		1	TVMFEYGMRLGREVRTLRGLEKQGNCYLAALNCLRLTRPEYAWI VQPVSGAVYDRPGASPKRNHDGECTAAPTNRQIEILELEDLEKE
	1		CSLARIRLTLAQHDPSAVAVAGSSSAEEMVTLLVQAGLFDTAIS
		1	LCQTFKLPLTPVFEGLAFKCIKLQFGGEAAQARAWAWLAANQLS
		1	SVITTRESSATDEAWRLLSTYLERYKVONNT, VHHCUTNYT I CHO
5826			VPLPNWLINSYKKVDAAELLRLYINVDI.I.DI.TDVOVITDIGGG
3020	3	8/1	KSQLLRDHSAPPPKPCTSVGAMGC*PRO/SPKEOOPOLVVOVND
	1	. [ .	MAAQKSKQKHTDKADALHOOHESLEKDNIALRKETOSLOARI NU
		1	WSKTLHVHERLCPMDCASCSAPGLIGCWDOAFGIJGPGDOCOUG
		j '	CREQUELFQTPGSCYPAOPLSPGPOPHDSPSI.I.OCDI.Det et CD
	i i	1.	AVVAEPPVQLSPSPLLFASHTGSSLOGSSSKLSALOPSLTAGTA
		1 -	PUPLELEHPTRGKLGSSPDNPSSALGLARIOSPEHKDALCAAT
5827	194		WQGLVVDPSPHPLLAFPLLSSAOVHF
		2287	MGSENSALKSYTLREPPFTLPSGLAVYPAVLQDGKFASVFVYK
		1 1	RENEDKVNKAAKVP**HLKTLRHPCLLRFLSCTVRADGTHTVTF
		1 2	*VQPLEVALETLSSAEVCAGIYDILLALIFLHDRGHI.THNINGCI.
	1	1.6	
		٤١	SSVFVSBDGHWKLGGMETVCKVSQATPEFLRSIQSIRDPASIPP
		F	EMSPEFTTLPECHGHARDAFSFGTLVESLITTINFOVENDUTE
		F	SSYFVSEDGHWKLGGMETVCKVSQATPEFLRSIQSIRDPASIPP SEMSPEFTTLPECHGHARDAFSFGTLVESLLTILNEQVSADVLS SFQQTLHSTLLNPIPKWRPALCTLLSHDFFRNDFLEVVNFLKSL SLKSREEKTEPFKFLLDRVSCLSEELIASRLVPLLLNQLVFAEP

•			
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l l	residue of	amino acid	W-Tryptophan, Y-Tyrosine, X-Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	-	\=possible nucleotide insertion)
			VAV\KSFLPYLLGPKKDHAQGETPCLLSPALFQSRVIPVLLQLF
	Í		EVHEEHVRMVLLSHIEAYVGALSLREQLKKV/IL/PQVLLG/LR
			D\TSDSIVAITLHSLAVLVSLLGPEVVVGGERTKIFKRTAP\SF
-		İ	TK\NTDLSLEGDPFSQPIKFPINGLSDVKNTSEDSENFPSSSKK
1	i		SEEWPDWSGPE\EPENQTVNI\QIWP\REP\CDDVKSQCTTLDV
ľ			EESSWDDCEPSSLDTKVNPGGGITATKPVTSGEQKPIPALLSLT
			EESMPWKSSLPQKISLVQRGDDADQIEPPKVSSQERPLKVPSEL
1	1		GLGEEFTIQVKKKPVKDPEMDWFADMIPEIKPSAAFLILPELRT
			EMVPKKDDVSPVMQFSSKFAAAEITEGEAEGWEEEGELNWEDNN
			W
5828	2	257	AREGGSLGAVAACGELSYSCDFCPARPHTSWLTRFVKMEFQAVV
			MAVGGGSRMTDLTSSIPKPLLPVGNKPLIWYPLNLLERVGFEEV
		1	IVVTTRDVQKALCABFKMKMKPDIVCIPDDADMGTADSLRYIYP
1		ľ	KLKTDVLVLSCDLITDVALHEVVDLFRAYDASLAMLMRKGQDSI
1			EPVPGQKGKKKAVEQRDFIGVDSTGKRLLFMANEADLDEELVIK
		1	GSILQKHPRIRFHTGLVDAHLYCLKKYIVDFLMENG\SITSIRS
ł		1	BL\IPYLV/RGKQFSSASSQQGTRKEKEGGSKGKRGLKSFRISY
<u> </u>			SFY*KEANYTGTGAPY\D\ACWI
5829	260	1259	PDGRLIVSCSEDKTIKIWDTTNKQCVNNFSDSVGFANFVDFNPS
	•	i	GTCIASAGSDQTVKVWDVRVNKLLQHYQVHSGGVNCISFHPSGN
1			YLITASSDGTLKILDLLKGRLIYTLQGHTGPVFTVSFSKGGELF
	1		ASGGADTQVLLWRTNFDELHCKGLTKRNLKRLHFDSPPHLLDIY
l	1		PRTPHPHEBKVETVEDFFLHLLRLIQSLR*SICRSLLPLLWISF
1	)		LLILPQQQKPVVGLCQTRVKRPVDIS*TLP*CHONVCOOPRKPK
	1		QKT*VTSPVKVK/VSIPLAVTDALEHIMEQLNVLTQTVSILEQR
<u></u>		•	LTLTEDKLKDCLENQQKLFSAVQOKS
5830	4496	3139	GGKMAAPEERDLTQEQTEKLLQFQDLTGIESMDOCRHTLEOHNW
ŀ			NIEAAVQDRLNEQEGVPSVFNPPPSRPLQVNTADHRIYSYVVSR
	1		POPRGLLGWGYYLIMLPFRFTYYTILDIFRFALRFTRPDPPSPV
	!		TDPVGDIVSFMHSFEEKYGRAHPVFYQGTYSOALNDAKRELRFI.
		•	LVYLHGDDHQDSDEFCRNTLCAPEVISLINTRMLFWACSTNKDE
1	1		GYRVSQALRENTYPFLAMIMLKDRRE*PV\VGRLEGLI\ODDDI.
1			INQLTFIMDANQTYLVSERLEREERNOTOVI.ROOODEAVI.AGI.D
1			ADQEKERKKREERERKRRKKEEVQOOKLAEERRRONT OEEKERK
	]		LECLPPEPSPDDPESVKIIFKLPNDSRVERRFHFSOSTTVTHDF
}	1		LFSLKESP\EKFQIEA\NFPRR\VLPCIPSEE\WPNPPTLOE\A
5831	<del></del>		GLSHTEVLFVQDLTDE
2027	71	2897	FCSKDKCCLYLPDSINRSKSCTAKPGAHSQDRHAVMDSERQVKD
	1		TDDIESPKRSIRDSGYIDCWDSERSDSLSPPRHGRDDSFDSLDS
i	!		FGSRSRQTPSPDVVLRGSSDGRGSDSESDLPHRKLPDVKKDDMS
	[		ARRTSHGEPKSAVPFNQYLPNKSNQTAYVPAPLRKKKARREEVR
	į į		KSWSTATSPAGLGKKALODYGPRT\PVS\DDAESTSMEDMPCPP
İ	İ		EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSRKRSVS
!	!	i	QDLIKKEEERKKMEKLLAGEDGTSERRKSIKTYREIVOEKERRE
			RELHEAYKNARSQEBAEGILQQYIERFTISEAVLERIEMPKILE
]			RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIARAS
1			VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSOPKNSODVLKTFK
	}		VDGKVSVNGETVHREEEKERECPTVAPAHSLTKSOMFEGVARVH
			GSPLELKQDNGSIEINIKKPNSVPQELAATTEKTEPNSORDKND
			GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVEEPSSPOLKND
	1	J	VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTPPFLD
	l l	!	KMPEANQLHLPNLNSQVDSPSSEKSPVTTPFKFWAWDPEERRRR
	1	i	QEKWQQEQERLLQERYQ\KEQDK\LKEE\WEKAOKEVERERRY
[	]		YEEEP*II\EDPVVPFTVSSSSADQLSTSSSMTEGSGTMNKIDI.
İ	į	İ	GNCQDEKQDRRWKKSFQGDDSDLLLKTRESDRLEEKGSLTEGAL
1	ļ	ŀ	AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPOLAODPSONOOTSN
1	ļ		PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSSCGL
ŀ	ì		PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDVRIR
5832			NGLLNCNDCYMRSRSAGQPTTL
2032	2454	829	PGRRFRHGSCAFQKQCIMLHICQYFLQGECKFGTSCKRSHDFSN
			SENLEKLEKLGMSSDLVSRLPTIYRNAHDIKNKSSAPSRVPPLF

WO 01/53312

PCT/US00/34263

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine.
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Ì	residue of	residue of	S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	seducuce	Codon, /=possible nucleotide deletion,
		<del></del>	\=possible nucleotide insertion)
1	}	1	VPQGTSERKDSSGSVSPNTLSQEEGDQICLYHIRKSCSFQDKCH
İ	į		RVHFHLPYRWQFLDRGKWEDLDNMELIEEAYCNPKIERILCSES ASTPHSHCLNFNAMTYGATQARRLSTASSVTKPPHFILTTDWIW
		İ	YWSDEFGSWQEYGRQGTVHPVTTVSSSDVEKAYLAY/WYTGV*R
		ĺ	PGSHLEVPGRKAQLRVRFQSLRSEKPGLWHN*KGLPQTQIR\AP
			QDVTTMQTCNTKFPGPKSIPDYWDSSALPDPGFQKITLSSSSEE
1			YQKVWNLFNRTLPFYFVQKIERVQNLALWEVYOWOKGOMOKONG
1			GKAVDERQLFHGTSAIFVDAICQQNFDWRVCGVHGTSYGKGSYF
1			ARDAAYSHHYSKSDTQTHTMFLARVLVGEFVRGNASFVRDDAKE
1			GWSNAFYDSCVNSVSDPSIFVIFEKHQVYPEYVIQYTTSSKPSV
5833	170	2000	TPSILLALGSLFSSRQ
1 -000	1/0	3289	SILCLLSPCVVQFGKPVVSILSSRSRHSPCTKKGWEGMRKHLHT
			RQGHK*VHVEISKALWVYRDDYFIRHSISVSAVIVRAWITHKYR
1			GRDWNVKWEENLLHAVAKNYTLLQTIPPFERPFKDHQVCLEWNM
1			GYIWNLRANRIPQCPLENDVVALLGFPYASSGENTGIVKKFPRF RNRELEATRRQRMDYFVFTVSLWLYLLHYCKANLCGILYFVDSN
]	1	•	EMYGTPSVFLTEEGYLHIQMHLVKGEDLAVKTKFIIPLKEWFRL
			DISFNGGQIVVTTSIGQDLKSYHNQTISFREDFHYNDTAGYFII
1 1	ł i		GGSRYVAGIEGFFGPLKYYRLRSLHPAQIFNPLLEKQLAEQIKL
1 :			YYERCAEVQEIVSVYASAAKHGGERQEACHLHNSYLDLORRYGR
1			PSMCRAFPWEKELKDKHPSLFQALLEMDLLTVPRNONESVSETG
1			GKIFEKAVKRLSSIDGLHQISSIVPFLTDSSCCGYHKASYYLAV
			FYETGLNVPRDQLQGMLYSLVGGQGSERLSSMNLGYKHYQGIDN
1	ľ		YPLDWELSYAYYSNIATKTPLDQHTLQGDQAYVETIRLKDDEIL
			KVQTKEDGDVFMWLKHEATRGNAAAQQRLAQMLFWGQQGVAKNP EAAIEWYAKGALETEDPALIYDYAIVLFKGQGVKKNRRLALELM
1			KKAASKGLHQAVNGLGWYYHKFKKNYA\KAAKYWLKA\EE\MGN
1			PDASYNLGVLHLDGIFPGVPGRNQTLAGEYFHKAAQGGHNEGTL
1			WCSLYYITGNLETFPRDPEKAVVWAKHVAEKNGYLGHVIRKGLN
	İ		AYLEGSWHEALLYYVLAAETGIEVSQTNLAHICEERPDLARRYL
	1		GVNCVWRYYNFSVFQIDAPSFAYLKMGDLYYYGHONOSODLELS
1 1			VQMYAQAALDGDSQGFFNLALLIEEGTIIPHHILDFLEIDSTLH
] }		İ	SNNISILQELYERCWSHSNEESFSPCSLAWLYLHLRLLWGAILH
		ļ	SALIYFIGTFLLSILIAWTVQYFQSVSASDPPPRPSQASPDTAT
5834	17	4020	STASPAVTPAADASDQDQPTVTNNPEPRG RFRRGGGRVFPGAFPASPSDSLGQGNSQGPFRTPKPPRT/QECG
)			SAAPGPIPGQSSS*VPLRLEQIQQKADCPLSLELALKPRMAAQV
i I		'	TLEDALSNVDLLEELPLPDQQPCIEPPPSSLLYQPNFNTNFEDR
1 1			NAFVTGIARYIEQATVHSSMNEMLEEGQEYAVMLYTWRSCSRAT
1	i		POVKCNEOPNRVEIYEKTVEVLEPEVTKLMNFMYFORNAIERFC
1	1		GEVRRLCHAERRKDFVSEAYLITLGKFINMFAVLDELKNMKCSV
i I	İ		KNDHSAYKRAAQFLRKMADPQSIQESQNLSMFLANHNKITQSLQ
1		1	QQLEVISGYEELLADIVNLCVDYYENRMYLTFSEKHMLLKVMGF
1	1	Ì	GLYLMDGSVSNIYKLDAKKRINLSKIDKYFKQLQVVPLFGDMQI ELARYIKTSAHYEENKSRWTCTSSGSSPQYNICEQMIQIREDHM
	ļ	j	RFISELARYSNSEVVTGSGRQEAQKTDAEYRKLFDLALQGLQLL
			SQWSAHVMEVYSWKLVHPTDKYSNKDCPDSAEEYERATRYNYTS
			EEKFALVEVIAMIKGLQVLMGRMESVFNHAIRHTVYAALQDFSO
		ļ	VTLMEPLRQAIKKKKNVIQSVLQAIRKTVCDWETGHEPFNDPAT.
		1	RGEKDPKSG*DIKVPRRAVGPSSTQLYMVRTMLESLIADKSGSK
1		}	KTLRSSLEGPTILDIEKFHRESFFYTHLINFSETLOOCCDLSOL
		1	WFREFFLELTMGRRIQFPIEMSMPWILTDHILETKEASMMEYVI.
ĺ		i i	YSLDLYNDSAHYALTRENKQFLYDEIEAEVNLCFDOFVYKLADO
ļ	1		IFAYYKVMAGSLLLDKRLRSECKNQGATIHLPPSNRYETLLKQR
İ			HVQLLGRSIDLNRLITQRVSAAMYKSLELAIGRFESEDLTSIVE
-		1	LDGLLEINRMTHKLLSRYLTLDGFDAMFREANHNVSAPYGRITL
			HVFWELNYDFLPNYCYNGSTNRFVRTVLPFSQEFQRDKQPNAQP QYLHGSKALNLAYSSIYGSYRNFVGPPHFQVICRLLGYQGIAVV
	1		MEELLKVVKSLLQGTILQYVKTLMEVMPKICRLPRHEYGSPGIL
	1	1	EFFHHQLKDIVEYAELKTVCFQNLREVGNAILFCLLIEQSLSLE
		l i	EVCDLLHAAPFQNILPRVHVKEGERLDAKMKRLESKYAPLHLVP
			THE PROPERTY OF THE PROPERTY O

Deginning   nucleotide   location   corresponding   cofirst   amino acid   cofirst   amino acid   cofirst   amino acid   cofirst   amino acid   cofirst   amino acid   cofirst	SEC	Predicted	Predicted end	I Amiro
MO: nucleotide corresponding to first amino acid residue of residue of amino acid residue of residue of amino acid sequence				
Cocation   Cocresponding   Cofirst   amino acid   amino acid   cosidue of   residue of   amino acid   amino	NO:			Glutamic Reid Berbarder DeAspartic Acid, Es
corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence    Servine, T-Threenine, N-Apparagine, S-Servine, N-Apparagine, N	1			H-Highiding T Including G=Glycine,
to first amino acid serious of serious of securing the personner the securing amino acid amino acid amino acid amino acid asequence of securing the	1	corresponding		I-leveine, Management, Kalysine,
amino acid residue of amino acid sequence  Sequence  Sequence  Sequence  Sequence  Lightyptophan, Yefyrosine, Authonown, *stop Codon, /spossible nucleotide deletion, /possible nucleotide	ļ			Paroline O-Clutamine B hardele
maino acid anino acid	İ	amino acid		Sasserine Tathreonine Water
sequence    Codon, /=possible nucleotide deletion,		residue of		Werrentonhan Verturesing Viving
A-possible nuclectide insertion		amino acid		Codon. /=possible pucleotide deletion
LIEBLATFOGIALAREGOLLITEBLECGISSFEVLITRIRES DE DEURGGPERGRUNDECCUPIATE DE DEURGGPERGRUNDECCUPIATE DE MONGGERE DE LIENVPLKNOWIGHER DEN MONGGERE DE LIENVPLKNOWIGHER LIENVPLKNOWIGHER ITT LICKYLKSGOBET PVE HVRCFCOPPINGSLASS  5815 4209 1904 5ENTRAGGSRIC DE GVILLED LITTLAGUE SCHENNING DE LIENVPLKNOWIGHER STREVELLSGOBET SE HVRCFCOPPINGSLASS  SENTRAGGSRIC DE GVILLED LITTLAGUE SCHENNING DE LITTLAGUE SCHENNING DE LITTLAGUE SCHENNING SCHEN SE GVILLED CONTRAGUE SCHEN LITTLAGUE SCHEN LIT		sequence	-	\=possible nucleotide incertion)
DPINGSFLESHOMMINDECUEFHRLMSAMGPVCLPVSHIEDRY ECCROGICHMAGEMUIVLIGGOREPAL/DECYLLKYQKINDEKU ELINNYLKKYVERIRKFQILMOSIITTLINKYLKSGOGETPVE HURCGOPEINGLASS  \$5835 4209 1904 \$\$\$NIRRAGGSHQIDEQULHDLRQKFPEVPEVWSKCMLQKNINLD CACAVLAGESTRIYLYGGGDINFSTENDGOLGGGGSMSLEVQCGE TAPAQVQGGYNVEYSSSSGASHAPHGPHILGSKOTSSLSQOY PRENPIMUTLANNIQTGRIYLYGGDINFSTENDGOLGGGGSMSLEVQCGE TAPAQVQGGYNVEYSSSSGASHAPHGPHILGSKOTSSLSQOY PRENPIMUTLANNIQTGRIYLYGGGINSHAPQVUYOPSQOGPHYTT RANNILSHTSQOPYQGGYNVEYSSSGASHAPHGPHILGSKOTSSLSQOY PRENPIMUTLANNIQTGRIYLYGGGINSHAPQVUYOPSQOGPHYTT RANNILSHTSQOPYQGGYNVGGGGTSHVWPISSTTSGPFTHISSGS SQSSARSQYNIQNISTTOPKNOLETIKLBEPQXMSSKLRSSGOP TSSTSSSVNSQTLMRNOPTVYIAASPPHTDEMSRGQFXVIYS SYSTSSSVNSQTLMRNOPTVYIAASPPHTDEMSRGQFXVIYS GVVSYTPELINLINGHPPEVYSTENHIHDTPDTLANNINGHSSTRK LSMSDDAATQDI*RISHPEWYSTENHIHDTPDTLANDRISSTRK LSMSDDAATQDI*RISHPEWYSTENHIHDTPDTLANDRISSTRK LSMSDDAATQDI*RISHPEWYSTENHIHDTPDTLANDRISSTRK LSMSDDAATQDI*RISHPEWYSTENHIHDTPDTLANDRISSTRK LSMSDDAATQDI*RISHSMLGMWAATCSSSLGGGOQNTI*LY QUEFTSWONINKALUKREY*NYAGWAATCSSSLGGGOQNTI*LY RANDRIGGGEORGERIPPTDTRIBUTTSTANDRISSTRK LSMSDDAATQDI*RISHPEWYSTENHIHDTPDTLANDRISSTRK LSMSDDAATQDI*RISHPEWYSTENHIHDTPDTLANDRISSTRK LSMSDDAATQDI*RISHDEWYSTENHIHDTPDTEDDEGAQMNCTA ARDEVOLCESTANDRISGDASCHAPSTRUKKSCCISSVOYTGTSANOMGE PETINLIPPTONICTORYPPERSODRESDILYMRIGGBORSKQLLK SOURCECTSANOMACHARCAULTCPUPEDERGNOPHIMGSIFSGUK VENDOTYOSILISILSFFENDINGHIHDTSTANDRISGTANOMGE PETINLIPPTONICTORYPPERSODRESDILYMRIGGBORSKQLLK PETINLIPPTONICTORYPPETATARSONRQMKCCISSVOYTGTSANOMGE PETINLIPPTONICTORYPPETATARSONRQMKCCISSVOYTGTSANOMGE PETINLIPPTONICTORYPPETATARSONRQMKCCISSVOYTGTSANOMGE PETINLIPPTONICTORYPPETATARSONRQMKCCISSVOYTGTSANOMGE PETINLIPPTONICTORYPPETATARSONRQMKCCISSVOYTGTSANOMGE PETINLIPPTONICTORYPPTATARSONRQMKCCISSVOYTGTSANOMGE PETINLIPPTONICTORYPPTATARSONRQMKCCISSVOYTGTSANOMGE PETINLIPPTONICTORYPPTATARSONRQMKCCISSVOYTGTSANOMGE PETINLIPPTONICTORYPPTATARSONRQMKCCISSVOYTGTSANOMGE PETINLIPPTONICTORYPPTATARSONRQMKCCISSVOYTGTSANOMGE PETINLIPPTONICTORYPPTATARSONRATARSONCHISTORYPTSINCHING PETINLIPPTONICTORYPPTATARSONRA				LIERLGTPOOTATAREGULTKERLCCGLEMPRATIERTE
ECCROGLINAGCMITULISQURREPAYLDFCHILLKVQKHIDDG EIINVPLKMVBERREPGILDDGITTILDRVIKSGGGETPVE HWRCFQPPINGSLASS  5815 4209 1904 5SNIRMAGSSRID LITTLICKYLKSGGGETPVE HWRCFQPPINGSLASS SINRAGSGRID LITTLICKYLKSGGGETPVE HWRCFQPPINGSLASS SINRAGSGRID LITTLICKYLKSGCASSLETQQDEQ SENTYHHGREGSRAMGSETTHIS SIGGLGGGGSSSLETQQDEQ FRENPI LITTLICKYLKSGGASSGASNASHLIGHLISSGTSLESQOP PERNPI LITTLICKYLTGATETPIST SIGGLGGGGGSSSLETQQDEQ FRENPI LITTLICKYLKSGGASSGASNASHLIGHLISSGASSLETQCDEQ FRENPI LITTLICKYLKSGASSGASNASHLIGHLISSGASSGASNASHLIGHTUS PANNELSHTSSQOPYQGGGTSTHAWPOLVYGSGASSLETQCDEQ FRENPI LITTLICKYLTSGASSGASSGASNASHLIGHTUS PANNELSHTSSQOP TSSTSSSUNSQTHINGTOTT ENTENSCHASPPOTTOMERSCHESSGAP TSSTSSSUNSQTHINGTOTT ENTENSCHASPPOTTOMERSCHESSGAP TSSTSSSUNSQTHINGPTY LITTLICKYLTSTEDGEYVISA NAATODEQVERQOPLE I STINSGASASRAMSQQVSGGAPTI VA QUEPTSHINLLNINDPHYVETEN HHLTDPLAHUDRISSTEN GWSPTFELINLLNINDPHYVETEN HHLTDPLAHUDRISSTEN GWSPTFELINLLNINDPHYVETEN HHLTDPLAHUDRISSTEN KARMELQRELIGHT KERNSCHEMENHITERIKERSSIS IS QUESTSHGNINZLLIKERF*HYAGWAHTCSBYSUD**ALLIVER KARMERLQRELIGHT KERNSCHEMENHITERIKERSSIS IS QUESTSHGNINZLLIKERF*HYAGWAHTCSBYSUD**ALLIVER KARMERLQRELIGHTSKKLICKKLICKKLEWREMENHITERIKERSSIS IS QUESTSHGNINZLLIKERF*HYAGWAHTCSBYSUD**ALLIVER KARMERLQRELIGHTSKKLICKKLICKKLICKERFENENHITERIKERSSIS IS QUESTSHGNINZLLIKERFYHYAGRAGHAGHAGHAGHAGHAGHAGHAGHAGHAGHAGHAGHAGHA	1	ŀ		DPIWRGPI.PSNGVMHVDFCVFFHPI.WCAMOPIVOI DVOTENTENT
5835 4209 1904 SENIRHAGGSHQIDFQULHDLRQKFPEVPEWVSKCMLQNININ DACCAULSQUSTRIVLOSDUDINESDOSIGSLENDED TAPAQVQGOTVENTSUSSGASSASHATIHISISDGQLQGQSMSSLFQQDE TAPAQVQGOTVENSSSASANSARICHISISDGQLQGQSMSSLFQQDE TAPAQVQGOTVENSSSASANSARHICHISISDGQLQGQSMSSLFQQDE TAPAQVQGOTVENSSSASANSARHICHISISDGQLQGQSMSSLFQQDE TAPAQVQGOTVENSSSASANSARHICHISISDGQLQGQSMSSLFQQDQ PRIFFE INVITARNIQTORIF PISHHHOVPPVUMSPQONSTIT REVITTEDGTTRETQCONSGWASQFININDQVUVQDSQOPPUTT PASMPLISHTSQQDYQQGGQTSHVWP ISSTTSQFPTIHSSS SQSSASANGYNIQNISTTE ISTPRKNOLE ISLBPPQNINSSKLRSSGPR TSSTSSSVMSQTLRRNQPTV VIAASPPHTDSLMSRQDFXVTS ANATODEQVRRQDPTL ISTMSRGASASRMSQQDQXMGPAFIHH HEPERSAL GBMSATSPRVVVTQPNT EVTFKTVSPMSPPASYS GVVSPTFELINLINIHAPPEWVSTER HHLTDPTLANDRISSTRK LSMSDDAATQD1*RINSPPLVVIENHHUNDRISSTRK LSMSDDAATQD1*RINSPPLVVIENHHUNDRISSTRK LSMSDDAATQD1*RINSPPLVTERHHUNDRISSTRK LSMSDDAATQD1*RINSPPLVTERHHUNDRISSTRK LSMSDDAATQD1*RINSPPLVTERHHUNDRISSTRK LSMSDDAATQD1*RINSPPLVTERHHUNDRISSTRK LSMSDDAATQD1*RINSPPLVTERHHUNDRISSTRK LSMSDDAATQD1*RINSPPLWAATCESSYSVQFMSTTVX QBENTYDNIGVGFVPPRCKNORGSIIKTPKTQDTEDDGGAQMCCTA ANDERFONLINGUENGCCOMPRIB FFINALITY GREECOMP	j	ľ		EOCFGDGLHWAGCMITVLLGOOPRFAVI.DECVULL VUOVUDGVD
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RPYITTPGGTTROTQHSGWVSQFNPMNPQQVVQPSQPGPWTTC PARNPLSHTSSQPNQGGGTGSHVWPLTSTQPTHISSGS SQSSAHSQYNIQNISTGPRKNQIEIKLEPQRNNSKRESGPRV ISSTSSVNSTQTHRNQPTVLARSPPNTDLMSRSQCKVVISA NAATGDEQWMRNQPTLFISTMSGGASERMSQOVSMGDAFIHH HPPKSRAIGNSATSPRVVTQDFY-EVETVYSPNKUPAVISA GVVSPTFELTHLIMIDEKVVTERN HHLTDPTLARVDRISETRK LSMSGDBAAYQOI-*RISMSWLGMVAHACMSSALGGQDKII-*A QEPETSWGNIWRIRLINTRY-NYAGWAHTCSPTSVDP-ALLUVEQ KAMMERLQREGERIQKKLDKKLDKLKSSVNEMENNLTRREKENSIS QEPETSWGNIWRIRLINTRY-NYAGWAHTCSPTSVDP-ALLUVEQ KAMMERLQREGERIQKKLDKKLDKLKSSVNEMENNLTRREKENSIS QEPETSWGNIWRIRLINTRY-NYAGWAHTCSPTSVDP-ALLUVEQ KAMMERLQREGERIQKKLDKKLDKLKSSVNEMENNLTRREKENSIS QEPETSWGNIWRIRLINTPY-NYAGWAHTCSPTSVDP-ALLUVEQ KAMMERLQREGERIQKKLDKKLDKLKSSVNEMENNLTRREKENSIS QEPETSWGNIWRIRLINTPY-NYAGWAHTCSPTSVDP-ALLUVEQ KAMMERLQREGERIQKKLDKKLDLSKKLDKGRONSKGLLK COPENSAMONITAL CSQCCMMPRIP  SANTYCLFSSANDERSPORT HNYSDNIGFVGPVPPPFCPGGRSIITTPKTDDTEDDEGQWNCTA CTTEINHPALIR CSQCCMMPRIP  FHITMGGICCSVNFSAEHFSQDLKKDLINIKGKRONSKGLLKS HIMPGGDFGRSLLMHFSGDLKKSTLLSVTOTGSGLANGVOR VPAS\DFSELITSLLSFPDALFYNCILONIFLERILLKKULLA- VKROGTYOHLVOR OMKRONICLKNULEPI-1*CCTARKRULLAP VKROGTYOHLVOR OMKRONICLKNULEPI-1*CCTARKRULLAP FPCCHLORRYRSPLIMYT*KEVIQQFIDULSVAVKRVULCIPR DENLTANEVLKTCDRKANVALIFSGGIDSWVARTANCHOPR PLOLIMVAFTAEEKTMYTTRAGGKKCKNCKGLIPSEFFSCDVAA AANDS PNKHVSVPDRITGRAGUKELQAVSPSRINNFVEINVSHE ELQKLRRTRITCHINFLDTULDDSIGCAVFRSIGIGHVVAQGG VKSYGSNAKVVLTGIGADEGLAGVSRRRVKFOSHGLEGLNKEIM MELGRISSRNCHCHDNINGLEGERSGIGHVNVSLIKLDFL KRENGGIDSPKTHVSSDAFGANGTERIGHVVSSLIKLDFL GERGARALTSSASSANDATHTRESGKGCKNAKTLLDFL GERGARALTSSASSANDATHTRESGKGCKNATULLDFL GERGARALTSSASSANDATHTRESGCGCREVWSLIKLDFL GERGARALTSSASSANDATHTRESGCGCREVWGLIKLDFFL GERGAREFFSCAGGRIVHCHMINSGSGEROFILKLURDFLIKY LLPHYTEISMKADCKINALGNENDHSRPPGGKSTARWSPL GERGAREFFSCAGGRIVHCHMINSGSGEROFILKLURDFLIKY LLPHYTEISMKADCKINALGNENDHSRPPGGKSTARWSPL GERGAREFFSCAGGRIVHTRUSSROPPUNCUSPTCHLIKNC DPCLYSG\ASSANDATHNOTTHRENGGSFCAGALVATREGGVERG GERGAREFELDGGGRIVAGALERGUNDANDAA GYHWILAVAGSACHLURKGLKSTLLPKSSLPPCOVUSSCHALLCHANSPL DPCLYSG\ASSANDATHNOTTHRENGGSFCAGGLIUVCLERGHVADAR G		1	1	PRENDIMVTLAPNIQTGRNTPTSLHIHGVPPPVLNSPOGNSIVI
PASNPLSHTSSQOPNQGHQTSHVYMPISSTTINGPTHISSSG SQSAHSQUTIQNISTINGPTWICHSTERRYPTISSTRISSPRINGHINLERPPGRNISSKIRSSGOPR SQSAHSQUTIQNISTINGGTTWICHSTERRYPTISHERSSERGER TSSTSSSVNSQTLINRQFTWILABPPHTDELMSRSQOPKWISA NAATGEQUMANQTUFISTINGGAAASROQVMGDAPIH HPPKSRAIGNNSATSSRVVVVTQNRTLEYTFKITVSBNIPAVSS GVVSPTSLINLLINHDPLVYSTENHHLIDDILAHDDILSFTIRK LSMSSDDAAYTQOI-PLENBULGWUHACNSSALGGQDGRII-A QEETSTWONINGRELRYPTSFYNGGWAITGPTUADTLAHDRISSTTRK LSMSSDDAAYTQOI-PLENBULGWUHACNSSALGGQDGRII-A QEETSTWONINGREDHIOLIDICLITEIDLFQARGPHRSPASI OISSLEBMQOLRSCONGOIDIDCLITEIDLFQARGPHRSPASI OISSLEBMQOLRSCONGOIDIDCLITEIDLFQARGPHRSPASI OISSLEBMQOLRSCONGOIDIDCLITEIDLFQARGPHRSPASI ANYFONIGFFGPPVP PKPKQGRSIIKTPTOUTBEDEGAQWACCA CTELNHPALLRCQCEMPRHY  FRINKGICCSVMFSAEHFSQDLKEBLLYNLKGRGPNSSKQLLK SDUNYQCLFSAHVLHAGVLTTOPVEDERGNVELMNCEIFSGIK VARCHTCLHYNLSSCKWESSEILSLESPAGAAGMGE VARASDTERGERSLILMHFSNLGKSFCLSSVOTOTSGLANGMGE VARASDTERGERSTLINHFSNLGKSFCLSSVOTOTSGLANGMGE VARASDTERGERSTLISHISFSDLKFSGLINKLLKKHLIAV VXRQQTYQHLYQR-QMKRNCILKNLLFL-1*CCHLLHKRLIAVI FFNCHLGERFKFSFLLMT KEVIQQFI UZHAVKKRVUCLPR DENLTANEVLKTCDKKANVALLFSGIDSWIATLADRHPDLDE PIOLINVAF TAEGEKTMUTTRRGGKKGKAVAVKKRVUCLPR DENLTANEVLKTCDKKANVALLFSGIDSWIATLADRHPDLDE PIOLINVAF TAEGEKTMUTTRRGGKKGKAVAVKKRVUCLPR DENLTANEVLKTCDKKANVALLFSGIDSWIATLADRHPDLDE PIOLINVAF TAEGEKTMUTTRRGGKKGKAVAVKKRVUCLPR DENLTANEVLKTCDKKANVALLFSGIDSWIATLADRHPDLDE PIOLINVAF TAEGEKTMUTTRRGGKKGKAVAKKRVUCLPR WASYGSNAKVULTGIGABCQLAOVSCHHVVRPGGIGEGINKRIM MELGRISSRAIGRDRVICHDDSGCGAVERSKIGWIKLMAL KMEKINERASDKCGRUINGLANGKARPFPIDENVSSITINLEPERSCLAMPI VKRYGGIGEKULLHADAVELQAVSSCFGGGWILKLEPT KARGGGIDFTVERLHWILHHSSNOPTQLVSSCFGGGLAQMIT QSWRKYLTERSSSEQQHISTRIVVENCHICTDDKQLLLSTSMD ROKKWILABLSKASSKGWILKHLAGNEDSSTEIRQUTGDKKGLARPT DDGKVGLYDTYSNKPGISSTTHKKTVYTILARGPVPPRSLGGG GDRSHALTSCGGGFLVYCLHENGTHKACCH PKAAPSSPSDPLGSPYRTPOGGTAQDYPWAASEPHILH-MEGL VCCPPILOYSTGACON PKAARGANACHTMIDTISKY LLPHTHISMKADKINAGLKINALGNEDSSPPQOKKSTELEKKALOG PKAAPSKKEVETLIKKKARSLLELSTSLDHRISEGHQDCL VCCPPILOYSTGACON PKAARGRUINGCSFFCILLKNC PKAAPSKKEVETLAVKGCGGRUVCCLEBLISHLAG GHYMULAWARAFA		ŀ	]	RPYITTPGGTTRQTQQHSGWVSQFNPMNPOOVYOPSOPGPWTTC
SQSSAHSQYNIGHISTOPRKNOLEIKLEPPQRINDSKURSSGPR TSSTSSVNSOTIANNIPPTVI YAASPPINTDELMSKSQPKVI SA NAATGDEQWMRNQPTLJ ISTNISGASAASRMSQQVSMGDAPIHH HPPKSRAIGNNSATSPRVVTQPRY-KYTTYPSKYPPANSP GVVSPTFELTNILMHPDHVVETEN HHLLTDPILAHVDRISSTRK LSMSSDDAAYQOL*RISSMSLGWAHGKSSALGGQDGRII*A QEFFTSWGNINRLELVRR?*WYAGWAHTCSPRYSVD*ALLVUQ KAMMELQRELBIOKKCLOKKLSEVNBMENNITREKKRNSIS; QIPSLEEMQQLRSCHRQLQIDICLITETDLFQARGHFNPSAI HNYTDNIGFVGPPPFRCHQRSIIKTPKTQDTEDDEGQANCTA CTEINHPALIRCEQCEMPHHF  S836  361  2303  FHITMGGICCSVNFSAEHSGOLKEDLVYNLKGRGPNSEKOLK VZAEENDTQILFRYLSSCKNESETISJFSVOJPWSIFTYQASS HYLWFGGTPGHLWGVLTTQPVEDERGNYFLMNGEIFSGIK VZAEENDTQILFRYLSSCKNESETISJFSVOJPWSIFTYQASS HYLWFGGTPGHLWGVLTGVPTLEBRGNYFLMNGEIFSGIK VZAEENDTQILFRYLSSCKNESETISJFSEVGPWSFITYQASS HYLWFGGTPGHLWGVLTGVRTWSTUTGVTLGNIFTGRILLKKULIAVI FPMCHLQRRYFKSFLMYT*KEVIQQPIDVLSVAVKKRULCLPR DENLTANSVLKTCORRANVAILPSGGIDSMVIATLADRHIPLDE PIDLLMVAFIAEEKTMPTTFREGNIKKCEIFSEFSKDVAA AAADSNNCHVSVDRITGSRACLKELQAVSSSRIKNVEINVSHE ECQKLRRTRICHLIRFLDTVLDDSIGCAVWASRGIGMVXAGE VKSYQSNAKVVLTGIGADEQLAGVSHRWRCEIFSEFSKDVAA AAADSNNCHVSVDRITGSRACLKELQAVSSSRIKNFETINVSHE ECQKLRRTRICHLIRFLDTVLDDSIGCAVWASRGIGMVXAGE VKSYQSNAKVVLTGIGADEQLAGVSHRWRCEIFSEFSKDVAA AAADSNNCHVSVDRITGSRACLKELQAVSSRIKKEIIVAGE VKSYGSNAKVVLTGIGADEQLAGVSHRWRCEIFSEFSKDVAA AAADSNNCHVSVDRITGSRACLKELQAVSSRIKKEILADRHIPLDE PIDLAMVAFIAERSTRICHDINGLENLISTKSTEVETINVSHE EKANLTLPGIGBKLLLKLAAVSIGJITASALLPRRAMOGGSRIA MEKKINERASDKCGRLGUMSLENLISTKSTALLDRHFREGELGELUNGIH MEKKINERASDKCGRLGUMSLENLISTKSTALLDRHFREGELGELUNGIH GERNSLALTSGSGGIVGHGEILVYNLCPLQTEDKGULLGUNDIT GONRKYTLSIKANDVOKNFRQGVKSKYTALCWHPTESGGLAFGT DDGKVGUTATLEGSTETPSLGGFAYSLLAFSSVOIGSLALGGGG GDRSSLALYSCGGGBGRIVGHNFRIKSGGGVEGGGELQAWSPL DDGKUTSGGAADSVARFBYOLVSTALCWHPTESGGLAFGT DDGKVGLUTTSSKADGGENGSTTTHKKTVTTLAWGFPPPBISLGGE GDRSSLALYSCGGGBGUTCHLKKRCASPL DPCTYSGGAADSVARRYBYCTPVSSGFEKKNGGPVENGSVD DCCTYGGGGGGGAADAVARRYGCHSTALCHTRINDTISKY LLPVHTRISKADGENGAADSVARRYPQCSCSFFTCHILKNC TPKARPSBODPLGDLAPAVSRPPJCTPVSSGFEKKVTINNKY TLLKERP PEGROPALAFAREGETPGDQCVKAASHLUSHKVVSSTSLIDPGVSDL GEEGAAREPELGCGLAPAVSRPPJC		i	1	PASNPLSHTSSQQPNQQGHQTSHVYMPISSPTTSOPPTIHSSGS
TSSTSSVNSGTINENOPTVYIAASPPNTDELMSRSQDKMQAPIH HPPKSRAIGNNSATSPRVVTOPNT\EYTEKITVSPMKPPAVSP GVVSTPTELINILMINENPHVVETENIHTDTLANUPRISTRK LSMGSDDAAYTODI*RISMSKLGWAHACNSALGGQDGRII*A QEPTSWGMIKRLRLYRRF*NYAGMVAHICSBYSVD*ALLVHQ KARMERLQRELBIQKKCLDKKJSVNYAGMVAHICSBYSVD*ALLVHQ KARMERLQRELBIQKKCLDKKJSVNYAGMVAHICSBYSVD*ALLVHQ KARMERLQRELBIQKKCLDKKJSVNYAGMVAHICSBYSVD*ALLVHQ KARMERLQRELBIQKKCLDKKJSVNYAGMSHITKPNIKRSNISS QIBSIBEMQQLRSCNRGROLGIDIDCLITEIDLEGARGHYNPSAI HNYYDNIGTVVPPPPRKPQRSIIKTPDTEDDEGAQNOCTA CTFLNNPALLIRCEGCEMPRHF FHITMGGIGSVNYSAEHPSQDLKEDLLYNLKQRGPRSSKQLLK SDVNYQCLFSAHVHHURGVLTTOPVEDEGRONYPHMGEIFSGIK VAREENDFOLLFSYLSKCNRSEILLSFEVQGPWSTYVQASS HYLMFGRDFFGRRSLLMHFSNLGKSFCLSSVJTQTSGLANQWQE VPAS\DFSELILSLSFPDALFYNCLIGNIFLGRILLKKHLLAV VARPOTYQHLYQR*QMKNCCLKNLEF!I*CCKHLHWRLIAVI FPMCHLGREYFKSFLLMT*KEVIQQFIDVSVAVKKRVLCLPR BENLTANBEVLETCDRKANVALTSGRSGCHSSFLINDVATALLARHIPLDE FIDLLNVAFIAEKTMPTTFRRSCNKQKKKCEIPSBEFSKDVAA AAADSPNKVLECTDRKANVALTGIGABYSLINTVETUNSME ELQKLRRTRICHLIRFLDTVLDDBIGCAVWFASRGIGNUTAOBG VKSYGSNAKVVLTGIGABOOLAGVSHRVAFOGSIGNIVAOBG VKSYGSNAKVVLTGIGABOOLAGVSHRVAFOGSIGNIELVADE ELQKLRRTRICHLIRFLDTVLDDBIGCAVWFASRGIGNILVAOBG VKSYGSNAKVVLTGIGABOOLAGVSHRVAFOGSIGNILKLEPT MELGRISSRNLGRDORVIGDHIGKBAPPPLDENVVSFLNSLPIW EKANLILPGGIGSKLLLRLAAVELGITASALLFRRAMOFGSRIA KMEKINEKASDKCGRLQIMSLENLSIKEGTKRUTILKDFL GWRKXTLESSASSGQNHGRIVYNLCPLQTCDDKQLLLSTSMD ROVKKWITASSGGORDJTANSFGVUNSCEGGELLQWDLT QSWRKXTLESSASSGGNHGRIVYNLCPLQTCDCKGLLLQWDLT GORNKKTTLESSASSGGNHGRIVYNLCPLQTCDCKGLLLQWDLT GROSGLAFTSCHALLWSADGSTHAKKYTALGCYDG MRVWNTISSKNNDVNRFNGGVKSKVTALCWPTTEGGLAFGT DDGKVGLYDTYSNKP DGISSTYHKKYTLAGFSVDIGSLAIGVDG MRVWNTISSKNNDDVNRFNGGVKSKVTALCWPTTEGGLAFGT DDGKVGLYDTYSNCPDGSTYHKKYTLAGFSVDGSTHKKTLTCTIQH HKLVNTISWHE\HGGPAQALSYLWFGGSGGCSFFTCHNLKNC P*KAAPBSPSDPLIGBFPTFPCGHTAQDYPVWAWEHHH*WEGIL VCCFPILGSFGCMDAFFROKEPANITALGCTTQGN HKLVNTISWHENADGSTHALLGNEGGSTHAKCLLGHOG UNLAWAGAGABOLACHARGSLUCHGUNGSTPPONKLICHTLICH PFRAPKKKKKFPLETPVKLKULSSTDIMERSELBHQDCL ULATAKHSPERSPEDICFGGDAPAVSRFYUCTFVSSGFKKVTINNKY ILLKKEPP KEKKPFLITTFVKLESSTGMARGGPVENNYGSDD GGEGAR		İ	}	SQSSAHSQYNIQNISTGPRKNQIEIKLEPPORNNSSKLESSGDP
NAATGDEOWAND, TIE ISTNGSAASARSMASCOWS GOWAPPE HIH HPPEKSRI LONNASTS PREVVOTOPEN; SYTEKTUSPEN HEPPENSE GUVSPTFELTHLINHEDHVA PETEN HHILTDPILARUDRISETEK LSMSSDDAAYTOO!* FISSENLEWAUHTCERSYSVD* ALLVEQ GEPETSWONIERLELYREP*NYAGWAHTCERSYSVD* ALLVEQ KARMERLQRELBIOKKCLDRIKSEVMEMENLTRERKENSES; QIPSLEBWOCKESCHOOLOIDLCLTE ILLFOARG PHEMPSAI HNEYDNIGFVCPVPPFKROQRSIIKTPKTQDTEDDEGAGWNCTA CTTEINHPALIRECCGEMPHH  SAGI  5836  361  2303  FHITMGICCS VNPSAEHPSQDLKEDLLVNILWGEOPRISEKOLLK SVANGCICSPANUHLRIGUTUPOPUEDRONVPLUMGEIFSGIK VZAERDDTOLLFRYLSSCKNESEILSLFSEVOCHWSTIYVQASS HYLMFGRDFPGRRSILMHERSLIKHSPCLSSVOTTGSLANGWGE VARSUPSELLISLISFPDALFYNCLIGHIFLGSILLKKWLIA* VXFQOTYGHLYQR* OKKENESEILSLFSEVOCHWSTIYVQASS HYLMFGRDFPGRRSILMHERSLIKHSPCLSSVOTTGSLANGWGE VARSUPSELLISLISFPDALFYNCLIGHIFLGSILLKKWLIA* VXFQOTYGHLYQR* OKKENESEILSLFSEVOCHWSTIYVQASS HYLMFGRDFPGRRSILMHERSLIKKSPCLSSVOTTGSLANGWGE PROCHLIGERYERSFLUMT* KEVYQGT IDVLSVAVKKRUCLOR DENLITANSVLKTCDRKANVALIFSGGIDSMVIATLARHIPLDE PIDLINVALTAEKKTHTYTFKRECHKOKKKCEIPSREFSKOVA AAADSPNCHYJAEKKTHTYTFKRECHKOKKKCEIPSREFSKOVA AAADSPNCHYJAEKKTHTYTFKRECHKOKKKCEIPSREFSKOVA AAADSPNCHYJAEKSTOTTHYTHRECHKOKKKCEIPSREFSKOVA AAADSPNCHYJAEKSTOTTHYTHRECHKOKKKCEIPSREFSKOVA AAADSPNCHYJAEKSTOTTHYTHRECHKOKKKCEIPSREFSKOVA AAADSPNCHYJAEKSTOTTHYTHRECHKOKKKCEIPSREFSKOVA AAADSPNCHYJAEKSTOTTHYTHRECHKOKKKCEIPSREFSKOVA AAADSPNCHYJAEKSTOTTHYTHYTHORTOKKKCEIPSREFSKOVA AAADSPNCHYJAEKSTOTTHYTHYTHYTHYTHYTHYTHYTHYTHYTHYTHYTHYTHY	1			TSSTSSSVNSQTLNRNOPTVYIAASPPNTDELMSRSOPKVYTCA
GWYSPTELINLIANDERVETENIHLHIDDELHARDRISLAGGOGRIITA QETETSWGNIMRLELYREF-NYAGMYAHCUSESSYSUD-ALLUVO KARMELLQRELBIQKKIDEKJSEVNEMENNITERLEKRISIS QIPSLEBMQOLRSCNRQLQIDIDCLIKEIDLFQARGPHRNESAI HNFYDNIGFVGEVPFKENQRSIIKTPKTQDTEDDEGAQWNCTA CTELNHPALIREQCCEMPRHF HTMGGICCSWNFSAEHFSODLKEDLLYNLKQRGPNSSKOLK SDWYQCLFSAHVLHLGVLTTQPVDERGWVFLWNGETSGKOLK VAREENDTQILFNYLSSCKNESEILSLPSPUCGFWSFIYYQASS HYLMFGROFFSREVLHGVLTTQPVDERGWVFLWNGETSGKOLK VAREENDTQILFNYLSSCKNESEILSLPSPUCGFWSFIYYQASS HYLMFGROFFSFFGREVLHGVLTCHOFFLGRILKKCHLTA- VKFQCTYCHLVQR-QMKPNCILKNLLFL-*I*CCHKLHWRLIAVI FFMCHLGRYKKSFLHYF*KEVIGTURUSVAVKRVLCLPR DENLITANSVLETCRKANVAILFSGGIDSWVIATLADRHIPLDE PIOLLUVAFILBEEKTHYT*KEVIGTURUSVAVKRVLCLPR DENLITANSVLETCRKANVAILFSGGIDSWVIATLADRHIPLDE PIOLLUVAFILBEEKTHYT*FKEVIGKNKCETPSEFSKDVAA AAADSPNHVSVPDRTTGRAGLKELQAVSDSRTWNFVETNVSME ELQKLRRFRICHLIFERDTYTLDGSGKOKKCETPSEFSKDVAA AAADSPNHVSVPDRTTGRAGLKELQAVSDSRTWNFVETNVSME ELGKLRRFRICHLIFERDTYTLDGSGKOKKCETPSEFSKDVAA AAADSPNHVSVPDRTTGRAGLKELQAVSDSRTWNFVETNVSME ELGKLRRFRICHLIFERDTYTLDGSGKOKKCETPSEFSKDVAA AAADSPNHVSVPDRTTGRAGLKELQAVSDSRTWNFVETNVSME ELGKLRRFRICHLIFERDTYTLDGSGLAVFASRGIGWUNGEG VKSYGSNAKVVLTGIGADEQLAGYSRHKVRFQSHGLEGINKEIM MELGRISSRNLGRDDRVTGDHGKERFFFLGEWVSFINSLPIW MELGRISSRNLGRDDRVTGDHGKERFFFLGEGELLQWDLT KANGAQADPVINCYLATASKNOTTHSSCSGRGGWMILKLDFL KRRGGIDPTVKRRLHLTLHWPSNQPTQUVSSCFGGELLQWDLT GNERKAYLTSASSEGGORISGRIVFNSCSGRGGWMILKLDFL KRRGGGIDPTVKRRLHLTLHWPSNQPTQUVSSCFGGELLQWDLT GNERKAYLTSASSEGGORISGRIVFNSCFGGELLQWDLT GNERKAYLTSASSEGGPTSTTONLIRGTNSIKY KLPVHTSISWALGSKIMALGREDGSTIFG\TPNLIKDTNSIKY KLPVHTSISWALGSKIMALGREDGSTIFG\TPNLIKNC PKAAPBSBDDPLQBFYRTPDGGTAPVVARWEHTH-WEGL VPCPIIGGSPGGCDVTYNKNFPURSGERFRILGTTONLVANSPL DPDCIYGG\ADDSCYHKKLTSHWDHSRPPTGRKSTHLWRD EGEGQAREFELPGGLAPAVSREPVICTPYSSGFESKYTINNKY ILLKKEPPKKEPTLIKKRARSLLPSTSLDHRSKEELHQDCL VLATAKHSRELWEDVSADVEERFFILGLPTDRATVYNKIDTEGGG HALWWAVAVEAPAKQLKGULGGLGGCGFESKKTINNKY ILLKKERPPKKEPTLIKKGDLKGULGGGGGFESKFCLURADAAA GYHWILMAVEAPAKQLGGDGOTVYCLLEBILTSRHLE EKQLESKERSSSYHTWINGTGGFFFULKLERGGHTAVAWAKSIFSLADFAGLE	1	1		NAATGDEQVMRNQPTLFISTNSGASAASRNMSGOVSMGPAFIHH
LSMSSDDAAYTQDI*RISMSHLEWAHARCKSALGGDORDI*A  QEPTEISMGNIMBLINIRTRF*NYAGMYAHTCSPSYSUP*ALLWBO KARMERLQRELBIOKKKLDKLSGEVMEMENNLTRRRLKRSNSIS QIPSLEMGQURSCNRQLQIDIDCLTKEIDAGRGPHENPSAI HNFYDNIGFVGPVPPKRKDQRSIIKTPKTQDTBDBSAQMNCTA CTFLNHPALIRCGCEWPRHF  FHIMGCICSVNPSABHFSODLKEDLLYNLKQRGPNSSKOLLK SDWNYQCLFSAHVLHLRGVLTTOFVEDERGRWPLWMGETFSGIK VAREEDPTOILFNISGCKNESSILFSEVGGFWSFIYYQASS HYLWFGRDFFGRRSLLWHFSNLGKSFCLSSVGTQTGGLANDWGE VPAS\DFSELINSLSSFDDALFYNCILGNIFLGRILLKKMLIA* VRPQGTYGHLYGR*QWFMCILKNIF-FX*CCHKHHRALIAVI FPMCHLQRRYFKSFLLMYT*KEVIQQFIDUSAVKKRVLCL.PR DENLITANEVLKTCDRKANVAILFSGIDSWVIATLADRHIPLDE PIDLLNVAFIAEKTWFTTFINEGGKKKNKCEIPSEEFSKDVAA AAADSPNHAVSVPDRITGRAGLKELQAVSPSRIWMFVEINVSME ELQKLRRTRICHLIRELDTVLDDSIGCAVWFASRGIGMIVAQGG VKSYGSNAKVVLTGIGADEQLAGYSRHKVFFGDGLNEGINKEIM MELGRISSRNLGRDBVIGDHKKERFFLDENVVSFINSLPIW EKANLTIPRGIGEKLLLRLAAVELGITASALDEKRAMOFGSRIA KMEKINEKASDKCGRIGOLNSLENIS,EKEYKL  SOMRKAVAQAPVTNCCYLATGSKDQTTRIWSCSRGRGWMILKLPFI KRRGGGIDFYVKSRLWITLHWPSNQFTQLVSSGEGGELLQWDLT GSWRKXVITESASSEQGHNSRIVFNLCPLGTEDDRXQLLISTSMD RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGWGDD MIRVMNTISIKNNYDVKSMYGAVSKALCHPPEREGCLAPGT DDGKWGWJPTYSNKFPQOISSTTHKKTYTLAWGPFVPPMSLGGE GDRPSLAJYSCGGGIVLQCHNPWLLSCEFTANLARDRYPPLWSPL PKAAPSSPEDPLQSFYRTPPGGHTSALIFNLINGTNSIKY KLPVHTBISWKADGKIMALGNEDSIEFFILDRINGFPH-WEGGL GPRSLAJYSCGGGGIVLQCHNPWLLSCEFTSCLAFGT DDGKWGWJPTYSNKFPQOISSTTHKKTYTLAWGPFVPPMSLGGE GDRPSLAJYSCGGGIVLYCHNFWLLSCHPPHERECLAFGT DDGKWGWJPTYSNKFPQOISSTTHKKTYTLAWGPFVPPMSLGGE GDRPSLAJYSCGGGIVLYCHNFWLLSCHPPHERECLAFGT DDGKWGWJPTYSNKFPQOISSTTHKKTYTTLAWGPFVPPMSLGGE GDRPSLAJYSCGGGIVLYCHNFWLLSCHPPHERECLAFGT DDGKWGWJPTYSNKFPQOISSTTHKKTYTLAWGPFVPPMSLGGE GDRPSLAJYSCGGGIVLYCHNFWLLSCHPPHERECLAFGT DDGKWGWJPTYSNKFPQOISSTTHKKTYTLAWGPFVPPMSLGGE GDRPSLAJYSCGGGIVTCTLURINNINGV ILLKKEBPPERPDLQFRYNTRIPGGPOYVAMBPHH-WEGL VVCCPFIIGYSPGCWD APPGRBAPVATRG\GNGLLCVAWSPL DPCTYSG\ADDECLYGAPAVSREPVICTPYSSGFEKKYTINNKV ILLKKEBPPERPDLQFRYNKLDGRAPAVSREPVICTPYSSGFEKKYTINNKV ILLKKEBPPERPEDPLOGAPAVSREPVICTPYSSGFEKKYTINNKV HLENGHFEDFOHWENGEDFOHUNDARAPELALIKENDLAGARG HLENGHFEDFOHUND	[			HPPKSRAIGNNSATSPRVVVTQPNT\EYTFKITVSPNKPPAVSD
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#MYYDNIGFVGPVPPKPRQRSIIKTPKTQDTBDBGQQMCTA CTFINIPALIRCGCCMPRHF SDWTYQCIFSARVIHLRCVLTTQPVEDERGNVPLWIGEIFSGIK VZAEEMDTQLIFNYLSSCKNESEILSIFSEVQOPWSFYTYQASS HYLWFGRDPFGRRSLLWHFSNLGKSFCLSSVGYQTSGLANQWGE VPAS\PSS\DFSELILSILFDALFYNCLIGNIFLGRILLKKMILA* VKFQQTYQHLYQR*QMKRNCILKNILEL*I*CKHKHKILAVI FPMCHIQERYFKSFLLWIT*KEVTQQFIDUSVAVKKRVLCLPR DENLTANSVLKTCORKANVALIFSGGIDSWLTATLADHRIPLDE PIOLINVAPIAEEKTMPPTFNREGNKQKNKCEIPSEEFSKDVAA AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIWMFVSINVSME ELQKURRTRICHLIRPLDTVLIDDSIGCAWFASRGIGNIVAQEG VKSYGSNAKVULTGIGADECLAGYSHRVRFQSHGLBGLNKEIM MELGRISSRNLEGDDRVTIGHREAFFFLDENVVSFLNSLPIW EKANLTLPRGIGEKLLLRLAAVSLGITASALDFKRAMQFGSRIA KMEKINEKASDKCGRLQIMSLENLSIRKFKL  S837 4792 903 NONAVAQAPVTNCCYLATGSKDGTFINSGSSGRGWMLKLDFL KRRGGGIDPTVKERLIMLTHWPSNQSTOLYEDKQLLLSTSMD GWRRKYTLFSASSEGQNHSRIVFNLCYFDDKQLLLSTSMD RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGUGDD MTRVWNTISIKNYDVKNTWQGYKSKVTALCWHFTKSGCLAFGT DGKWGYLYTTYSNRPPQISSTTWATVTLAWGPVPPMSLGGE GDRPSLALYSCGGEGIVLCHNPWKLSGEAFDINKLIRDTNSIKY KLPVHTBISWKADGKIMALGNEGSIEIFO, IPALKLICTIQOH HKLNWTISWHEPURSPACKSTYLLWSGSQOCSFTCHNLKNC P*KAAPBSBSDPLQSPYRTPPQGHTAQDYFWMAMEPHIH*WEGL VCCPFIGGSBGCOMD\AFPGKEAPVAIFRG\URSCKISSQ PKAAFKKKKRFTLRTPVKLGSIDGHESSWENGSPVENGVSDQ BGRGQAREPSLPGCLAPAVSRFPLOYDESRPPQKKSIBLEKKGLSQ PKAAFKKKKKPTLRTPVKLGSIDGHESSWENGSPVENGVSDQ BGRGQAREPSLPGLAPAVSRFPLOYTEVSSGFEKSKYTINNKV ILLKKEPPKEKPFTLIKKKKARSLLPLSTSLDHRSKEELHQDCL VLATAKHSRELNEDVSADVEERFHLGJETTRATLYRNIDISGKG HLENGHEELPHQLMLWKGDLKGVLQTARERGEITDNIVAMAPAA GYHWUMAVBAFAKQLCFDQDYVKAASHLLSIHKVVEAVELLKS NHYKREAIATAKARLPSDDVUKQDLYKAASHLLSIHKVVEAVELLKS NHYKREAIATAKARLPSDDVUKQASHCLSHIKVEADHELLKS NHYKREAIATAKARLPSDDPUKKQDLKGVUKCLLELLSRILE EKQLSEKSSSSYHTMYTTSTBOPFERVTAWWSTSDTPFOOY				OTHER FENON RECEIPT OF THE PROPERTY OF THE PRO
S836  361  2303  SHITMCGICGSWPSAEHSGOLKEDLLVNLKQRGBNSKQLLK SDWNYQCLFSAHVLHLRGVLTTQPVEDERGNVFLWNGEIFSGIK VZAEENDTQILFNY_SCKNESEILSFEVQGPWSFYYYQASS HYLWFGRDFFGRRS.LWHESNLGKSFCLSVYGTYGGLANGWGE VPAS\DFSELILSLSFDALFYNCLLGNIFLGRILLKKMLIA* VXFQCTYGHLYQNF*OKMPRGILKNLLFL*!*CCHKLHWRLIAVI FPMCHLQERYFKSFLLMYT*KEVIQQFLDUSVAVKKRVLCLPR DENLTANBVLKTCDRKANVAILFSGSIDSMVIATLADRHIPLDE ELQKLRTRIECILLRFDTVLFNEGKKQKNKCEIPSEFSKDVAA AAADSPNKHVSVDPRITGRAGLKELQAVSPSRINNFVEINVSME ELQKLRTRIECILLRFDTVLDDSIGCAVWFASRGIGWLVAQBG VKSYQSNAKVVLTGIGADEQLAGYSRHEVRFQSHGLEGLNKEIM MELGRISSRNLGRDDRVIGDHGKEARPFFLDENVVSFINSLPIW EKANLTLPRGIGEKLLLKLAAVELGITASALDFRAWQFGSRIA KMEKINEKASDKCGRLQTMSLENLSIRKETKL  SRAWAQAQAVTNCCYLATGSKQDTITRIWSCSRGRGVMILKLPFL KRRCGGIDFTVKERLMUTLHWPSNQFYQLVSSCFGGELLQMDLT GSWRKKYTLFSASSEGQNHSRIVFNLCPLGTEDDKQLLLSTSMD RDVKCWDIATLECSWTLFSLGGFAYSLAFSSVDIGSLAIGVGDG MIRVWNTISIKNNYDVKNFWQGVKSKVTALCWHFTKEGCLAFGT DDGKVGLYDTYSNKPPQISSTYHKVTYLAWGFPYPMSLGGE GDRPSLALYSCGSGSIVLQHNPWKLSGEAPDINKLIRDTNSIKY KLPVHTEISWKADCKIHALGNEGGSIFFQ\HGRKLACCAWGPL HKLUWITISWHHE\KGSPAQKLSYL\MPSGSQCSFFTCHNIKNC P*KAAPBSPSDPLQSPRTPPQGHTAQDYPVWAWEPHIH*WEGL VFCFFIDGYSPGCWD\AFFOKEAPVALFGR\HQGRLCVAWSPL DPDCIYSG\ADDFCVHKALTSWQDHSRPPQGKKSIBLEKKRLSQ PKARFKKKKKFTLTPYKLESIDONEESMKENSGPVERGVSDQ EGESCARFPELLGCLAPAVSREPVICTPYSSGFSKKVTINKV ILLKKEPPKEKPETLIKKRKARSLLPLSTSLDHRSKEELHQDCL VLATAKHSRELNEDVSADVEERPHLGTPTATLYRMIDISGKG HLENGHPELFPQUTLWKGUKGVGQCYPTCALLTNNKV ILLKKEPPKEKPETLIKKRKARSLLPLSTSLDHRSKEELHQDCL VLATAKHSRELNEDVSADVEERPHLGLFTDRATLYRMIDISGKG HLENGHPELFPQUTLWKGUKGVGQCAPFCIENTUNAWAPAA GYHWUMAVSAFAKQLCFQDOYVKAASHLLSHKVYEAVELLKS NHFYREAIATAKARLPPDDFVLKULJSWGTVLERGGHYAVAAK CYLGATCAYDAAKVLAKKGDASLKTAAELAAIVGEDELISASLA LRCAGELLLANNWGAQEALQHEJSCOGGLUFCLLEBLISRHILE EKQLSEKSSSSYSTHTNTTTEGGFFFUERVIYAWKSTYSLDTPDOY				HNEYDNIGEWODURDKENDODGIIKMINGARGPHFNPSAI
S836  SPHITMCGICCSNMFSAEHFSQDLKEDLLYNLKQRGPNSSKQLLK SDWNYQCLFSAHVLHLRGVLTTQPVEDERGNVFLWNGSIFSGIK VZAEENDTQILFNYLSSCKNESEILSLFSEVGPWSFIFYQASS HYLWFGRDFGRRSLLWHFSNLGKSFCLSSVJTQTSGLANGMQE VPAS\DFSELILSLSFPBLYSTVCLGNIPLGRILLKKMLIA* VXFQQTYQHLYQR*QMKPNCILKNLFF*I*CCKHLHRRLTAVI FFMCHLGREYFKSFLLMYT*KEVIQGFIDVLSVAVKKRVLCLPR DENLITANEVLKTCDRKANVAIFTSGIDSWITATLADRHIPLDE PIDLLNVAFIAEEKTMPTFFNEGGKQKNKCEIPSEFFSKDVAA AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIWNFVEINNSHE ELQKLRRTRICHLIRFLDTVLDDBIGCAVWFASRGIGMUAQGE VKSYQSNAKVVLTGIGADEQLAGYSRHHVROGSGISLKMEIM MELGRISSRNLGEDDNVIGDREARPFFIDENVVSFINSLPIW EKANLTLPRGIGEKLLLRLAAVELGLTASALLPKRAMQFGSRIA KMEKINEKABDKCRGLOTMSLENDSIRKETKL NGRGGIDPTVKERIWLTLHWPSNOFTQLVSSCFGGELLQMDLT GSWRKYTLFSASSEGQMHSRIVPHLCPLQTEDDKQLLLSTSMD RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGDG MIRVWNTISIKNNTDVNFMGGVKSKVTALCWHFTKEGCLAFGT DDGKWGLDTTSNKPPGIGSFTKKTVTTLAWGPVPPMBLGGE GDRSLAIJSCCSGBIVLQHNPWKLSGEAFDINKLIRDTNSIKY KLPVHTBISWKADGKIMALGNMEDGSTFTCINLKNC P*KAAPBSPSDPLGSPYRTPPGGHTAQDYPWWAWEHHI*WEGL VFCPPIGGSPSGCMD\AFPGKSPVATFRG\HGGRLLCVAWSPL DPDCIYSG\ADDFCVHKWLTSMQDHSRPPQGKKSILLEKKRLSQ PKARFKKKKKPTLRTPVKLESIDGNEESMKENSGSPERGWSDQ EGESQAEPSLBLPGCLAPAVSREPVICTPVSSGFEKSKVTINNKV ILLKKEPPKKKPTLIKKRKARSLLPLSTLDHRSKEELHQDCL VLATAKKSPELTETPVKLESIDGNFAREESMKENSGFVERGVSDQ EGESQAREPSLPGCLAPAVSREPVICTPVSSGFEKSKVTINNKV ILLKKEPPKKRPTLIKKRKARSLLPLSTLDHRSKEELHQDCL VLATAKHSRELNEDVSADVERFPHIGFTPATLIVMIDIGSKG HLENGHPELFHQLMMKGDLKGVLQTAARERGELTDNLVAMAPAA GYHWLMAVSAFAKQLCFQDOYVKAASHLISTHKVYEAVELLKS NHFYREAIALKARLRFSDPVVKLVLISMGTVLERDGHYAVAAK CYLGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSASLA LECAGELLLANNWGAQEALQHJESGFGVRUFCLEBLISRHILE EKQLSEKSSSSYSTHTNTTTEGFFFVURCPFVURCHSLFSSALA	1			CTFINHPALTECEOCEMPBUR
SDWNYQCLFSAHULHLRGVLTTQPVEDERGNVFLWNGEIFSGIK VZAERDHDTJLIFNYLSSCKESEILSIFSEVQGFWSFIYYQASS HYLWFGDFFGRRSLLWHFSNLGKSFCLSSVGTQTSGLANQMQE VPAS\JFSELILSILSFPDALFYNCLIGNIFIGHILLKKMLIA* VKFQQTYGHLYQR*OMKPHCLKNLLEL*I*CKCHKLHRRLIAVI FPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRRANVAILFSGGDSMVIATLADRHIPLDE PIDLLMVAFIAEEKTMPTTFNRSGNKQKNKCETPSEFSKDVAA AAADSPNKHVSVPDRITGRRGLKELQAVSPSRIWNPVEINVSME ELQKLRRTRICHLIRPLDTVLDDSIGGAVWFASRGIGMUVAQEG VKSYGSNAKVVLTGIGADEQLAGYSHRVKFOSHGLEGLNKEIM MELGRISSRNLGRDDRVIGDHGKEARPPFLDENVVSFLNSLPIW EKNNITLPRGIGEKLLLRLAVELGILTASALLPKRAMQFGSRIA KMEKINEKASDKCGRLQINSLENLSIKEKTKL  NONAVAQAPVTNCCVLATGSKDTTFIWSGSRGGGWMILKLPPI KRRGGIDPTVKERLWLTLHWPSNQFTQLVSSCFGGELLQWDLT QSWRRKYTLFSASSEGQNHSRIVFNLCPLQTEDDKQLLLSTSMD RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGGB MIRVWNTISISINNTPVNKWRGVKSKVTALCHPTKEGCLAPGT DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGPPVPPMSLGGE GDRPSLALYSCGGGIVLQHNFWKLSGEAFDINKLIRDTNSIKY KLPUHTEISWKADGKIMALGNEDGSIEIPQ\TPNLKLICTIQQH HKLVWTISWHHE\HOSPAQKLSYL\MPSGSQCSPFTCHNLKNC P*KAAPBSPSDPLQSPYRTPPQGHTAQDYPVWAWEPHH*WEGL VFCFPIDGYSSGCND\APPGKBAPVAIFRG\MGGELLCTAWSPL DPDCTYSG\ADDFCVHKWLTSMODHSRPPQGKKSIELEKKZLSQ PKAKPKKKKPLRTPVKLESIDGNEESMKENSGPVENGVSDQ EGEEQARPELPCGLAPAVSRPPVLCTPVSSGFEKSKVTINNKV ILLKKEPPKEKPFTLIKGRKARSLLPLSTSLDHRSKEELHODCL VLATAKHSRELREDVSADVASRPPVLCTPVSSGFEKSKVTINNKV ILLKKEPPKEKPFTLIKKRKARSLLPLSTSLDHRSKEELHODCL VLATAKHSRELREDVSADVASRPPVLCTPVSSGFEKSKVTINNKV ILLKKEPPKEKPFTLIKGRKARSLLPLSTSLDHRSKEELHODCL VLATAKHSRELREDVSADVASRPPVLCTPVSSGFEKSKVTINNKV ILLKKEPPKEKPFTLIKGRKARSLLPLSTSLDHRSKEELHODCL VLATAKHSRELREDVSADVASRPPVLCTPVSSGFEKSKVTINNKV ILLKKEPPKEKPFTLIKGRKARSLLPLSTSLDHRSKEELHODCL VLATAKHSRELREDVSADVASRPVLCTPVSSGFEKSKVTINNKV ILLKKEPPKEKPFTLIKGRKARSLLPLSTSLDHRSKEELHODCL VLATAKHSRELREDVSADVASRPVLCTPVSSGFEKSKVTINNKV ILLKKEPPKERPFTLAKRARLREDBFUKDLYSLEGGELTDNIVMAMPAAA GYHWLMAVEAFFAKQLCFODQYVKAASHLLSIHKVYRAVELLKS MFFFREAITALARALREPEDFUKDLYLSLEGGRUFVERDGHYAVAAK CYLGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSSALA LRCAQELLLANNWUGAQBALLLEBLGORLVFCLEBLLSSHLE EKQLSEKSSSSSSTHTMNTGTFGFFFFFFFFFFFF	5836	361	2303	FHITMCGICCSUNFEARUPCODI VEDI I VOI VORGRUSCULT
VÄÄEENDTQILFNYLSSCKWESEILSIFSEVOGPWSFITYYQASS HYLWFGRDFGRSLLWFFDRAKFSCLSSVOTOTSGLANQWQE VPAS\DFSELILSLISFPDALFYNCLIGNIFLGRILKKKHIAY VKPQOTYQHLYQR*QMKPNCILKNLLFL*I*CKHKLHKKHIAYI FPMCHLQERKFKSFLLMYLKVORPIOULSVAVKKKVLCLPR DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADRHIPLDE PIDLLNVAFIAEEKTMPTTFNREGNIKUNKCEIPSEEFSKDVAA AAADSPNKHVSVPDRITGRAGLELQAVSPSRIWNFVEINVSME ELQKLRRTRICHLIRPLDTVLDDSIGCAVWFASRGIGWLVAQEG VKSYOSNAKVUTGIGADEQLAGYSRHRVRFQSHGLEGLNKEIM MELGRISSRNLGRDDRVIGDHGKEARFPFLDENVVSFLNSLPIW EKANLTLPRGIGEKLLLRLAAVELGITASALLPKRAMGFGSRIA KMEKLNEKASDKCGRLQINSENLSIKKETKL  5837 4792 903 NONAVAQAPVINCCYLATGSKDOTIRIWSCSRGRGVMILKLPFL KRRGGIDFTVKERLWLTLHWPSNGPTQLVSSCFGGELLQWDLIT GSWRKXYLTFSASSEQONISRIVFNLCPLJGTEDDKGLLISTSMD RDVKKWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGDG MIRVNNTLSIKNNYDVKNFWQDVKKKVTALCWHPTKEGCLAFGT DDGKVGLVDTYSNKFPQLISSTTHKKTVYTLAWGPPVPPWSLGGE GDRPSLALYSCGGEGIVLQHNPWKLSGEAFDINKLIRDINSIKY KLPPVHTEISWKADGKIMALGNEGSIEIPO, IPNLKLICTIQQH HKLVNTISWHHE\HGSPAQKLSYL\MPSGSQCSFFTCHNLKNC P*KAAPBSPSDPLOSPYRTPDGHTAQDYPVWAWBPHIH*WEGL VFCFFIDGYSPGCWD\AFPGKBAPVAIFRG\NGGKLICVAWSPL DPDCTYSG\ADDFCVHKWLISNDDHSRPPQGKKSIBLEKKRLSQ PKAKPKKKKPTLRTPVKLESIDGHSRFRENGVSNGVSDQ EGESQAREPELPCCLAPAVSREPVICTPVSSGFESKVTINNKV ILLKKEPPKEKPFTIIKKRKARSLLPLSTSLDHRSKEELHQDCL VLATAKHSRELINDVSADVEEFFHLGLFTDRATLYRMIDISGKG HLENGHPELPPQLMLWKGDLKGVLQTAAERGELTDNIVMAMAPAA GYHWLMAVBAFARQLCFOPQYVKAASHLLSIHKVYBAVELLKS NHFFREAIAILAKARLRPEDPUKDLYLLGVGTVEREDGHYAVAAK CYLGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSSALA LRCAQELLLANNWVGAQBALQLHESLGQGRUFYCLLBELSSHLE EKQLSEKKSSSSYHTWNTGTFGFFFVERFTDFFOF				SDVNYOCLESAWY, ULDCVI TEODY EDERGARD INTO THE
HYWMFGRDFGRRSLLMHFSNLGKSFCLSSVGTGTSGLANGWGE  VPAS\DFSELILSLLSSPGTLATYNCILIGNIFLGRILLKKNLIA*  VXFQQTYQHLYQR*QMKPNCILKNLIGH** 1*CCHKLHWRLIAVI  FPMCHLGERYFKSFLLMY1** KEVIQQFIDULSVAVKKRVLCLPR  DEBLITANEVLKTCDRKANNLFSGGIDSWIJATLADRHIPLDE  PIDLLHVAFIAEEKTMPTTFNREGNKQKNKCEIPSEEFSKDVAA  AAADSPNKHVSVPDRITGRAGLEELQAVSPSRIWNFVEINVSME  ELQKLRFRISCHLHIPRLDTVLDDSIGCAVMFASRGIGWLVAQEG  VKSYGSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLEGLNKEIM  MELGRISSRNLEGIGEKLLLKLAAVELGITASALLPKRAMQFGSRIA  KMEKINEKASDKCGRLQIMSLENLSIEKETKL  MGHANAQAPVTNCCYLATGSKDGTIRIWSCSRGRGWMILKLPFL  KRRGGGIPTVKERLMLTHWPSNQFTGLVSSCFGGELLQWDLT  CSWRRKYTLFSASSEQNISRIVFNLCPLQTEDDKQLLLSTSMD  RDVKCMDIATLECSWTLPSLGFAYSLAFSSVDISSLATGVCGBG  MIRVWNTLSIKNNYDVKNFWQGVKSKVTALCHHPTEEGCLAFGT  DDGKVGLVDTYSNKPPQISSTYHKKTVYTLAMSPPVPPMSLGGE  GDRPSLALYSCGSGGIVLQHNPWKLSGEAFDINKLIRDTNSIKY  KLPVHTEISWRADGKIMALGNEDGSIEIPQ\TPNLKLIGTTQQH  HKLVWTISWHE\KHSPAQKLSYL\MPSGSQCSFTCCHNLKNC  P*KAAPBSPSDLQSPYRTPGGHTAQDYPVWAWEPHIH*WEGL  VFCFPIDGYSPGCWD\AFPGKRAVAIFRG\HGGRLLCVAWSPL  DPDCIYSG\ADDFCVHKALTSMDDHSPPOGKKSIELEKKZLSQ  PKAKPKKKKPLFPVNLESDGMSPPOGKSIELEKKZLSQ  PKAKPKKKKPLFPVNLESDGMSPPOGKSIELEKKZLSQ  PKAKPKKKKPLFPTPVLESDGFESMKNSGPVENGVSDQ  EGEEQARFELPCGLAPAVSREPVICTPVSSGFEKSKVTINNKV  ILLKKEPPKEKPETLIKKRKARSLLPLSTLDHRSKEELHODCL  VLATAKHSRELENDVSADVERFFHLGLETDRATLYRMIDIEGKG  HLENGHPELPHQLMLWKGDLKGVLQTAAERGELTDNLVAMAPAA  GYHWLMAVBAFAKQLCFQDQYVKAASHLLSIHKVYRAVELLKS  NHFYREAIALAKARRLPEDDVADVERFFHLGLETDRATLYRMIDIEGKE  HLENGHPELPHQLMLWKGDLKGVLQTAAERGELTDNLVAMAPAA  GYHWLMAVBAFAKQLCFQDQYVKAASHLLSIHKVYRAVELLKS  NHFYREAIALAKARRLPEDGLAQUEVFLERDGHAVANAK  CYLGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSASLA  LRCAGELLLAANNWQAQBAALQLEBLGQGRUVFCLLBELLSRHLE  EKQLSEKSSSSYHTWMTGTGGFFUERDTAWKSIFSLDFFDOV	1	į i		VZAEENDTOTI.FNYT.SSCKNESETT.ST.ESPUSCEMSETTINGS
VPAS_DFSELILSILSFPDALFYNCILGNIFLGRIILLKKMILAY VKROQTYOGHYOR OMKPOLILKNILFL*1*CCHKLHWRLIAVI FPMCHLQERYFKSFLLMYT*KEVIQOFIDVLSVAVKKRULCLPR DENLTANEVLKTCDRKANVAILFSGSIDSMVIATLADRHIPLDE PIDLINVAFTAEEKTMPTTFNREGMKQKNKCEIPSEEFSKDVAA AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIWMFVEINVSNE ELQKLRTRICHLIRPLDTVLDDGIGCAVWFASRGIGWLVAQEG VKSYQSNAKVVLTGIGADEQLAGYSHRVRFQSHGLEGLINKEIM MELGRISSRNLGRDDRVIGDHGKEARFFFLDENVVSFLNSLPIW EKANLTLPRGIGEKLLLRLAAVELGLTASALLBKRAMQFGSRIA KMEKINEKASDKCGRLQIMSIENLSIRKETKL NGNAVAQAPVINCCYLAATGSKDCTTRIWSCSRGRGVWILKLPFL KRRGGGIDPTVKRRLWLTLHWPSNQFTQLVSSCFGGELLQWDLT QSWRRKYTLFSASSEGQNHSRIVFNLCPLQTEDDKQLLISTSMD RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGDG MIRVNNTISIKNNYDVKNFRQGVKSKVTALCWPPTKEGCLAFGT DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGPVPPMSLGGE GDRPSLALYSCGGGGTVLQHNPWKLSGFAFFINKLIRDTNSIKY KLPVHTEISWKADGKIMALGNEDGSIEIFQ\IPMLKLICTIQQH HKLVNTISWHHE\HGSPAQKLSYL\MPSGSQQCSFFTCHNLKNC P*KAAPBEPSDPLQGFYRTPPQGHTAQDYPVWAMEPHIH*WEGL VFCFFIDGYSGCWD\AFFGKEAPVAFFRG\HQGRLLCVAWSPL DPDCIYSG\ADDFCVHKWLTSMQDHSRPPQGKKSIBLEKKALSQ PKAAPKKKKKFTLRTPVKLESIDGNEESSNKENSGPVENGUSDQ EGESQARPELPCGLAPAVSREPVICTPVSSGFEKSKVTINNKV ILLKKEPPKEKPETLIKKRKARSILPLSTSLDHRSKEELHDCL VLATAKHSRELMEDVSADVERFPHLGLFTDRATLYRMIDISGKG HLENGHPELPFQLMWKGDLKGVLGYTAAERGELTDNIVAMAPAA GYHVWLMAVEAFRAKQLCFODQVVKAASHLLSHIKVVEAVELLKS NHFYREAIAIAKARLRPEDPVLKDLYLLSHIKVVEAVELLKS NHFYREAIAIAKARLRPEDPVLKDLYLLSHIKVVEAVELLKS NHFYREAIAIAKARLRPEDPVLKDLYLLSHIKVVEAVELLKS NHFYREAIAIAKARLRPEDPVLKDLYLLSHIGVTULERGGHYAVAAK CYLGATCAYDAAKULAKKGDASLRTAAELAAIVGEDELSASLA LRCAQELLLANNWUGAGSALQHESLQCGRLVFCLLELLSRHLE EKQLSEKSSSSYHTWNTOTBGPFVERVTAWKSITSLDTPFOV		1		HYLWFGRDFFGRRSIJ.WHFSNI.GKSECI.GSVGTOTGGI ANOMOR
VAPQOTYQHLYQR*QMKENCILKNILFL*I*CCHKLHWRLIAVI FPMCHLQERYKSFLHW*KEVIQQFIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILFSGSIDSMVIATLADRHIPLDE PIDLLNVAFIAEEKTMPTTFRREGKQKMKCEIPSEEFSKDVAA AAADSPNKHVSVPDRIJORGGLKELQAVSPSRIWNFVEINVSME ELQKLRRTRICHLIRPLDTVLDDSIGCAVWFASRGIGMTVAQEG VKSYGSNAKVVLTGIGADEQLAGGSRHRVRFQSHGLEGINKEIM MELGRISSRNIGRDDRVIGDHGKEARPFFLDENVVSFLNSLPIW EKANLTLPRGIGEKLLLRLAAVELGITASALDPKRAMQFGSRIA KMEKLNEKASDKGGRLQIMSLENLSIRKETKL  5837 4792 903 NONAVAQADYDNCCYLATGSKDOTTRIWGCSRGGRGVMILKLPFL KRCGGIDPTVKERLWLTLHWPSNQPTQLVSSCFGGELLQWDLT GSWRRKYTLFSASSEQGNHSRIVVRLCPLQTCEDDKQLLLSTSMD RDVKCWDIATLEGSWIDJSLAFSSVDIGSLAIGVCDG MIRVWNTLSIKNNYDVKNFWQGVKSKVTALCWHPTKEGCLAPGT DDGKVGLYDTYSNKPPQISSTYHKTYTLAWGPFVPPMSLGGE GDRSSLALYSCGGEGLUQHNPWKLSGEAPINLKIRDTNSIKY KLPVHTEISWKADGKIMALGNEDGSIEIFQ\IPNLKLICTTQQH HKLVNTISWHEF-HGSPAQKLSYL\MPSGSQCGSFTCHNLKNC P*KAAPESPSDPLQSFYRTPPQGHTAQDYPWAWEPHIH*WEGL VFCFPIDGYSPGCWD\AFPGKEAPVAIFRG\HQGRLLCVAWSPL DPDCIYSG\ADDFCYHKWLTSMQDHSRPPQGKKSIBLEKKRLSQ PKAAPKKKKKKPPLRTPVKLESIDGNEESKMENSGPVENGUSDQ GESCOARPELPCGLAPAVSREPVICTPVSSGFEKSKVTINNKV ILLKKEPPKEKPETLIKKRKARSLEPLSTSLDHRSKEELHQDCL VLATAKHSRELMEDVSADVEERPHLGLFTDRATLYRMIDISGKG HLENGHPELPFQLMLWKGDLKGVLQTAAERGELTDNIVAMAPAA GYHVWLMAVEAFAKQLCFQDQVVKAASHLLSIHKVYEAVELLKS NHFYREAIAIAKARLRPEDPVLKAUTVLGWTVLENGOHYAAVAAK CYJGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSASLA LRCAQELLLANNWUGAGSALQLHESLQGGRLVFCLLELLSRHLE EKQLSEKSSSYMTWMTOTBGPFVERVYLWWKSISLDTPFGVV				VPAS DESELLISLISEPDALE YNCILGNIEL COLLINGUE
FPMCHLQERYFKSFILMYT*KEVIQQFIDVLSVAVKKRVLCLPR DENLTARDEVLKTCDRKANVAILPSGGIDSMVIATLADRHIPLDE PIDLLNVAFIAEEKTMPTTFNREGNKÇKNKCEIPSEEFSKQVAA AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIMMFVEINVSME ELQKLRRTRICHLIRPLDTVLDDSIGCAVWFASRGIGMUNQGSG VKSYGSNAKVVLTGIGADEQLAGYSKHRVRFQSHLGEINKEIM MELGRISSRNLGRDDRVIGDHGKEARFPFLDENVVSFLNSLPIW EKANLTLPRGIGEKLLLRAVELGITASALLPKRAMQFGSRIA KMEKINEKASDKCGRCQIMSLENLSIKEFTKL  S837 4792 903 NONAVAQAPVTNCCYLATGSKDQTTRIWSCSRGRGVMILKLPFL KRRGGIDPTVKERLWUTLHWBNQPTGULVSCFGGELLQWDLT QSWRRKYTIFSASSEGGMHSRIVFNLCPLQTEDDKQLLISTSMD RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGDG MIRVWNTLSIKNYDVNNFWQGVSKVTALCWHPTKEGCLAFGT DDGKVGLYDTYNSKYPQOTKSTYHKKTVYTLAWGPPVPPMSLGGE GDRPSLALYSCGGEGIVQHNPWKLSGEAFDINKLIRDTNSIKY KLPVHTEISWKADGKIMALGNEDGSIEIFQ\IDNIKLICTIQQH HKLWNTISHHE\HGSPAKLSYL\MPSGSQCGSPFTCHNLKNC P*KAAPESPSDPLQSPYRTPPQGHTAQDYPVWAWEHHH*WEGL VFCFPIDGYSPGCWD\AFPGKEAPVAIFRG\HGGRLLCVAWSPL DPDCIYSG\JADDFCVHMLISMQDHSRPPQGKKSIBLEKKRLSQ PKARPKKKKKPTLRTPVKLESIDGMEESMKENSGEVENGVSDQ EGESQAREPELPCGLAPAVSREPVICTPYSSGFEKSKVTINNKV ILLKKEPPBEKPPTLIKKRARSLLPLSTSLDHRSKEELHQDCL VLATAKHSRELMEDVSADVEERFHLGLFTDRATLYRMIDITSGKG HLENGHPELFHQLMLWKGDLKGVLQTAAERGELTDNLVAMAPAA GYHVWLMAVEAFAKQLCFQDQYVKAASHLLISHKVYEAVELLKS NHFYREAIAIAKARLRPEDPVLKDLYLSWGTVLERGGHYAVAAK CYLGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSASLA LRCAQELLLANNWVGAQEALQLEBSLGCGUFFCLLLELSRHLE EKQLSEGKSSSYHTWNTOTEGFFVERVTAWKSTFSLDPPEOV				VKFQQTYQHLYQR*OMKPNCILKNIJ.FI.*I*CCHKI.HWPI.TAVT
DENLTANEVLEKTORKANVAILESGGIDSMVIATLADRHIPLDE PIDLINVAFIAEEKTMPTTFINEGNKOKNKCEIPSEEFSKDVAR AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIWMFVEINVSME ELQKLRRTRICHLIRPLDTVLDDSIGCAVWFASRGIGWLVAQEG VKSYQSNAKVVLTGIGADEQLAGYSHRVRRQSHGLEGINKEIM MELGRISSRNLGRDDRVIGDHGKEARPFFLDENVVSFLMSLPIW EKANLTLPRGIGEKLLLRLAAVELGLTASALLPRRAMGPGSRIA KMEKANTLPRGIGEKLLLRLAAVELGLTASALLPRRAMGPGSRIA KMEKINEKASDKCGRLQIMSLENLSIEKETKL  SRAGGIDPTVKERLHWILHWBSNQFTQLVSSCFGGELLQWDLT QSWRRKYTLFSASSEGQNHSRIVFNLCPLQTEDDKQLLLSTSMD RDVKCWDIATLECSWTLPSLGGFAYSLAFSVDIGSLAIGVCDG MIRVWNTLSIKNNYDVNNFWQGVKSKVTALCWHFIKEGCLAFGT DGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGPPVPPMSLGGE GDRPSLALYSCGGEGIVLQHNPKLSGEAFDINKLIETIONSIKY KLPVHTEISWKADCS HAALGMEDGSEIFQ\IPNLKLICTIQQH HKLVNTISWHHE\HGSPAQKLSYL\MPSGSQCSPFTCHNLKNC P*KAAPESPSDPLQSPPRTPPGGHTAQDYPWWAWEPHIH*WEGL VFCFPIDGYSPGCMD\AFPGKEAPVAIFRG\HQGRLLCVAWSPL DPDCIYSG\ADDFCVHKWLTSMQDHSRPPQGKKSIBLEKKRLSQ PKAKPKKKKKPTLRTPVKLESIDGNEESMKENSGPVENGVSDQ EGEQAREPELPCGLAPAVSREPVICTEVSSGFEKSKVTINNKV ILLKKEPPKEKPETILKKRKARSLLPLSTSLDHRSKEELHQDCL VLATAKHSRELNEDVSADVEERFHLGLFTDRATLYRMIDIEGKG HLENGHPELFFHQLMLWKGDLKGVLQTAAERGELTDNLVAMAPAA GYHWULMAVEAFAKQLCFQDQYVKAASHLLSIHKVYEAVELLKS NHFYREAIAIAKARLRPEDPVLKDLYLSWGTVLERGGHYAVAAK CYLGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSASLA LRCAQELLLANNWVGAQEALQLHESLQGQRLVFCLLELLSRHLE EKQLSEGKSSSSYHTMITTGEGFFURRTVAWKSIFSLDTPEOV	İ			FPMCHLQERYFKSFLLMYT*KEVIOOFIDVLSVAVKKRVLCI.PD
PIDLLNVAFIAEEKTMPTTRIREGIKQKNKCEIPSEEFSKDVAA AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIWNFVEINUSME ELQKLRRTRICHLIRPLDTVLDDSIGCAWFASRGIGRIVAQDSG VKSYGSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLEGLNKEIM MELGRISSRNLGRDDRVIGDHGKEARFPFLDENVVSFINSLPIW EKANLTLPRGIGEKLLKRLAVELGITASALLPKRAMQFGSRIA KMEKINEKASDKCGRLQIMSLENLSIEKETKL  5837  4792  903  MGNAVAQAPVINCCYLATGSKDQTTRIWSCSRGRGWNIKLLPFL KRRGGGIDPTVKERLHUTLHWPSNQPTQLVSSCFGGELLQWDLT QSWRRKYTLFSASSEGQNHSRIVFNLCPLQTEDDKQLLLSTSMD RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGDG MIRVNNTLSIKNNYDVKNFWQGVKSKVTALCWHPTKEGCLAFGT DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGPFVPPMSLGGE GDRPSLALYSCGGRGIVLQHNPWKLSGEAFDINKLIRDTNSIKY KLPVHTEISWKADGKIMALGNEDGSIEIFQ\IPNLKLICTIQQH HKLWNTISWHHE\UGSPAQKLSYL\MPSGSQCCSFFTCHNLKNC P*KAAPESPSDPLQSPYRTPPQGHTAQDYPVWAWEPHIH*WEGL VFCFFIDGYSFGCWD\AFFGKEAPVAIFRG\HQGRLLCVAWSPL DPDCIYSG\ADDFCVHKMLTSMQDHSRPPQGKSIBLEKKRLSQ PKAKPKKKKKPTLRTPVKLESIDGNEESMKENSGPVENGVSDQ EGESQAREPELPGCLAPAVSRPVICTPVSSGFEKSKVTINNKV ILLKKEPPKEKPETLIKKRKARSLLPLSTSLDHRSKEELHQDCL VLATAKHSRELNEDVSADVEERFHLGLFTDRATLYRMIDIEGKG HLERGHPELFFHQLMLWKGDLKGVLQTAÆRGELTDNIVAMAPAA GYHWLWAVEAFAKQLCFDQQYVKAASHLLSIHKVYEAVELKS NHFYREATAIAKARRLRPEDFVLKDLYLSWGTVLERDGHVAVAAK CYLGATCAYDAAKVLAKKGDAASLRTAÆELAAIVGEDELSASLA LRCAQELLLANNWVGAQEALQHESLQGGRUFCLLBLLSRHLE EKQLSECKSSSSYHTNITGTEGFFVERVITAWKSIFSLDTPEOV		-		DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADRHIPLDE
AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIWNFVEINVSME BLQKLRRTRICHLIPPLDTVLDDSIGCAVWFASRGIGWILVAQEG VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLEGLNKEIM MELGRISSRNLGRDDRVIGDHGKEARFPFLDENVVSFLNSLPIW EKANLTIPRGIGEKLLIRLAAVELGITASALLIPKRAMQFGSRIA KMEKINEKASUKCGRLQIMSLENLSIBKETKIL  S837  4792  903  NGNAVAQAPVTNCCYLATGSKDQTIRIWSCSRGRGVMILKLIPFL KRRGGGIDPTVKERLIWLTLHWPSNQPTQLVSSCFGGELLQWDLT QSWRRKYTLFSASSEQNHSRIVFRLCPLQTEDDKQLLLSTSMD RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGDG MIRVWNTLSIKNNYDVKNFWQGVKSKVTALCWHPTKEGCLAFGT DDGKVGLYDTYSNKPPQISSTYHKRTYYTLAWGPPVPPMSLGGE GDRPSLALYSCGSGIVLQHNPWKLSGEAFDINKLIRDTNSIKY KLPVHTEISWKADGKIMALGNEDGSIEIFQ\IPPLKLICTIQQH HKLVWTISWHHE\HGSPAQKLSYL\MPSGSQQCSPFTCHNLKNC P*KAAPBSPSDPLQSPYRTPPQGHTAQDYPVWAMEPHIH*WEGL VFCFFIDGTSPGCWD\AFPGKEAPVAIFRG\HQGRLLCVAWSPL DPDCIYSG\ADDFCVHKWLTSMQDHSRPPQGKKSIELEKKRLSQ PKARYKKKKKPTLRTPVKLESIDGNEEESMKENSGPVENGUNDQ EGGEQAREPELPCGLAPAVNSEPVICTPVSSGFEKSKVTINNKV ILLKKEPPKEKPETLIKKRKARSLLPLSTSLDHRSKEELHQDCL VLATAKHSRELNEDVNADVEERFHLGLFTDRATLYRMIDIEGKG HLENGHPELFHQLMLWKGDLKGYLQTAAERGELTDNIVAMAPAAA GYHWUMAVVAFARAKQLCFQDQYVKAASHLLSIHKVYEAVELLKS NHFYREAIAIAKARLRPEDDFVLKDLYLEWGTVLERDGHYAVAAK CYLGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSASLA LRCAQELLLANNWGAQGAALQLHESLQGQRLVFCLLEBLLSRHLE EKQLSEGKSSSSYHTWNTGTEGFFVERVTAVWKSIFSLDTPEGY	1	1		PIDLLNVAFIAEEKTMPTTFNREGNKOKNKCEIPSEEFSKDVAA
ELQKLRRTRICHLIRPLDTVLDDSIGCAVWFASRGIGWLVAQEG VKSYQSNAKVVLTGIGADEQLAGYSRHRVZRFQSHGLEGLINKSIM MELGRISSRNLGRDDRVIGDHGKEARPFFLDENVVSFLNSLPIW EKANLTLPRGIGEKLLLRLAAVELGLTASALLPKRAMQFGSRIA KMEKINEKASDKCGRLDJIMSLENLSITKETKL  MGNAVAQAPVTNCCYLATGSKDQTIRIWSCSRGRGWMILKLPFL KRRGGIDPTVKERLWLITLHWPSNQPTQLVSSCFGGELLQWDLT QSWRRKYTLFSASSEGQNHSRIVFNLCPLQTEDDKQLLLSTSMD RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGDG MIRVWNTLSIKNNYDVKNFWQGVKSKVTALCWHPTKEGCLAFGT DDGKVGLYPDTYSNKPPQISSTYHKKTVYTLAWGPPVPPMSLGGE GDRPSLALYSCGGEGIVLQHNPWKLSGEAFDINKLIRDTNSIKY KLPVHTEISWKADGKIMALGNEDGSIEIFQ\IPNLKLICTIQQH HKLVNTISWHHE\HGSPAQKLSYL\MPSGSQQCSFFTCHNLKNC P*KAAPESPSDPLGSPYRTPPQGHTAQDYPVWAMEPHIH*WEGL VFCFFIDGYSPGCWD\AFPGKEAPVAIFRG\HQGRLLCVAWSPL DPDCIYSG\ADDFCVHKWLTSMQDHSRPPQGKKSIELEKKRLSQ PKAKPKKKKKPTLRTPVKLESIDGNEEESMKENSGPVENGVSDQ EGESQARPELPCGLAPAVSREPVICTPVSSGFKKSVTINNKV ILLKKEPPKEKPETLIKKRKARSLLPLSTSLDHRSKEELHQDCL VLATAKHSRELNEDVSADVEERFHLGLFTDRATLYRNIDIEGKG HLENGHPELFHQLMLWKGDLKGDLKGVLQTAAERGELTDNLVAMAPAA GYHWLWAVEAFFAKQLCFQDQVVKAASHLLSIHKVVEAVELLKS NHFYREAIAIAKARLRPEDPVLKDLYLSWGTVLERDGHYAVAAK CYLGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSASLA LRCAGELLLANNWCGAQEALQLHESLQGQRLVFCLLELLSRHLE EKQLSEGKSSSSYHTWNTGTEGFFVERVITAVWKSIFSLDTPEGV	ł	1 .		AAADSPNKHVSVPDRITGRAGLKELOAVSPSRIWNFVEINUSME
VKSYQSNAKVVLTGIGADEQLAGYSRHRVARQSHGLEGLNKEIM MELGRISSRNLGRDDRVIGDHGKEARFPFLDENVVSFLNSLPIW EKANLTLPRGIGEKLLLRLAAVELGITASALLPKRAMQFGSRIA KMEKINEKASDKCGRLQIMSLENLSIRKETKL SNAVAQAPVTNCCYLATGSKDCTTRIWSCSGGRGVMILKLPFL KRRGGIDPTVKERLWLTLHWPSNQFTQLVSSCFGGELLQWDLT CSWRRKYTLFSASSEGQMHSRIVFNLCPLQTEDDKQLLLSTSMD RDVKCMDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGDG MIRVWNTLSIKNNYDVNNFWQGYKSKVTALCWHPTKEGCLAFGT DDGKVGLYDTTYSKKPPQISSTYHKKTVYTLAWGPFVPPMSLGGE GDRPSLALYSCGGEGIVLQHNPWKLSGEAFDINKLIRDTNSIKY KLPVHTEISWKADGKIMALGNEDGSIEIFQ\IPNLKLICTIQQH HKLVNTISWHHE\HGSPAQKLSYL\MPSGSQQCSFFTCHNLKNC P*KAAPESPSDPLQSPYRTPPDGHTAQDYPVWAWEPHIH*WEGL VFCFFIDGYSPGCWD\AFPGKEAPVATFRG\HGGRLLCVAWSPL DPDCIYSG\ADDFCVHKWLTSMQDHSRPPQGKKSIELEKKRLSQ PKAKPKKKKKPTLRTPVKLESIDGNEESMKENSGPVENGVSDQ EGESQAREPELPCGLAPAVSREPVICTPVSSGFEKSKVTINNKV ILLKKEPPKEKPETLIKKRKARSLLPLSTSLDHRSKEELHQDCL VLATAKHSRELNEDVSADVEERFHLGLFTDRATLYRMIDIEGKG HLENGHPELFHQLMLWKGDLKGVLQTAAERGELIDNIVAMAPAA GYHWLWAVEAFAKQLCFQDQYVKAASHLLSIHKVVEAVELLKS NHFYREAIAIAKARLRPEDFVLKDLYLSWGTVLERGHYAVAAK CYLGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSASLA LRCAQELLLANNWVGAQEALQLHESLQGQRLVFCLLELLSRHLE EKQLSEGKSSSSYHTWNTGTEGFFVERVTAWKSIFSLDTPROY		1		ELQKLRRTRICHLIRPLDTVLDDSIGCAVWFASRGIGWLVAOEG
EKANLTIPRGIGEKLLKRLAAVELGITASALLPKRAMQFGSRIA KMEKINEKASDKCGRLQIMSLENLSIKKETKL  MANAVAQAPVINCCYLATGSKDQTIRIWSCSRGRGVMILKLPFL KRRGGGIDPTVKERLWLTHWPSNQPTQLVSSCFGGELLQWDLT QSWRRKYTLFSASSEGQNHSRIVFNLCPLQTEDDKQLLLSTSMD RDVKCKDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGDG MIRVWNTLSIKNNYDVKNFWQGVKSKVTALCHPPTKEGCLAFGT DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGPPVPPMSLGGE GDRPSLALYSCGGEGIVLQHNPWKLSGEAFDINKLIRDINSIKY KLPVHTBISWKADGKIMALGNEDGSIEIFQ\IPNLKLICTIQQH HKLVWTISWHHE\HGSPAQKLSYL\MPSGSQQCSPFTCHNLKNC P*KAAPESPSDPLQSPYRTPPQGHTAQDYPWAWMEPHIH*WEGL VFCFILOGYSPGCMD\AFPGKEAPVAIFRG\HQGRLLCVAWSPL DPDCIYSG\ADDFCVHKWLTSMQDHSRPPQGKKSIBLEKKRLSQ PKAKPKKKKKPTLRTPVKLESIDGNEEESMKENSGPVENGVSDQ EGESQAREPELPCGLAPAVSREPVICTPVSSGFEKSKVTINNKV ILLKKEPPKEKPETLIKKRKARSLLPLSTSLDHRSKEELHQDCL VLATAKHSRELNEDVSADVEERFHLGLFTDRATLYRMIDIEGKG HLENGHPELFHQLMLWKGDLKGVLQTAAERGELTDNIVAMAPAA GYHVWLWAVEAFAKQLCFQDQYVKAASHLLSIHKVYEAVELLKS NHFYREAIAIAKARLRPEDPVLKDLYLSWGTVLERDGHYAVAAK CYLGATCAYDAAKVLAKKGDAASJRTAAELAAIVGEDELSASLA LRCAGELLLANNWVGAQEALQLHESLQGQRLVFCLILELLSRHLE EKQLSEGKSSSYHTWNTGTBGPFVERVTAVWKSIFSLDTPFOV		1 1		VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFOSHGLEGLNKEIM
MEKINEKASDKCGRLQIMSLENLSIRKETKL  MGNAVAQAPUTNCCYLATGSKDQTTIRIWSCSRGRGVMILKLPFL KRRGGIDPTVKERLWLTLHWPSNQPTQLVSSCFGGELLQWDLT QSWRRKYLLFSASSEGQNHSRIVFNLCPLQTEDDKQLLLSTSMD RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGDG MIRVMNTLSIKNNYDVKNFWQGVKSKVTALCWHPTKEGCLAFGT DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGPFVPPMSLGGE GDRPSLALYSCGGEGIVLQHNPWKLSGEAFDINKLIRDTNSIKY KLPVHTEISWKADGKIMALGNEDGSIEIFQ\IPNIKLICTIQQH HKLVNTISWHHE\HGSPAQKLSYL\MPSGSQQCSPFTCHNLKNC P*KAAPESPSDPLQSPYRTPPQGHTAQDYPVWAWSPHIH*WEGL VFCFFIDGYSPGCWD\AFPGKEAPVAIFRG\HQGRLLCVAWSPL DPDCIYSG\ADDFCVHKWLTSMQDHSRPPQGKKSIBLEKKRLSQ PKAKPKKKKKPTLRTPVKLESIDGNEEESMKENSGPVENGVSDQ EGEEQAREPELPCGLAPAVSREPVICTPVSSGFEKSKVTINNKV ILLKKEPPKEKPETLIKKRKARSLLPLSTSLDHRSKEELHQDCL VLATAKHSRELINEDVSADVEERFHLGLFTDRATLYRMIDIEGKG HLENGHPELFHQLMLWKGDLKGVLQTAAERGELTDNLVAMAPAA GYHVWLWAVEAFAKQLCFQDQYVKAASHLLSIHKVYEAVELLKS NHFYREAIAIAKARLRPEDPVLKDLYLSWGTVLERDGHYAVAAK CYYGATCAYDAAKVLAKKGDAASLKTAAELAAIVGEDELSASIA LRCAQELLLANNWVGAQCALQLHESLQGQRLVFCLLELLSRHLE EKQLSEGKSSSSYHTWNTGTEGPFVERVTAWWKSIFSLDTPFOOY		1		MELGRISSRNLGRDDRVIGDHGKEARFPFLDENVVSFLNSLPIW
MGNAVAQAPVINCCYLATGSKDQTIRIWSCSRGRGVMILKLPFL KRRGGGIDPTVKERLWLITLHWBSNQPTQLVSSCFGGELLQWDLT QSWRKYTLFSASSEGQNHSRIVFNLCPLQTEDDKQLLLSTSMD RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGDG MIRVWNTLSIKNNYDVKNFWQGVKSKVTALCWHPTKEGCLAFGT DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGPPVPPMSLGGE GDRPSLALYSCGGBGIVLQHNPWKLSGEAFDINKLIRDTNSIKY KLPVHTEISWKADGKIMALGNEDGSIEIFQ\IPNLKLICTIQQH HKLVNTISWHHE\HGSPAQKLSYL\MPSGSQQCSPFTCHNLKNC P*KAAPESPSDPLQSPYRTPPQGHTAQDYPVWAWEPHIH*WEGL VFCFFIDGYSPGCWD\AFPGKEAPVAIFRG\HQGRLLCVAWSPL DPDCIYSG\ADDFCVHKWLTSMQDHSRPPQGKKSIELEKKRLSQ PKARPKKKKKPTLRTPVKLESIDGNEESSMKENSGPVENGVSDQ EGEGAREPELPCGLAPAVSREPVICTPVSSGFEKSKVTINNKV ILLKKEPPKEKPETLIKKRKARSLLPLSTSLDHRSKEELHQDCL VLATAKHSRELNEDVSADVEERFHLGLFTDRATLYRMIDIEGKG HLENGHPELPHQLMLWKGDLKGVLQTAAERGEITDNLVAMAPAA GYHVWLWAVEAFAKQLCFQDQYVKAASHLLSIHKVYEAVELLKS NHFYREAIAIAKARLRPEDFPUKDLYLSWGTVLERDGHYAVAAK CYLGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSASIA LRCAQELLLANNWVGAQEALQLHESLQGQRLVFCLLELLSRHLE EKQLSEGKSSSSYHTWNTGTEGPFVERVTAWWKSIFSLDTPFOV		1 1		EKANLTLPRGIGEKLLLRLAAVELGLTASALLPKRAMQFGSRIA
KRRGGIDPTVKERLWLTLHWPSNQFTQLVSSCFGGELLQMDLT  QSWRRYTLFSASSEGQNHSRTVFNLCPLQTEDDKQLLLSTSMD  RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGDG  MIRVMNTLSIKNNYDVKNFWQGVKSKVTALCWHPTKEGCLAFGT  DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGPFVPPMSLGGE  GDRPSLALYSCGGEGIVLQHNPWKLSGEAFDINKLIRDTNSIKY  KLPVHTEISWKADGKIMALGNEDGSIEIFQ\IPNIKLICTIQQH  HKLVNTISWHHE\HGSPAQKLSYL\MPSGSQQCSPFTCHNLKNC  P*KAAPBSPSDPLQBPYRTPPQGHTAQDYPVWAWBPHIH*WEGL  VFCFFIDGYSPGCWD\AFPGKEAPVAIFRG\HQGRLLCVAWGFL  DPDCTYSG\ADDFCVHKWLTSMQDHSRPPQGKKSIBLEKKRLSQ  PKAKPKKKKKPTLRTPVKLESIDGNEEESMKENSGPVENGVSDQ  EGEEQAREPELPCGLAPAVSREPVICTPVSSGFEKSKVTINNKV  ILLKKEPPKEKPETLIKKRKARSLLPLSTSLDHRSKEELHQDCL  VLATAKHSRELNEDVSADVEERFHLGLFTDRATLYRMIDIEGKG  HLEENGHPELFQLMLWKGDLKGVLQTAAERGELTDNLVAMAPAA  GYHVWLWAVBAFAKQLCFQDQYVKAASHLLSIHKVYEAVELLKS  NHFYREAIAIAKARLRPEDPVLKDLYLSWGTVLERDGHYAVAAK  CYYGATCAYDAAKVLAKKGDAASLKTAAELAAIVGEDELSASLA  LRCAQELLLANNWVGAQCALQLHESLQGQRLVFCLLELLSRHLE  EKQLSEGKSSSSYHTWNTGTEGPFVERVTAWWKSIFSLDTPFOV	5837	4792	007	KMEKINEKASDKCGRLQIMSLENLSIRKETKL
QSWRRYTLFSASSEQNHSRIVFNLCPLQTEDDKQLLLSTSMD RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGDG MIRVWNTLSIKNNYDVKNFWQGVKSKVTALCWHPTKEGCLAFGT DDGKVCLYDTYSNKPFQISSTHKKTVYTLAWGPFVPPMSLGGE GDRPSLALYSCGGEGIVLQHNPWKLSGEAFDINKLIRDTNSIKY KLPVHTBISWKADCKIMALGNEDGSIEIFQ\IPNLKLICTIQQH HKLVNTISWHHEHGSPAQKLSYL\MPSGSQQCSFFTCHNLKNC P*KAAPBSPSDPLQSPYRTPPQGHTAQDYPVWAWEPHIH*WEGL VFCFFIDGYSPGCWD\AFFGKEAPVAIFRG\HQGRLLCVAWSPL DPDCIYSG\ADDFCVHKWLTSMQDHSRPPQGKKSIELEKKRLSQ PKARPKKKKKPTLRTPVKLESIDGNEEESMKENSGPVENGVSDQ EGEEQAREPELPCGLAPAVSREPVICTPVSSGFEKSKVTINNKV ILLKKEPPKEKPETLIKKRKARSLLPLSTSLDHRSKEELHQDCL VLATAKHSRELNEDVSADVEERFHLGLFTDRATLYRMIDIEGKG HLENGHPELFHQLMLWKGDLKGVLQTAAERGEITDNLVAMAPAA GYHVWLWAVEAFAKQLCFQDQYVKAASHLLSIHKVYEAVELLKS NHFYREAIAIAKARLRPEDFVLKDLYLSWGTVLERDGHYAVAAK CYLGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSASIA LRCAQELLLANNWVGAQCALQLHESLQGQRLVFCLLELLSRHLE EKQLSEGKSSSSYHTWNTGTEGPFVERVTAWWKSIFSLDTPFOV		1	903	NGNAVAQAPVTNCCYLATGSKDQTIRIWSCSRGRGVMILKLPFL
RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGDG MIRVWNTLSIKNNYDVKNFWQGVKSKVYTALCWHPTKEGCLAFGT DDGKVGLJVDTYSNKPPQISSTYHKKTVYTLAWGPPVPPMSLGGE GDRPSLALYSCGGEGIVLQHNPWKLSGEAFDINKLIRDTNSIKY KLPVHTBISWKADGKIMALGNEDGSIEIFQ\IPNLKLICTIQQH HKLVWTISWHHE\HGSPAQKLSYL\MPSGSQQCSPFTCHNLKNC P*KAAPBSPSDPLQSPYRTPPQGHTAQDYPVWAWBPHIH*WEGL VFCFFIDGYSPGCWD\AFPGKEAPVAIFRG\HQGRLLCVAWSPL DPDCIYSG\ADDFCVHKWLTSMQDHSRPPQGKKSLELEKKRLSQ PKAKPKKKKKPTLRTPVKLESIDGNEEESMKENSGPVENGVSDQ EGESQAREPELPCGLAPAVSREPVICTPVSSGFEKSKVTINNKV ILLKKEPPKEKPETLIKKRKARSLLPLSTSLDHRSKEELHQDCL VLATAKHSRELNEDVSADVEERFHLGLFTDRATLYRMIDIEGKG HLENGHPELFHQLMLWKGDLKGVLQTAAERGELTDNLVAMAPAA GYHVWLWAVEAFAKQLCFQDQYVKAASHLLSIHKVYEAVELLKS NHFYREAIALAKARLRPEDPVLKDLYLSWGTVLERDGHYAVAAK CYLGATCAYDAAKVLAKKGDAASLKTAAELAAIVGEDELSASLA LRCAQELLLANNWVGAQCALQLHESLQGQRLVFCLLELLSRHLE EKQLSEGKSSSSYHTWNTGTEGPFVERVTAWWKSIFSLDTPFOV		1		OCHERVATI FOR CORCONTIGUE THE TOTAL CONTIGUE TO THE TOTAL CONTIGUE
MIRVMTLSIKNNYDYKNFWQGYKSKUTALCWHPTKEGCLAFGT  DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGPFVPPMSLGGE GDRPSLALYSCGGEGIVLQHNPWKLSGEAFDINKLIRDTNSIKY KLPVHTEISWKADGKIMALGNEDGSIEIFQ\IPNIKLICTIQQH HKLVMTISWHHE\HGSPAQKLSYL\MPSGSQQCSPFTCHNLKNC P*KAAPESPSDPLQBFYRTPPQGHTAQDYPVWAWEPHIH*WEGL VFCFFIDGYSPGCWD\AFPGKEAPVAIFRG\HQGRLLCVAWGFL DPDCIYSG\ADDFCVHKWLTSMQDHSRPPQGKKSIBLEKKRLSQ PKAKPKKKKKPTLRTPVKLESIDGNEEESMKENSGPVENGVSDQ EGEEQAREPELPCGLAPAVSREPVICTPVSSGFEKSKVTINNKV ILKKEPPKEKPETLIKKRKARSLLPLSTSLDHRSKEELHQDCL VLATAKHSRELNEDVSADVEERFHLGLFTDRATLYRMIDIEGKG HLENGHPELFHQLMLWKGDLKGVLQTAAERGELTDNLVAMAPAA GYHVWLWAVEAFAKQLCFQDQYVKAASHLLSIHKVYEAVELLKS NHFYREAIAIAKARLRPEDPVLKDLYLSWGTVLERDGHYAVAAK CYYGATCAYDAAKVLAKKGDAASLKTAAELAAIVGEDELSASLA LRCAQELLLANNWVGAQEALQLHESLQGQRLVFCLLELLSRHLE EKQLSEGKSSSSYHTWNTGTEGPFVERVTAWWKSIFSLDTPFOV		1	•	PDVKCWDIATI ECCUMU DCI COER VOL PROTECTION
DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGPPVPPMSLGGE GDRPSLALYSCGGEGIVLQHNPWKLSGEAFDINKLIRDTNSIKY KLPVHTBISWKADGKIMALGNEDGSIEIFQ\IPNLKLICTIQQH HKLVMTISWHHE\HGSPAQKLSYL\MPSGSQQCSPFTCHNLKNC P*KAAPESPSDPLQSPYRTPPQGHTAQDYPVWAMEPHIH*WEGL VFCFFIDGYSPGCWD\AFPGKEAPVAIFRG\HQGRLLCVAWSPL DPDCIYSG\ADDFCVHKWLTSMQDHSRPPQGKKSIBLEKKRLSQ PKAKPKKKKKPLTERTPVKLESIDGNEEESMKENSGPVENGVSDQ EGEEQAREPELPCGLAPAVSREPVICTPVSSGFEKSKVTINNKV ILLKKEPPKEKPETLIKKRKARSLLPLSTSLDHRSKEELHQDCL VLATAKHSRELNEDVSADVEERFHLGLFTDRATLYRMIDIEGKG HLENGHPELFHQLMLWKGDLKGVLQTAAERGELTDNLVAMAPAA GYHWLWAVEAFAKQLCFQDQYVKAASHLLSIHKVYEAVELLKS NHFYREAIAIAKARLRFEDFVLKDLYLSWGTVLERDGHYAVAAK CYLGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSASIA LRCAQELLLANNWVGAQEALQLHESLQGQRLVFCLLELLSRHLE EKQLSEGKSSSSYHTWNTGTEGPFVERVTAWKSIFSLDTPFOV		1		MIRVWNTLSTKNNYDYKNEWOCHKOCHTEN CHUDWYDGG 2 222
GDRPSLALYSCGGEGIVLQHNPWKLSGEAFDINKLIRDTNSIKY KLPVHTEISWKADGKIMALGNEDGSIEIFQ\IPNLKLICTIQQH HKLVNTISWHHE\HGSPAQKLSYL\MPSGSQCSPFTCHNLKNC P*KAAPBSPSDPLQSPYRTPPQGHTAQDYPVWAWEPHIH*WEGL VFCFFIDGYSPGCWD\AFFGKEAPVAIFRG\HQGRLLCVAWSPL DPDCIYSG\ADDFCVHKWLTSMQDHSRPPQGKKSIELEKKRLSQ PKARPKKKKKPTLRTPVKLESIDGNEEESMKENSGPVENGVSDQ EGEQAREPELPCGLAPAVSREPVICTPVSSGFEKSKVTINNKV ILLKKEPPKEKPFTLIKKRKARSLLPLSTSLDHRSKEELHQDCL VLATAKHSRELNEDVSADVEERFHLGLFTDRATLYRMIDIEGKG HLENGHPELPHQLMLWKGDLKGVLQTAAERGEITDNLVAMAPAA GYHVWLWAVEAFAKQLCFQDQYVKAASHLLSIHKVYEAVELLKS NHFYREAIAIAKARLRPEDFVLKDLYLSWGTVLERDGHYAVAAK CYLGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSASIA LRCAQELLLANNWVGAQEALQLHESLQGQRLVFCLLELLSRHLE EKQLSEGKSSSSYHTWNTGTEGPFVERVTAWWKSIFSLDTPFOV		1		DDGKVGI.YDTYSNKPPOISSTYHKKTIVTI.NKCRDICDNKS.CCC
KLPVHTEISWKADCKIMALGNEDGSIEIFQ\IPNLKLICTIQQH HKLVNTISWHHE\HGSPAQKLSYL\MPSGSQQCSPFTCHNLKNC P*KAAPBSPSDPLQSPYRTPPQGHTAQDYPVWAWEPHIH*WEGL VFCFFIDGYSPGCWD\AFPGKEAPVAIFRG\HQGRLLCVAWSPL DPDCIYSG\ADDFCVHKWLTSMQDHSRPPQGKKSIELEKKRLSQ PKARPKKKKKPTLRTPVKLESIDGNEEESMKENSGPVENGVSDQ EGEEQAREPELPCGLAPAVSREPVICTPVSSGFEKSKVTINNKV ILLKKEPPKEKPETLIKKRKARSLLPLSTSLDHRSKEELHQDCL VLATAKHSRELNEDVSADVEERFHLGLFTDRATLYRMIDIEGKG HLENGHPELPHQLMLWKGDLKGVLQTAAERGEITDNLVAMAPAA GYHVWLWAVEAFAKQLCFQDQYVKAASHLLSIHKVYEAVELLKS NHFYREAIATAKARLRPEDPVLKDLYLSWGTVLERDGHYAVAAK CYLGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSASIA LRCAQELLLANNWVGAQEALQLHESLQGQRLVFCLLELLSRHLE EKQLSEGKSSSSYHTWNTGTEGPFVERVTAVWKSIFSLDTPPGOY		1		GDRPSLALYSCGGRGIVIOHNPWKI.SGFAFOTNKI.TRDTNGTVV
HKLVNTISWHHE\HGSPAQKLSYL\MPSGSQQCSPFTCHNLKNC P*KAAPESPSDPLQSPYRTPPQGHTAQDYPVWAMEPHIH*WEGL VFCFPIDGYSPGCWD\AFPGKEAPVAIFRG\HQGRLLCVAWSPL DPDCIYSG\ADDFCVHKWLTSMQDHSRPPQGKKSLBLEKKRLSQ PKAKPKKKKKPTLRTPVKLESIDGNEEESMKENSGPVENGVSDQ EGEEQAREPELPCGLAPAVSREPVICTPVSSGFEKSKVTINNKV ILLKKEPPKEKPETLIKKRKARSLLPLSTSLDHRSKEELHQDCL VLATAKHSRELNEDVSADVEERFHLGLFTDRATLYRMIDIEGKG HLENGHPELFHQLMLWKGDLKGVLQTAAERGELTDNLVAMAPAA GYHVWLWAVBAFAKQLCFQDQYVKAASHLLSIHKVYEAVELLKS NHFYREAIALAKARLRPEDPVLKDLYLSWGTVLERDGHYAVAAK CYYLGATCAYDAAKVLAKKGDAASLKTAAELAAIVGEDELSASLA LRCAQELLLANNWVGAQEALQLHESLQGQRLVFCLLELLSRHLE EKQLSEGKSSSSYHTWNTGTEGPFVERVTAVWKSIFSLDTPPGOY				KLPVHTBISWKADGKIMALGNEDGSTEIFO\ IDNI.KI.TCTTOOU
P*KAAPESPSDPLQSPYRTPPQGHTAQDYPVWAWEPHIH*WEGL VFCFP IDGYSPGCWD\AFFGKEAPVAIFRG\HQGRLCVAWSPL DPDCIYSG\ADDFCVHKWLTSWQDHSRPPQGKKSIBLEKKRLSQ PKAKPKKKKPTLRTPVKLESIDGNEEESMKENSGPVENGVSDQ EGESQAREPELPCGLAPAVSREPVICTPVSSGFEKSKVTINNKV ILLKKEPPKEKPETLIKKRKARSLLPLSTSLDHRSKEELHQDCL VLATAKHSRELNEDVSADVEERFHLGLFTDRATLYRMIDISGKG HLENGHPELFHQLMLWKGDLKGVLQTAAERGELTDNLVAMAPAA GYHVWLWAVBAFAKQLCFQDQYVKAASHLLSIHKVYEAVELLKS NHFYREAIAIAKARLRPEDFVLKDLYLSWGTVLERDGHYAVAAK CYLGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSASLA LRCAQELLLANNWVGAQEALQLHESLQGQRLVFCLLBLLSRHLE EKQLSEGKSSSSYHTWNTGTEGPFVERVTAVWKSIFSLDTPFOV		1	ŀ	HKLVNTISWHHE\HGSPAOKLSYL\MPSGSOOCSPETCHNIKNC
VFCFFIDGYSPGCWD\AFPGKEAPVAIFRG\HQGRLLCVAWSPL DPDCIYSG\ADDFCVHKWLTSMQDHSRPPQGKKSIBLEKKRLSQ PKAKPKKKKKPTLRTPVKLESIDGNEEESMKEMSGPVENGVSDQ EGEEQAREPELPCGLAPAVSREPVICTPVSSGFEKSKVTINNKV ILLKKEPPKEKPETLIKKRKARSLLPLSTSLDHRSKEELHQDCL VLATAKHSRELNEDVSADVEERFHLGLFTDRATLYRMIDIEGKG HLENGHPELFHQLMLWKGDLKGVLQTAAERGELTDNLVAMAPAA GYHWILWAVEAFAKQLCFQDQYVKAASHLLSIHKVYEAVELLKS NHFYREAIAIAKARLRFEDFVLKDLYLSWGTVLERDGHYAVAAK CYLGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSASLA LRCAQELLLANNWVGAQEALQLHESLQGQRLVFCLLELLSRHLE EKQLSEGKSSSSYHTMNTGTEGPFVERVTAWKSIFSLDTPFOV		1		P*KAAPESPSDPLQSPYRTPPQGHTAODYPVWAWEPHTH*WEGI.
DPDCIYSG\ADDFCVHKWLTSMQDHSRPPQGKKSIBLEKKRLSQ PKAKPKKKKPILRTPVKLES IDGNEEESMKENSGPVENGVSDQ EGEEQAREPELPCGLAPAVSREPVICTPVSSGFEKSKVTINNKV ILLKKEPPKEKPETLIKKRKARSLLPLSTSLDHRSKEELHQDCL VLATAKHSRELNEDVSADVEERFHLGLFTDRATLYRMIDIEGKG HLENGHPELPHQLMLWKGDLKGVLQTAAERGELTDNLVAMAPAA GYHWLWAVEAFAKQLCFQDQYVKAASHLLSIHKVYEAVELLKS NHFYREAIAIAKARLRPEDFVLKDLYLSWGTVLERDGHYAVAAK CYLGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSASIA LRCAQELLLANNWVGAQEALQLHESLQGQRLVFCLLELLSRHLE EKQLSEGKSSSSYHTMNTGTEGPFVERVTAWKSIFSLDTPFOV		1		VFCFPIDGYSPGCWD\AFPGKEAPVAIFRG\HOGRLLCVAWSPI.
PKAKKKKPTLRTPVKLESIDGNEEESMKENSGPVENGVSDQ EGEQAREPELPCGLAPAVSREPVICTPVSSGFEKSKVTINNKV ILLKKEPPKEKPETLIKKRKARSLLPLSTSLDHRSKEELHODCL VLATAKHSRELNEDVSADVEERFHLGLFTDRATLYRMIDIEGKG HLENGHPELPHOLMLWKGDLKGVLQTAAERGEITDNLVAMAPAA GYHVWLWAVEAFAKQLCFQDQYVKAASHLLSIHKVYEAVELLKS NHFYREAIAIAKARLRPEDPVLKDLYLSWGTVLERDGHYAVAAK CYLGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSASIA LRCAQELLLANNWVGAQEALQLHESLQGQRLVFCLLELLSRHLE EKQLSEGKSSSSYHTWNTGTEGPFVERVTAVWKSIFSLDTPPEOV		1		DPDCIYSG\ADDFCVHKWLTSMQDHSRPPOGKKSIELEKKRLSO
EGEEQAREPELPCGLAPAVSREPVICTPVSSGFEKSKVTINNKV ILLKKEPPKERPETLIKKRKARSLLPLSTSLDHRSKEELHQDCL VLATAKHSRELINEDVSADVEERFHLGLFTDRATLYRMIDIEGKG HLENGHPELFHQLMLWKGDLKGVLQTAAERGELTDNLVAMAPAA GYHVWLWAVBAFAKQLCFQDQYVKAASHLLSIHKVYEAVELLKS NHFYREAIATAKARLRPEDPVLKDLYLSWGTVLERDGHYAVAAK CYLGATCAYDAAKVLAKKGDAASLKTAAELAAIVGEDELSASLA LRCAQELLLANNWVGAQEALQLHESLQGQRLVFCLLELLSRHLE EKQLSEGKSSSSYHTWNTGTEGPFVERVTAVWKSIFSLDTPFOV			ì	PKAKPKKKKRTLRTPVKLESIDGNEEESMKENSGPVENGVSDO
ILLKKEPPKEKPETLIKKRKARSLLPLSTSLDHRSKEELHQDCL VLATAKHSRELNEDVSADVEERFHLGLFTDRATLYRMIDIEGKG HLENGHPELFHQLMLWKGDLKGVLQTAAERGELTDNLVAMAPAA GYHVWLWAVBAFAKQLCFQDQYVKAASHLLSIHKVYEAVELLKS NHFYREAIAIAKARLRPEDPVLKDLYLSWGTVLERDGHYAVAAK CYLGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSASLA LRCAQELLLANNWVGAQEALQLHESLQGQRLVFCLLBLLSRHLE EKQLSEGKSSSSYHTWNTGTEGPFVERVTAVWKSIFSLDTPFOV			Į	EGEEQAREPELPCGLAPAVSREPVICTPVSSGFEKSKVTINNKV
VLATAKHSRELNEDVSADVEERFHLGLFTDRATLYRMIDIEGKG HLENGHPELFHQLMLWKGDLKGVLQTAAERGELTDNLVAMAPAA GYHVWLWAVEAFAKQLCFQDQYVKAASHLLSIHKVYEAVELLKS NHFYREAIAIAKARLRPEDFVLKDLYLSWGTVLERDGHYAVAAK CYLGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSASLA LRCAQELLLANNWVGAQEALQLHESLQGQRLVFCLLELLSRHLE EKQLSEGKSSSSYHTMNTGTEGPFVERVTAVWKSIFSLDTPFOY			J	ILLKKEPPKEKPETLIKKRKARSLLPLSTSLDHRSKEELHODGL
GYHWLWAVEAFAKQLCFQDQYVKAASHLLSIHKVYEAVELLKS NHFYREAIATAKARLRFEDFVLKDLYLSWGTVLERDGHYAVAAK CYLGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSASLA LRCAQELLLANNWVGAQEALQLHESLQGQRLVFCLLELLSRHLE EKQLSEGKSSSYHTMNTGTEGPFVERVTAVWKSIFSLDTPFOY		1	]	VLATAKHSRELNEDVSADVEERFHLGLFTDRATLYRMIDIEGKG
NHFYREAIATAKARLRPEDPVLKDLYLSWGTVLERDGHYAVAAK CYLGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSASLA LRCAQELLLANNWVGAQEALQLHESLQGQRLVFCLLELLSRHLE EKQLSEGKSSSSYHTWNTGTEGPFVERVTAVWKSIFSLDTPEOV			ĺ	HLENGHPELPHQLMLWKGDLKGVLQTAAERGELTDNLVAMAPAA
CYLGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSASLA LRCAQELLLANNWVGAQEALQLHESLQGQRLVFCLLELLSRHLE EKQLSEGKSSSSYHTWNTGTEGPFVERVTAVWKSIFSLDTPFOY			i	GYHVWLWAVEAFAKQLCFQDQYVKAASHLLSIHKVYEAVELLKS
LRCAQELLLANNWVGAQEALQLHESLQGQRLVFCLLELLSRHLE EKQLSEGKSSSSYHTWNTGTEGPFVERVTAVWKSIFSLDTPFOY		1		NHFYREAIAIAKARLRPEDPVLKDLYLSWGTVLERDGHYAVAAK
EKQLSEGKSSSSYHTWNTGTEGPFVERVTAVWKSIFSLDTPEOV			}	CYLGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSASLA
EKQLSEGKSSSYHTMTGTEGPFVERVTAVWKSIFSLDTPEQY QEAFQKLQNIKYPSATNNTPAKQLLLHICHDLTLAVLSQQMASW				LKCAQELLLANNWVGAQEALQLHESLQGQRLVFCLLELLSRHLE
QEAFQKLQN I KYPSATNNTPAKQLLLHI CHDLTLAVLSQQMASW				ANQLISEGRSSSSYHTWNTGTEGPFVERVTAVWKSIFSLDTPEQY
		<u> </u>		QEAT QALQAIKYPSATANTPAKQLLLHICHDLTLAVLSQQMASW

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1			DEAVQALLRAVVRSYDSGSFTIMQEVYSAFLPDGCDHLRDKLGD
			HOSPATPAFKSLEAFFLYGRLYEFWWSLSRPCPNSSVWVRAGHR
1			TLSVEPSQQLDTASTEETDPETSQPEPNRPSELDLRLTEEGERM
1		1	LSTFKELFSEKHASLQNSQRTVAEVQETLAEMIRQHQKSQLCKS
i			TANGPOKNEPEVEAEQPLCSSQSQCKEEKNEPLSLPELTKRLTE
1			ANQRMAKFPESIKAWPFPDVLECCLVLLLIRSHFPGCLAQEMQQ QAQELLQKYGNTKTYRRHCQTFCM
5838	110	98	KIMPHLLVTFRDVAIDFSQEEWECLDPAQRDLYRDVMLENYSNL
			ISLDLESSCVTKKLSPEKEIYEMES\PSGRIWGNVSTITFQYNG
			LGDNMECKGNLEGQVSKSEGLYMCVKITCBEKATESHSTSSTFH
1			RII/HYQGKIVKCKECRQGFSYLSCLIQHEENHNI*KCSEVNKH
			RNTFSKKPSYI*HQ\KFRLGEKPYECMECGKAFGRTSDLIQHQK
			IHTNEKPYQCNACGKAFIRGSQLTEHQRVHTGEKPYDCKKCGKA
			FSYCSQYTLHQRIHSGEKPYECKDCGKAFILGSQLTYHQRIHSG
	į į		EKPYECKECGKAFILGSHLTYHQRVHTGEKPYICKECGKAFLCA
1			SQLNEHQRIHTGEKPYECKECGKTFFRGSQLTYHLRVHSGERPY
			KCKECGKAFISNSNLIQHQRIHTGEKPYKCKECGKAFICGKQLS
			EHQRIHTGEKPFECKECGKAFIRVAYLTQHEKIHGEKHYECKEC
			GKTFVRATQLTYHQRIHTGEKPYKCKECDKAF/HLWLTILSEHQ
			RIHRGEKPYECKQCGR/LFIRGSHL/NEHLRTHTGEKPYECKEC
			GRAFSRGSEHTLHQRIHTGEKPYTCVQCGKDFRCPSQLTQHTRL
5839	1	2425	HN*EYSSHKICMHSIALASLDFAHLQEKNPEN
3035	-	2425	GRPFPRPPRALPRLPLRGRRQDGRWTVDFEBCLKD\SPRFRAAL
Į į	ĺ.		EEVEGDVAELELKL\DKLVKLCIA\MIDTGKAFCVANKQFMNGI RD\LAQNS\NNDA\VVETKFAPSFLDSLQEMINFHTIL/L+PNS
1 1	·		EIN*GHSFQNFVKEDLRKFKDAKKQFENSQ*KRKKIALVKNAPV
1			PSRPASLEL*KPPNILTATRKCFRHIALDYVLQINVLQSKRRSE
			ILKSMLSFMYAHLAFFHQGYDLFSELGPYMKDLGAQLDRLVGDA
			AKEKREMECKHSTIQQKDFSRDDSKLKYNVDAANGIVMEGYLFK
			RASNAFKTWNRRWFSIQNNQVVYQKKFKDNPTVVVEDLRLCTVK
			HCEDIERRFCFEVVSPTKSCMLQADSEKLRQAWIKAVQTSI\AT
			AYREKDDESEKLDKKSSPSTGSLDSGNESKEKLLKGESALQRVQ
			CIPGNASCCDCGLADPRWASINLGITLCIECSGIHRSLGVHFSK
1 1			VRSLTLDTWEPELLKLMCELGNDVINRVYEANVEKMGIKKPQPG
1 1			QRQEKEAYIRAKYVERKFVDKIFL*SLSPP\EQQKK\FVSKSSE
1			EKRLSISKFGP\GDQVRASAQSSVRSNDSGIQQSSDDGRESLPS TVSANSLYEPEGERQDSSMFLDSKHLNPGLQLYRASYEKNLPKM
]	'		AEALAHGADVNWANSEENKATPLIQAVLGGSLVTCEFLLQNGAN
			VNQRDVQGRGPLHHATVLGHTGQVCLFLKRGANQHATDEBGKDP
1	1		LSIAVEAANADIVTLLRLARMNEEMRESEGLYGQPGDETYQDIF
			RDFSQMASNNPEKLNRFQQDSQKF
5840	698	3610	KHLHLPRQHLTTLWQISSPRWRSPQRAFMSALSKTQTQSAPALQ
]	j	j	GLSSLLQSVTGNPVPASEAASQSTSASPANTTVYTIKGRNLPSS
	į	İ	AQPFIPKSFNYSPNSSTSEVSSTSASKASIGQSPGLPSTAFKLP
	[		SNTKGFTATHNTSPAAPPTEVTICQSSEVSKPKL\ESESTSPSL
1 1			\EMKIHNFLKGNPGFSVA*NLKHPNPAGSLGSSAPSESHPSDFQ
ļ l	į		RGPTSTSIDNIDGTPVRDERSGTPTQDEMMDKPTSSSVDTMSLL
; !	İ		SKIISPGSSTPSSTRSPPPGRDESYPRELSNSVSTYRPFGLGSE SPYKQPSDGMERPSSLMDSSQEKFYPDTSFQEDEDYRDFEYSGP
	l		PPSAMMNLQKKPAKSILKSSKLSDTTEYQPILSSYSHRAOEFGV
1		į	KSAFPPSVRALLDSSENCDRLSSSPGLFGAFSVRGNEPGSDRSP
1	j		SPSKNDSFFTPDSNHNSLSQSTTGHLSLPQKQYPDSPHPVPHRS
1 1			LFSPONTLAAPTGHPPTSGVEKVLASTISTTSTIEFKNMLKNAS
i I	, ]		RKPSDDKHFGQAPSKGTPSDGVSLSNLTQPSLTATDQQQQBEHY
ı İ			RIETRVSSSCLDLPDSTEEKGAPIETLGYHSASNRRMSGEPIQT
	į	ł	VESIRVPGKGNRGHGREASRVGWFDLSTSGSSFDNGPSSASELA
]	1	ļ	SLGGGGGGGLTGFKTAPYKERAPQFQESVGSFRSNSFNSTFEHH
		1	LPPSPLEHGTPFQREPVGPSSAPPVPPKDHGGIFSRDAPTHLPS
		İ	VDLSNPFTKEAALAHAAPPPPPGEHSGIPFPTPPPPPPPGEHSS
		ł	SGGSGVPFSTPPPPPPPVDHSGVVPFPAPPLAEHGVAGAVAVFP
L			KDHSSLLQGTLAEHFGVLPGPRDHGGPTQRDLNGPGLSRVRESL

	SEQ	Predicted	Predicted end	
	ID	beginning	nucleotide	
	NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	i	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		amino acid	sequence	Codon, /=possible nucleotide deletion,
	ļ	sequence	_	\=possible nucleotide insertion)
	1			TLPSHSLEHLGPPHGGGGGGGGSNSSSGPPLGPSHRDTISRSGII
	1		ļ	LRSPRPDFRPREPFLSRDPFHSLKRPRPPFARGPPFFAPKRPFF
			į.	PPRY
	5841	1908	762	GLRLFLVLTVWPMMKPSWLSRTEFSKRLLCRTLWCQSGWSSRSY
	1	1		TREMLEMITES INFRESTRICT SAFERING TO SECOND
	1			RHCWMTARSCSGERGGHWAPROVGVYLLPGBVGCVCCDVCDCCD
	ļ	ļ		GDGDDSGLARKGSAVSALASGLVFFDMI.CDDFUDTDDFU31/03/
	Ī			SKEDLVSQGFTEFTIEDFHNTFMDIJEOVFKOTGVADI I ACIDIO
	ı		Í	QSTSDILVVYLRLLTSGYLORESKFFEHFTEGGPTUKPEGO\OR
	ł	1		\VEPMCKESDHIHIIALAOGLORVHPGWRYMGDDDDDDDDDDDDD
	i			FF. GDPSPKVYDDYRPG\HYDILYKIGI.GSSPI.GCDGCDTIADA
	5842	307		LGHCYRGFSVVVKWSYFTPFFLSHDPPPMFY
		] 307	1918	QEPTADFKLRSTCGCGREMTCPDKPGQLINWFICSLCVPRVRKL
				WSSKRPRTRRNLLLGTACALYLGFLUSOUGPASTOUGOAAEUGD
				HRSKDIAEPSFPEIPLDGTLAPPESOCNGSTLODMINITER DOV
				RSKPANIRGTVKPKRRKKHAVASAAPGQEALVGPSLQPQEA\EG
ı				KLML*HLGTLREQTWLRLESDPGGWCGVRE/WRAGGPDFLQPSS
				RESNIRIYSESAPSWLSKDDIRRMRLLADSAVAGLRPVSSRSGA RLIVLEGGAPGAVLRCGPSPCGLLKOPLDMSEVFAFHLDRILGL
				NRTLPSVSRKAEFIQDGRPCPIILWDASLSSASNDTHSSVKLTW
-				GTYQQLLKQKCWQNGRVPKPESGCTEIHHHBWSKMALFDFLLQI
1				YNRLDTNCCGFRPRKEDACVQNGLRPKCDDQGSAALAHIIQRKH
1				DPRHLVFIDNKGFFDRSEDNLNFKLLEGIKEFPASAVYVLKSQH
ı		1		LRQKLLQSLFLDKGYWESQGGRQGIEKLIDVIEHRAKILITYIN
ł	5843	500		ANGVEVENE
1	2013	200	1453	GTARLVTCWVLHGQ*VKKPAWEPGVVWL*Q*RCRPKGWGLGAGM
1				KGSKMSQPPQCLRRAOSSCCHFMVKTJ.DDCTRMTDCFKVZHTGT
ı	1			DALVITAQQXVIEPRRELLTOPCROKDDANUDVEDT.ET.VONAVA
ı	i			LEACTVSAPEEASPKPVLCHOSKERKPSAFM/PONNEGGERET
l	Į.			LPPKIPSWRDPPETLEEPONAPRERPEGDAAAKKDDBUGDIIN
ı	I	1		LGCPEIHGDLRPWDRKRQPRSLRGSHLGGQRLHGSLCGHISQKP
l	- 1	1		LTAPGTKROKGPHQEGREVGQLH*GDPRGQELAPNGSESPILPG VQARAPGLGRA
Γ	5844	202	2471	
l				FDSAVLSSINVMAVLPGPLQLLGVLLTISLSSIRLIQAGAYYGI KPLPPOIPPOMPROIPGYONI GOODHAAAAAA
l		į	•	KPLPPQIPPQMPPQIPQYQPLGQQVPHMPLAKDGLAMGKEMPHL QYGKEYPHLPQYMKEIQPAPRMGKEAVPKKGKEIPLASLRGEQG
l	1			PRGEPGPRGPPGPPGLPGHGIPGIKGKPGPQGYPGVGKPGMPGM
l	1			PGREGAMGMPGAKGEIGOKGEIGPMGTD* DOGDDGDUGLDGTGT
l	1		j	PGGPGLPGQPGPKGDRGPKGLPGPCGLPGPKGDKGPCNDCA DCV
l			ļ	AGPPGMAGPFGPVGLPGVGKPGVTGFPGP\AGDIGK\BCABCER
	į	1	1	GPQGPIGVPGVQGPPGIPGIGKPGODG\ TPGODGFPGGFGPCOT
l	- 1			PGLPGPPGDPGIGKPGFPGPKGDRGMCGVPGAIGDPGPKCDTCA
	J		į	FGLGGPPGEPGLPGIPGPMGPPGATGRDGDKGRGGTVGDAGDDG
	ļ	1		PRGEFGLQGFPGKPGFLGEVGPPGMRGFPGDTGPKGFUGOVGF
	į			GDPGVPGLLGPKGEPGIPGDOGLOCDPGTPGTGGDGCDTGDDGT
	1			PGPKGEPGLPGPPGFPGIGKPGVAGLHGPPGKPGALGPQGQPGL
				PGPPGPPGPPGPPAVMPPTPPPPQGEYLPDMGLGIDGVKPPHAYG
	ļ	ļ	İ	AKKGKNGGPAYEMPAFTAELTAPFPPVGAPVKFNKLLYNGRONY NPOTGIFTCEVPGVYVFAYDVGCONDENN
			ļ	NPQTGIFTCEVPGVYYFAYHVHCKGGNVWVALFKNNEPVMYTYD EYKKGFLDQASGSAVLLLRPGDRVFLQMPSEQAAGLYAGQYVHS
	- L			SFSGYLLYPM
	5845	215	2061	HASNKSASLQDKMANPKEKTAMCI JINELAPENBUODOVKI I NOD
	İ		1 '	GPANSKMESVQLSLGEOTWESEGSSIKKAOOAVCNKALTEROMER
		ļ	<u>.</u>	KP1*KPPKSNVNNNPGCITPTVELNGLAMKPG/KDATHDDLDDK
	1	-		FEPNIKAN INFOVMINORYHOPI PKI PYVOLTVONNE PROBOKO (
	ĺ	1	1 -	RQAARHNAAMKALQALONEPIPERSPONGESGKOMDDDVDANVC
			] 1	SISLVFEIALKRNMPVSFEVIKESGPPHMKSFVTRVSVGFPCAF
	- 1		1,0	SEGNSKKLSKKRAATTVLQELKKLPPLPVVEKPK\HPFKKDDVT
	1		j -	LVKAGPEYGQGMNPISRLAOIOOAKKEKEPDVVIJSEPGMDDDD
			1 1	FVMQVKVGNEVATGTGPNKKIAKKNAAEAMILOIGVKASTNIO
_			L	OQLEKTGENKGWSGPKPGFPEPTNNTPKGILHLSPDVYQEMEAS

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Grucamic Acid, F=Phenylalanine Godlynia
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid		P=Proline, Q=Glutamine, R=Arginine,
1	residue of	residue of	S=Serine, T=Threonine, V=Valine,
i	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
	1		RHKVISGTTLGYLSPKDMNOPSSSFFSISPTSNSSATIABELLM
ļ		<u> </u>	NGTSSTAEAIGLKGSSPTPPCSPVOPSKOLEVI.ARTOGROUPVC
i	1		DRUSGKECVTCLTLAPVOMIFHAIGSSIEASHDOU#VATATILG
		1	YGPARKWKAIKMEAMCAHAALLSLIHYLLAPSARLEKSKLFALG
ļ			N.
5846	1126	456	FSKLIMKTFIIGISGVTNSGKTTLAKNLQKHLPNCSVISQDDFF
Į.	i		KPESEIETDKNGFLQYDVLEALNMEKMMSAISCWMESARHSVVS
i			TDQESAEEIPILIIEGFLLFNYKPLDTIWNRSYFLTIPYEECKR
1			RRSTRVYQPPDSPGYFDGHVWPMYLKYRQEMQDITWEVVYLDGT
ĺ	1		KSEEDLELOVYEDLIOELAVOYOLOWNA + DRIVENSE A 4
	1		KSEEDLFLQVYEDLIQELAKQKCLQVTA*RRNTTNPS/CK*IRK
5847	2769	505	
1	]	203	APEMEDLSSPDSTLLQGGHNLLSSASFQESVTFKDVIVDFTQEE
I			WKQLDPGQRDLFRDVTLENYTHLVSIGLQVSKPDVISQLEQGTE
1			PWIMEPSIPVGTCADWETRLENSVSAPEPDISEERLSPEVIVEV
1			hkkddswssnllesweyegslerooanooti.pkgikurputtpg
i			WEKGPVNNEFGKSVNVSSNLVTOEPSPEETSTKRSIKONSNDVV
1			KEKSCKCNECGKAFSYCSALIRHORTHTGEKPYKCN*/CVEKAP
1	i		SRSENLINHQRIHTGDKPYKCDOCGKGFIEGPSLTOHODIUTGP
į			KPYKCDECGKAFSQRTHLVOHORIHTGEKPYTCNECGKAFGODC
			HEMEHOKIHTGEKPFKCDECDKTFTRSTHLTOHOKIHTGEKTVK
i l			CNECGRAFNGPSTFIRHHMIHTGERPYECNECGRAFSOHSNITTO
	ļ		HORTHTGEKPYDCAECGKSFSYWSSLAOHLKTHTGEKPYKCNEC
1 1	İ		GRAFSYCSSLTQHRRIHTREKPFECSECGKAFSYLSNINOUOVE
) [	1		HTQEKAYECKECGKAFIRSSSLAKHERIHTGEKDYOCHECGVTB
			SYGSSLIQHRKIHTGERPYKCNECGRAFNONIHI.TOHKDTUTCA
1 1	ſ		KFIECA±CGKAFRHCSSLAOHOKTHTEEKPYOCNKCEKTEGOGG
1	ì		HLTQHQRIHTGEKPYKCNECDKAFSRSTHLTQHQRIHTGEKPYK
i i			CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSALN
<del> </del>			[ KHQKLHPGI
5848	22	2961	AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK
ĺ	į į		GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL
1	1		DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG
	1		YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV
-		,	GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL
	1		VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV
1	i		SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY
			PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA
	i	ŀ	ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA
1	1		SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN
i	}	i	APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD
		Í	TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ
]			APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL
- 1		1	CSVPTRALLLSTYIKFVNLFPEVKPTIQDVLRSDSQLRNADVEL
1	i	İ	OOPAVEVI DI CENTA CEDITA DELLE CONTRADIVEL
1		!	QQRAVEYLRLSTVASTDILATVLEEMPPFPERESSILAKLKKKK
	1	1	GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG
1	-	•	LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA
I	}	l	RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFL
Į.	1	l	NFTPTLICSDDLQPNLNI.OTKPVDPTVEGGAOVOOVANTECTED
I			FTEAPVLNIQFRYGGTFONVSVOLPITLNKFFOPTFMASODERO
ſ		<b>i</b>	RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKITGFGSALLPEUDB
1	j	1	NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV
5849	3545		SQRLCELLSAQF
	2242	1895	KRREIKETVFHHVAQAGLELLSSSNPPSSASRSAGITGMRHQVQ
J		ŀ	P*DPCMSLSPPCFTEEDRFSLEALOTIHKOMDDDKDGGTEVERS
ľ	1	1	DEFIREDMKYKDATNKHSHLHREDKHITIEDLWKRWKTSFULMW
ı	İ		TLEDTLQWLIEFVELPQYEKNFRDNNVKGTTLPRIAVHEPSFMI
ŀ	[	İ	SQLKISDRSHRQKLQLKALDVVLFGPLTRPPHNWMKDFILTVSI
ł	İ	] -	VIGVGGCWFAYTQNKTSKEHVAKMMKDLESLQTAEQSLMDLQER
i	ĺ	. 1:	LEKAQEENRNVAVEKQNL+RKMMDEINYAKBEACRLRELREGAE
ı		.	CELSRRQYAEQELEQVRMALKKAEKEFELRSSWSVPDALQKWLQ
		1	LTHEVEVQYYNIKRONAEMQLAIAKDEAEKIKKKRSTVFGTLHV
			THV TOTAL TO

SEQ	Predicted	Predicted end	Amino acid secretary
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
- 1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
İ	residue of	amino acid	Water Manham W. Tames and Manham Manh
ı	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	bequence	Codon, /-possible nucleotide deletion,
ļ			\=possible nucleotide insertion)
	İ	ì	AHSSSLDEVDHKILEAKKALSELTTCLRERLFRWQQIEKICGFQ
	1		IAHNSGLPSLTSSLYSDHSWVVMPRVSIPPYPIAGGVDDLDEDT
İ			PPIVSQFPGTMAKPPGSLARSSSLCRSRRSIVPSSPQPQRAQLA
1	1		PHAPHPSHPRHPHHPQHTPHSLPSPDPDILSVSSCPALYRNBEE
ł	1		EEAIYFSAEKQWEVPDTASECDSLNSSIGRKQSPP/SKPRDIPN
5850	3	1005	IIS/DERYQEMRCP*RIPSGGIL
3030	3	1895	KAVLNFSASGSVISLTGSNPMHDASMWHLKKNGIIVYLDVPLLN
1	i		LICRLKLMKTDRIVGQNSGTSMKDLLKFRRQYYKKWYDARVFCE
1	1		SGASPEEVADKVLNAIKRYQDVDSETFISTRHVWPEDCEQKVSA
ì			EFFIEAVIEGLASDGGLFVPAKEFPKLSCGEWKSLVGATYVERA
	ļ		QILLERCIHPADIPAARLGEMIETAYGENFACSKIAPVRHLSGN
	1		QFILELFHGPTGSFKDLSLQLMPHIFAQCIPPSCNYMILVATSG
	Į.		DTGSAVLNGFSRLNKNDKQRIAVVAFFPENGVSDFQKAQIIGSQ
	1		RENGWAVGVESDFDFCQTAIKRIFNDSDFTGFLTVEYGTILSSA
1	}		NSINWGRLLPQVVYHASAYLDLVSQGFISFGSPVDVCIPTGNFG
			NILAAVYAKMMGIPIRKFICASNQNHVWTDFIKTG\HYDLRGKE
			N*AQTFFTVQ*IFLPNLSNLERHLHLMANKDGQLMTELFNRLES
j	1		QHHFQIEKALVEKLQQDFVADWCSEGECLAAINSTYNTSGYILD
1			PHTAVAKVVADRVQDKTCPVIISSTAHYSKFAPAIMQALKIKEI
1			NETSSSQLYLLGSYNALPPLHEALLERTKQQEKMEYQVCAADMN
5851	3120		VLKSHVEQLVQNQFI
3051	3120	1802	RCYLQFLALLLTSTSARAAAIAAAEEPAGSPSVMTRAGDHNRQ
1			RGCCGSLADYLTSAKFLLYLGHSLSTWGDRMWHFAVSVFLVELY
			GNSLLLTAVYGLVVAGSVLVLGAI IGDWVDKNARLKVAQTSLVV
			QNVSVILCGIILMMVFLHKHELLTMYHGWVLTSCYILIITIANI
	1		ANLASTATAITIQRDWIVVVAGEDRSKLANMNATIRRIDQLTNI
			LAPMAVGQIMTFGSPVIGCGFISGWNLVSMCVEYVLLWKVYQKT
1 .			PALAVKAGLKEEETELKQLNLHKDTEPKPLEGTHLMGVKDSNIH
1			ELEHEQEPTCASQMAEPFRTFRDGWVSYYNQPVF/LGWHGSCFP
1			LYDCPGL*LHHHRVRLHSGTEWFHPQYFDGSISYNWNNGNCSFY
			LATSKMWFGSDRSDLRIGTAFLFDLVCDLCIHAWKPPGLVRFSF
5852	1	422	KTTFPSSLCPLRQLPEVRGYSGQPLTDPLISLCRSHKCRGKGWG
	l i		SSSYPSLPALLRARSAPGHCTHRSCGPEWRIDSISRLEMQGARR
1			SGWAQAQPTILLLVPRLRKSLPSIWG/SLMGFFITSGPG/WFRQ
			YYFFISGRH*VLFTESDFYYVAMDFGGHGL9SHYSPGVPYYLOT
	1		FVSBIRRVVAGKKQSVYFRRCGGCSRAPPLITGGGVGSRKQRWP
			ESGAWALAPGLPAIHGRSWES
5853	223	1346	RLLGLSRVKGLHGPAASAWISDPETRGDPGGPWGMWRGSDLRPR
1	Í		PVSLTGLTLVCK*AAQGPQV\HSVKLCFGLGG\PCLL\FPIFRP
.	}		LLLHPRRPRLHPGTRGVAVEPHALRVVHVAHGEEAGIRAAGPGH
] [	1		GGVEIPQG/VGSLGARRGLRPSRPSSRHRNRVPAPPPGRPLATP
1 1			HRRRFPPDPALTCPGLGQDQGPREQQKQGSGRHDTILGDWGESE
1 1		i	SRWVRGNFRTGTAATLIGFSRNPTLNGSENWGSLVSIQEEGPDT
1		l	GWEREKRNPAEMGNPORWASPIHTPPLGPEILRAMPEALRAMDE
ļ .		l	ALGLRPDPATSVPSALS/QTF/PESWPRSCLRNQGETLGMGPVP
<b></b>			LSSLCITESPSQNWTPCLLLLTCPRGLF
5854	86	938	KGRNTAPEKKGAALNNRENASS*NGY/SRWKQDIRRIENHIIQE
[			LKHLCAMIKRVLLERLENTRKLRELTEGRTLDWPONRITEVSAK
			RQIVTEYREKGKRN*EEKKRDLEGRSRRYNLCIIGIPETEDRAS
1	1		GAETIKOLLE/ENFPELKNELDLOMEKAHRIPLKFNEKKAASRH
i I		i	IRVTFL/KFQRRNILQASSQRKQVTYKGAKVRLTSDFSPAILNA
		i	RRQW/N/PISRVLRENNFEPRIIYSAKLSFLYKGNWKTFLDIQG
			LGKYINQELSLKILLKDLLQLTENLN
5855	536	2391	LRSYGCKAPSRISHLHK\FLFLLLPSLLMGYSESPPPITDSWAP
1	į	ļ	FISLTHHVLSQSQSPLSSNCWICLSTHTO*FTALPADLITWTOS
( )	1	1	NVSLHISYLAIPFLADSFLKPV/L*PGNSAKHLSFKLSSLSMVS
1 1	į	1	GRAVALLHLIASGLTSIQTNTASSKPPIWGY\LSTQTSFISPPP
		ł	LCLSRTYPNPAHATMVGQVPQSLCGLIFTL/RTPCRPSILHPNY
1 1		ĺ	KIISTSAWQKVLCFSGSPTIHTSLHLTTGSSFLSFHPIPGFPAA
		ł	NSALYVSSLKGPPGKNVTIPSPVTGT*QPPHRGSN/RLTVDKDN
			THE TITLE THE YEAR ON THE VOKON

SEQ	Predicted	Predicted end	Amino acid
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ı	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ſ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	· -	\=possible nucleotide insertion)
			FFLSPKPNSLHQLPSQ\TPYQALTGAALAGSYPIWENENTLSWL
1			PTFTYNFCLSTPSLFFLCDTN+YLCLPANWSGTCTLVFQAPTIN
ı	<b>1</b> '	1	ILPPNOTILISVEASISSSPIRNKWALHLITLLTGLGITAALGT
	}		GIAGITTSITSYQTLFTTLSNTVEDMHTSITSLQRQLDFLVGVI
	1	1	LQNWRVLDLLTTEKGGTCIYLQEECCFCVNESGIVHIAVRRLHD
1	-		RAAEL*HQVADSWWQGSSLLRWIPWVAPFLGPLIFLFLLLMIGP
1		}	CIFNLVSRFISQRLNCFIQASMQKHIDNIFHLCHV*YQSLRGNH
	L		SEAPEPRP
5856	173	1137	PWLHGLGLSAVFLFYL*/YVTFHLYGGIILLLLIFISIAGILYK
1	1		FQDVLLYFPEQPSSSRLYVPMPTGIPHENIFIRTKDGIRLNLIL
1			IRYTGDNSPYSPTIIYFHGNAGNIGHRLPNALLMLVNLKVNLLL
Í			VDYRGYGKSEGEASEEGLYLDSEAVLDYVMTSPDLDKTKIYLSG
1			RSLG/GAAAIHLASDNSHRISAIMVENTFLSIPHMASTLFSFFP
ļ			MRYLPLWCYKNKFLSYRKISQCRMPSLFISGLSDQLIPPVMMKQ
			LYELSPSRTKRLAIFPDGTHNDTWQCQGYFTALEQFIKEVVKSH
i i			SPEEMAKTSSNVTII
5857	1597	563	KLIGKVLVLSVVADAMAAFAVEPQGPALGSEPMMLGSPTSPKPG
			VNAQFLPGFLMGDLPAPVTPQFRSISGPSVGVMEMRSPLLAGGS
1 1			PPQPVVPAHKDKSGAPPVRSIYDDISSPGLGSTPLTSRRQPNIS
1 1			VMQSPLVGVTSTPGTGQSMFSPASIGQPRKTTLSPAQLDPFYTQ
1 1			GDSLTSEDH\LDDSWGDCIWGFLKASA\SYILL\QFAQYGGIS*
1 [			NMWMSNTGNWMHIRYQSKLQARKALSKDGRIFGESIMIGVKPCI
j			DKSVMESSDRCALSSPSLAFTPPIKTLGTPTQPGSTPRISTMRP
			LATAYKASTSDYQVISDRQTPKKDESLVSKAMEYMFGW
5858	355	1419	PPHQPAAASTSXHQQQQPPPPPQDSSKPVVAQGPGPAPGVGSAP
1 1			PASSAPPATPPTSGAPPGSGPGPTPTPPPAVTSAPPGAPPPTP
1 1	1		PSSGVPTTPPQAGGPPPPPPAAVPGPGPGCPKQGPGPGGPKGGKMP
1 1			GGPKPGGGPGLSTPGGHPKPPHRGGGEPRGGRQHHPPYHQQHHQ
1 1			GPPPGGPGGRSEEKISGPRRGFKANLSLLRRPGEKTYTQRCRFC
] [	}		LLGIYLLISRRMNSRRLFAKIWENQEKFLSTKAKDSEFIKLESR
1 1			ALA+NCPKPELG*YTP*GGRQLPSSLFPTHACLPLSCSVIFSPF
1	ł	ł	MPPQ*NCWGRKPFRPNLGPHLKGAVCNRWDDPWEGPTGKGHCLN
			FAS
5859	307	1503	GGSSARPRASSRRMLSRKKTKNEVSKPAEVQGKYVKKETSPLLR
1			NLMPSFIRHGPTIPRRTDICLPDSSPNAFSTSGDGVVSRNQSFL
1 1			RTPIQRTPHEIMRRESNRLSAPSYLARSLADVPREYGSSQSFVT
1 1	1	ļ	EVSFAVENGDSGSRYYYSDNFFDGQRKRPLGDRAHEDYRYYEYN
1 1	1	i	HDLFQRMPQNQGRHASGIGRVAATSLGNLTNHGSEDLPLPPGWS
1		ļ	VDWTMRGRKYYIDHNTNTTHWSHPLEREGLPPGWERVESSERGT
1		1	YYVDHTNKKAQY\RHPCAPTCTSV*STCSCHI/AS/ROOTEPMO
1 !	j.	İ	SLLVPANPYHTAEIPDWLQVYARAPVKYDHILKWELFOLADLDT
l i			YQGMLKLLFMKELEQIVKMYEAYRQALLTELENRKQRQQWYAQQ
F0/2			HGKNF
5860	2956	1270	TIRVEEFPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFP
1	İ	1	LLLFSRLCGALAGPIIVEPHVTAVWGKNVSLKCLIEVNETTTOT
1			SWEKIHGKSSQTVAVHHPQYGFSVOGEYOGRVLFKNYSINDATT
1 1		1	TLHNIGFSDSGKYICKAVTFPLGNAOSSTTVTVLVEPTVSLTKG
1 .		ĺ	PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFP
!!	İ		NETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFILDI
		ŀ	QYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDG
1 1	1		QWPDGLLASDNTLHFVHPLTFNYSGVYICKVT\NSPGSKEUTOK
	l	4	VHPTFQDPSLPTYPPLPALQFQWASPSTA*TSRD\LATEP*KIA
j 1	1	1	PSPLSTL\ATIKGWTQLPTIIA*CSGVGALFIV\LVKCFGLGIF
] [			CYRRRTFRGDYFAKNYIPPSDMQKESOIDVLOODELDDYPDSV
į į	1	[1]	KKENKNPVNNLIRKDYLEEPEKTQWNNVENLNRFERPMDYVEDI.
			KMGMKFVSDEHYDENEDDLVSHVDGSVISRREWYV
5861	2051	1305	EVCACVQAFNLVASSGDDSQGGDKCGCEVGSWVGSMRVVMARLL
		1:	SEGEQGIPTACAAFAQQPAG/EPRRGLAGVGEGGPOCSWANVEC
			TLEFLVSLLGTDLARGRGNSASGPTAPADSKQL/ML*DVHRRVI
	<b></b>	l i	LE*RMNSGSPARDNAPSQRFCTNLSEGLRFGISPSWREALYGCH
			O DOME OTOT DIRECTOR

SEQ	Predicted	Predicted end	Amino acid regment gentaining
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ļ	to first	amino acid	P-Proline O-Clubarian P Parisi
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
- }	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ı	sequence	sequence	Codon, /=possible nucleotide deletion,
<del></del>	- Judgaenee	ļ	\=possible nucleotide insertion)
5862	1556	483	A
	1330	453	PPFQLIMGEIKVSPDYNWFRGTVPLKKIIVDDDDSKIWSLYDAG
		ĺ	PRSIRCPLIFLPPVSGTADVFFRQILALTGWGYRVIALQYPVYW
Į			DHLEFCDGFRKLLDHLQLDKVHLFGASLGGFLAQKFAEYTHKSP
1			RVHSLILCNSFSDTSIFNQTWTANSFWLMPAFMLKKIVLGNFSS
İ			GPVDPMMADAIDFMVDRLESLGQSELASRLTLNCQNSYVEPHKI
1	1		RDIPVTIMDVFDQSALSTEAKEEMYKLYPNARRAHLKTGGNFPY
1			LCRSAEVNLYVQIHL/R/RNSMEPNTRPLTHQWSVPRSLRCRKA
j			ALASARRSSSVSLAVNDELTRCVLV*SVASAPVSRPFPSGSSGS
5863	2714		PVLTVSGK
	2,14	249	PFPSRGSLPLAAPREDTMGPLMVLFCLLFLYPGLADSAPSCPQN
1			VNISGGTFTLSHGWAPGSLLTYSCPQGLYPSPASRLCKSSGQWQ
1	[		TPGATRSLSKAVCKPVRCPAPVSFENGIYTPRLGSYPVGGNVSF
1	·		ECEDGFI\LRGSPVRQCRPNGMWDGETAVCDNGAGHCPNPGISL
1			GP\VRTGFRFGHGDKVRYRCSSNLVLTGSSERECQGNGVWSGTE
1	ĺ		PICROPYSYDFFEDVAPALGTSFSHMLGATNPTQKTKESLGRKI
			QIQRSGHLNLYLLLDCSQSVSENDFLIFKESASLMVDRIFSFEI
1 .			NVSVAIITFASEPKVLMSVLNDNSRDMTEVISSLENANYKDHEN
			GTGTNTYAALNSVYLMMNNQMRLLGMETMAW\QEIRHAIILL\T
ļ			DGK\SHMGGSPKTAVDHIREILNINQKRNDYLDIYAIGVGKLDV
			DWRELNELGSKKDGERHAFILQDTKALHQVFEHMLDVSKLTDTI
			CGVGNMSANASDQERTPWHVTIKPKSQET\C\RGALISDQWVLT
ſ			AAHCFRDGNDHSLWRVNVGDPKSQWGKEFLIEKAVISPGFDVFA
			KKNQGIL\EFYGD\DIALL\KLAQKVKM\STHCQGPSCLP\CTM
1 1			\EANLGFLRETFKGSTCR\DHENEL/VWNKQSV\PAHF\VAL\N
1 1			GSKLEHLTLRMGVEWTSCCRGLSPKKKTM\FPNLT\DVRB\VVT
1 1	1		D\QFL\CS\GPQEDESP\CK*E\SGGA\VFLERRFRLSAGGVWC
			SWGL\YNP\CLGSA\DKNSPKKGPSVAKVPPPTR/DFHIN\LFP
			Q*SPWLRQHPGGMS*IFLPLLANGHLSPFACPARICRPLHFLPS
5864	173	1012	EWATLRTL
3001	1/3	1013	PLISVPQSLISLPQPLLCFPGGQEPSAPSPCLYSFLWACSFTMG
1 1			KLPPSIPPSSPLACVLKNLKPLQLTPDLKPKCLIFFCNTAWPQY
1 1	ŀ		KLDNDSK*PENGTFEFSILQVLDNSCHKMGKWSEVPDVQAFF\S
1			HWSLPSLCSQC/GLIPNLSSFSPFCSFG/PPPQVPSP/TESFFS
1			MDSSDLPPSPQAAPRQAEPGPNSHLASAPPPYNPFITSPPHTWS
1 1			SLQFHSVTSPPPPAQQFTLKKVAGAKGIVKVSAPFSLSQIR*RL
5865	568	1.64	GSFSSNIKIQPSSWLIWQQP
	200	1684	CLPGPRWGEGWRAGHTIVGCIFFKTAIISHFKGGMYLCVCMCTC
		ļ	LSVCVCVQVGSWICV/CVSMCACVSLCTC\ICRCISMYTREHAC
	İ		ACTRV*VYMCMS/VCTCVSTCIDVRVCAHVCVYMCLCLGYA*AC
1			TCV*MCVCMHEHVCMC/VCACSCVLL/CRGHICM/MCMSAYICI
į į	1	ļ	/CVYVCVLCVWACMRMSTCVWLVYG*ACTCVWMHM/CSCTCR/C
1	i	1	VHVCCMSMHACECLCVYLHICGCAGTRRWWAGSARGSRSCSRLP
	1	ļ	CWAPGPGLSLPGPSCPSVEQGLGGGPGQLQGRSGEARLGEHRGW
	1	J	GSPAAVCSRNCTVSPRRGADCFEAPDVPKQPPGWGRASFEERGC
5866	98	3197	GGRGWYCAPPLNGPQCCCFSIKPELKAKKKK
		3131	ARPEVPAPPAWLSRRGAAKMGDKKDDKDSPKKNKGKERRDLDDL
		1	KKEVAMTEHKMSVEEVCRKYNTDCVQGLTHSKAQEILARDGPNA
			LTPPPTTPEWVKFCRQLFGGFSILLWIGAILCFLAYGIQAGTED
- 1	1		DPSGDNLYLGIVLAAVVIITGCFSYYQEAKSSKIMESFKNMVPQ
l			QALVIREGEKMQVNAEEVVVGDLVEIKGGDRVPADLRIISAHGC
j			KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNNFVEGTA
1			RGVVVATGDRTVMGRIATLASGLEVGKTPIAIEIEHFIQLITGV
j			AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPEGLLATVTV
1	j	1	CLTLTAKRMARKNCLVKNLEAVETLGS'ISTICSDKTGTLTQNRM
- 1	1	1	TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*H/LLGFC
		1	NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE
1		1	RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD
1			RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGFCHYYL
- 1	1		PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG
<u> </u>	<u></u>		KCRSAGIKVIMVTGDHPITAKAIAKGVGIIFEGNETVEDIAARL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ſ	location	corresponding	H=Histidine, I=Isoleucine, K=Lusine
	corresponding	to first	hebeucine, MeMethionine, NeAsparagine
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
1	residue of	residue of	S=Serine, T=Threonine, V=Valine
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- 1	sequence	sequence	Codon, /spossible nucleotide deletion,
			\=possible nucleotide insertion)
1			NIPVSQVNPRDAKACVIHGTDLKDFTSEQIDEILQNHTEIVFAR
}			TSPOOKLIIVEGCOROGAIVAVTGDGVNDSPALKKADIGVAMGI
1			AGSDVSKQAADMILLDDNFASIVTGVBEGRLIFDNLKKSIAYTL TSNIPEITPFLLFIMANIPLPLGTITILCIDLGTDMVPAISLAY
ľ	}	·	EAAESDIMKRQPRNPRTDKLVNERLISMAYGQIGMIQALGGFFS
	1		YFVILAENGFLPGNLVGIRLNWDDRTVNDLEDSYGQQWTYEQRK
			VVEFTCHTAFFVSIVVVQWADLIICKTRRNSVFQQGMKNKILIF
		1	GLFEETALAAFLSYCPGMDVALRMYPLKPSWWFCAFPYSFLIFV
			YDEIRKLILRRNPGGWVEKETYY
5867	3	1485	LPGRRARGGRGLGWPPAQALDGSRMGKAKVPASKRAPSSPVAKP
1	1		GPVKTLTRKKNKKKKRFWKSKAREVSKKPASGPGAVVRPDKAPE
			DPSQNWKALQEWLLKQKSQAPEKPLVISOMGSKKKPKITOONKK
		İ	ETSPQVKGEEMPAGKDQEASRGSVPSGSKMDRRAPVPRTKASGT
ļ			EHNKKGTKERTNGDIVPERGDIEHKKRKAK\GOPOPHPPP/TDT
İ			WFDDVDPADIEAAIGPEAAKIARKQLGQSEGSVSLSLVKEQAFG
1			GLTRALALDCEMVGVGPKGEESMAARVSIVNQYGKCVYDKYVKP
			TEPVTDYRTAVSGIRPENLKQGEELEVVQKEVAEMLKGRILVGH
i			ALHNDLKVLFLDHPKKKIRDTQKYKPFKSQVKSGRPSLRLLSEK ILGLQVQQAEHCSIQDAQAAMRLYVMVKKEWESMARDRRPLLTA
			PDHCSDDA*QSCPAAAAAPLQRQCDQSQQQITSPQSGNSGETFS
			ESWQRGVAWCY
5868	2122	833	LTAGASHTQDASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR
			AVTVYDKPASFFKETPLDLOHRLFMKLGSMHSDFRARSEDEDDU
1			TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSTI.LAA
			LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRI.THOKHEOU
1			IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG
i i			CCLPVCAVNFKCLHELVKHEENGLVFEDSBELAAQIQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT
5869	2122	833	LTAGASHTQDASQSTSAKYPAAQNL/CVTNAMREDLADIWYIR
1 1	ł		AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV
!!			TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA
1 1			LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHOKHFOH
} }		·	IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDI.PMKVVDMFG
			CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAOLOMLFSNFP
5870	2122	077	DPAGKLNQFRKNLRESQQLRWDESWVOTVLPLVMDT
55,7	2122	833	LTAGASHTQDASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR
, [	1		AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV
1 1	Į		TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHQKHFQH
1	j		IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG
	,	ì	CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP
			DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT
5871	3	3465	FFFCRFLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS
			VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFRFLKV\GSVVPD
]		i	LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYOSPTTGLEDTKT
	ĺ	ĺ	CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAT
	1	]	KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS
	i	1	YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF
		!	CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KOFNGFNLFGNQGCSWSVIFVDLDAHNRNRQTLCSLLPRESR
			SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR
·			FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG
		İ	VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE
1			KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI
			DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESORI.OV
1	1	. 1	FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR
1	1	1	PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSODVFLLID
- 1		i i	DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA
		i	LKKGIIGGVKVHVDRLQTLISGAVVEOLDFLRISDTEELPEFKS
}	İ		FEELEPPKHSKVKRQSSTPSAPELGQQPDVNISEWKDKPTHEIL
		<u>-</u> L	QKLNDCSCLASQAILLGILLKREGPNFITKEGTVSDHIERVYRR

SEQ Predicted Predicted end nucleotide nucleotide nucleotide nucleotide (A=Alanine, C=Cysteine, D=Asparti (A=Alanine, C=Cysteine, D=Asparti (A=Alanine, C=Cysteine, D=Asparti (A=Alanine, C=Cysteine, D=Asparti (A=Alanine, C=Cysteine, D=Asparti (A=Alanine, C=Cysteine, D=Asparti (A=Alanine, C=Cysteine, N=Asparti (A=Alanine, C=Cysteine, N=Asparti (A=Alanine, C=Cysteine, N=Asparti (A=Alanine, C=Cysteine, N=Asparti (A=Alanine, C=Cysteine, N=Asparti (A=Alanine, C=Cysteine, D=Asparti (A	c Acid, E=
NO: nucleotide location corresponding to first amino acid residue of location corresponding to first amino acid residue of service corresponding to first amino acid residue corresponding to first amino acid residue corresponding to first amino acid residue corresponding to first amino acid residue corresponding to first amino acid residue corresponding to first amino acid residue corresponding to first amino acid residue corresponding to first amino acid residue corresponding to first amino acid residue	c Acid, E=
location corresponding H=Histidine, I=Isoleucine, K=Lysi corresponding to first L=Leucine, M=Methionine, N=Aspara to first amino acid residue of S=Serine, T=Threonine, V=Valine,	=GIVCine.
corresponding to first L=Leucine, M=Methionine, N=Appara to first amino acid P=Proline, Q=Glutamine, R=Arginin amino acid residue of S=Serine, T=Threonine, V=Valine,	
to first amino acid P=Proline, Q=Glutamine, R=Arginin amino acid residue of S=Serine, T=Threonine, V=Valine,	
amino acid residue of S=Serine, T=Threonine, V=Valine,	
	e,
i testude of I amino acid I walivocobnan. Ysivrosine, Xsunkno	
amino acid sequence Codon. /=nossible nucleoride dele	wn, *=Stop
The state of the s	tion,
The state of the s	
AGSQKLWSVVRRAASLLSKVVDSLAPSITNVLV	
HEEEVISNPLSPRVIQNIIYYKCNTHDEREAVI	
ISNNPELFSGTLKIRIGWIIHAMEYELQIRGGD	
SEVKQLLLDILQPQQNGRCWLNRRQIDGSLNRT	
LERTPNGIIVAGKHLPQQPTLSDMTMYEMNFSL	
PQYRQIVVELLMVVSIVLERNPELEFQDKVDLD	
KDQSRLKEIEKQDDMTSFYNTPPLGKRGTCSYL	TKAVMNLLLEG
EVKPNNDDPCLIS	
5872 68 665 VQGYMYRFVIKINSCYSEKTSICRHRCCPELPA	
NIAIDSESLGCI\SFKLFADKV/PKRWKKNFVL	
GPCFYRIIPG\LCQGGDFTHHNGTGGKSLYSKE	
TAPGVLSTANAGPTINGSQFFICTAKTEDG*QH	VVFGKVKDGMS
IVEALERSGSRNGKTSKKITAANCGQL	
5873 2240 506 RRPPEGGSGGGRRTRARMPLPWSLALPLLLSWV	
HHGLLASARQPGVCHYGTKLACCYGWRRNSKGV	CEATCEPGCKF
GECVGPNKCRCFPGYTGKTCSQDVNECGMKPRP	
YKCFCLSGHMLMPDATCVNSRTCAMINCQYSCE	DTEEGPQCLCP
SSGLRLAPNGRDCLDIDECASGKVICPYNRRCV	NTFGSYYCKCH
IGFELQYISGRYDCIDINECTMDSHTCSHHANC	FNTQGSFKCKC
KQGYKGNGLRCSAIPENSVKEVLRAPGTIKDRI	KKLLAHKNSMK
KKAKIKNVTPEPTRTPTPKVNLQPFNYEEIVSR	GGNSHGG\KKG
NEEKMKEGLEDEKREEKALKD*HRRERPFRG\D'	VFFPKVNEAGE
FGLIL\VQRKALTSKLEHKADLNISVDCSFNHG	\ICDW\KQDR\
EDDFDW\NPADR\DNAI\GFY\MAVPGLWQGHK	
PDLQPQSNFCLLFDYRLAGDKVGKLRVFVKNSM	NALAWEKTTSE
DEKWKTGKIQLYQGTDATKSIIFEAERGKGKTG	
GLCPDSLLSVDD	
5874 2 3387 ACPRLARRRRVRSLRRRRGWLRARWSRGQNNM	AARRITOETFD
AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAY	
VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPS	
SYFRKECGRDLEFSHSNSRDQVIGHRKLGHFRS	
EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRI	
SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALI	
. KGETQGLLTAKGGVGKLVTLRNV5TKKIPTVNR	
QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDL	
FDIIDKSDVFSRFGIEIIKWAGFHTIKDDIKFSC	
ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSAI	KTPRVDNEFL
NMLLDKGAVKTKNCFFEIIKPFDKYIMRLQDRIJ	
NAYELSVKMKTLSNPLDLALALETTNSLCRKSL7	LLGOTFSLAS
SFRQEKIL*AVGLQDIAPSPAAFPNFEDSTLFGF	REYIDHLKAWL
VSSGCPLQVKKABPEPMREEBKMIPPTKPEIQAF	
QRADHRVVGTIDQLVKRVIEGSLSPKERTLLKEI	PAYWFLSDEN
SLEYKYYKLKLAEMQRMSENLRGADQKPTSADCF	VRAMLYSRAV
RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\1	TGTQTLLFLR
APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\C	
QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADI	DMKDNGRTAE
KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\	HDQNSS\AFK
FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\G	
GEAEFEDEPPPREAELESPEVMPEEEDEDDEDGG	EEAPA\PGRG
GPSLEGSTPADGLPGEA\AEDDL/ALGAPALFTG	
RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIA	
KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWK	
GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSF	
IFVF	
5875 296 1848 LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAM	RSVSVVODUA
LEFSGSLFPHAICLGDVDNDTLNELVVGDTSGKV	
WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSAEGW	
VLDASGHHETLIGEEQRPVFKQHIPANTKVMLIS	
\	
VVGYTDRVVRAFRWEELGEGPEHLTGQLVSLKKW	
VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSP	
/SGDPSCPRRGAAPDIWPYPQQECLHSPNWQHQT	/2001 P2262

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1,10.	location	t .	Glutamic Acid, F=Phenylalanine, G=Glycine,
ı	corresponding	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	to first	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	residue of	S=Serine, T=Threonine, V=Valine,
i	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		sequence	Codon, /-possible nucleotide deletion,
<u> </u>	sequence		\=possible nucleotide insertion)
	j		GLFALCTLDGTLKLMEEMEEADKLLWSVQVDHQLFALEKLDVTG
			NGHEEVVACAWDGQTYIIDHNRTVVRFQVDENIRAFCAGLYACK
			EGRNSPCLVYVTFNQKIYVYWEVQLERMESTNLVKLLETKP\ST
1			TACCRSWAWILTTSL*LVPCFTKRSTIQTSHHSVLPQASRIPPS
5876	1122		WTCLIAGEGFF*TPTLPPKGVFGSHCAAAGSITKQ
3876	1122	224	HLPLGVPSKVAGAAAMEPQEERETQVAAWLKKIFGDHPIPQYEV
Ī			NPRTTEILHHLSERNRVRDRDVYLVIEDLKQKASEYESEAKYLQ
	į ;		DLLMESVNFSPANLSSTGSRYLNALVDSAVALETKDTSLASFIP
1	1		AVNDLTSDLFRTKSKSEEIKIELEKLEKNLTATLVLEKCLQEDV
			KKAELHLSTER\AKVDNRRQNM\DFLKAKSEEFRFGIQAAGEQL
ł			SARGQ\DAFSVPIQSLVALIRENWPRLKQQTIPLK\KKLESYLD
			LMP\NPSHCSK*RIEEAK\RELA\SIEAELTRRVS\MMEL
5877	2030	1907	GTLGKMAASSSGEKEKERLGGGLGVAGGNSTRERLLSALEDLEV
1			LSRELIEMLAISRNQKLLQAGEENQVLELLIHRDGEFQELMKLA
•			LNQGKIHHEMQVLEKEVEKRDSDIQQLQKQLKEAEQILATAVYQ
			AKEKLKSIEKARKGAISSEEIIKYAHRISASNAVCAPLTWVPGD
			PRRPYPTDLEMRSGLLGQMNNPSTNGVNGHLPGDALA/RRKIAR
			CPCSTVS/NGSQMTCR*INIILILQKSVCEL
5878	950	2113	GLWKCMQLQGPHTHRVQP+PTPRQQGPQ\VPVAVIAGNRPNYLY
	1		RMLRSLLSAQGV9PQMITVFIDGYYEEPMDVVALFGLRGIQHTP
1			ISIKNARVSQHYKASLTATFNLFPEAKFAVVLEEDLDIAVDFFS
			FLSQSIHLLEEDDSLYCISAWNDQGYEHTAEDPALLYRVETMPG
1			LGWVLRRSLYKEELEPKWPTPEKLWDWDMWMRMPEQRRGRECII
			PDVSRSYHFGIVGLNMNGYFHEAYFKKHKFNTVPGVQLRNVDSL
1			KKEAYEVEVHRLLSEAEVLDHSKNPCEDSFLPDTEGHTYVAFIR
			MEKDDDFTTWTQLAKCLHIWDLDVRGNHRGLWRLFRKKNHFLVV
5879			GVPASPYSVKKPPSVTPIFLEPPPKEEGAPGAPEQT
36/9	3	981	RLTEAAAAGSGSRAAGWAGSPPTLLPLSPTSPRCAATMASSDED
) ,	· ,		GTNGGASEAGEDREAPGKRRRLGFLATAWLTFYDIAMTAGWLVL
			AIAMVRFYMEKGTHRGLYKSIQKTLKFFQTFALLEIVHCLIGIV
1			PTSVIVTGVQVSSRIFMVWLITHSIKPIQNEESVVLFLVAWTVT
			EITRYSFYTFSLLDHLPYFIKWARYNFFIILYPVGVAGELLTIY
	1		AALPHVKKTGMFSIRLPNKYNVSFDYYYFLLITMASYIPLFPQL
1	i		YFHMLRQRRKVLHG\G*L*KRMIK*SLQTRCFFQNNQDYLSPSF
5880	1138	1334	NNKNKQLCEISWIVWFLKI
3000	1136	1324	SLWCLVAGGLGLGPSSQNPLQRAGILARPREARGTFSALTACSA
1			SVTSKGKSSSGMWPSAASDRDSPVPLRPPGPVQLPSGTGWVLSD
1 1			*KKKRGRCSS/WLSQPQHEREKEVVLLRRSMAEGERARAASDVL
1	ľ		CRSLANETHQLRRTLTATAHMCQHLAKCLDERQHAQRNVGERSP
1 1	1		DQSEHTDGHTSVQSVIEKLQEENRLLKQKVTHVEDLNAKWQRYN
			ASRDEYVRGLHAQLRGLQIPHEPELMRKEISRLNRQLEEKINDC
j ł			AEVKQELAASRTARDAALERVQMLEQQILAYKDDFMSERADRER
1			AQSRIQELEEKVASLLHQVSWRQDSREPDAGRIHAGSKTAKYLA
1			ADALELMVPGGWRPGTGSQQPEPPAEGGHPGAAQRGQGDLQCPH
5881	26		CLQCFSDEQGEELLRHVABCCQ
5001	20	441	GGIHPSPTEAPRAQHLTMDCTWRILFLVAAATGTHAQVQLLQSG
j ĺ	!	ļ	SEVKKPGASVMVSCYVSGYTLTKLSMHWVRQAPGKGLE*MGPFD
1	1		LQDVETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV
5882	2407	0010	HHCATDTV
3002	2407	2216	SGCVEMLYSHSLEYNPEWISVQSAVAPAQLALNSDGDL*LHSGE
[ }			RTRRD*QLPEAGGPGLQEPLQLGELDITSDEFILDEVDG\VDLR
			HYSKQVELELQQIEQKSIRDYIQESENIASLHNQITACDAVLER
) ]			MEQMLGAFQSDLSSISSEIRTLQEQSGAMNIRLRNRQAVRGKLG
	(		ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVREQE
]	j	j	ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMTNYQ
	ł	1	IPQTALLKYRFFYQFLLGNERATAKEIRDEYVETLSKIYLSYYR
	İ	i	SYLGRLMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLRSRNTIF
		}	TLGTRGSVISPTELEAPILVPHTAQRGEQRYPFEALFRSQHYAL
		i	LDNSCREYLFICEFFVVSGPAAHDLFHAVMGRTLSMTLKHLDSY
			LADCYDAIAVFLCIHIVLRFRNIAAKRDVPALDRYWEQVLALLW

SEO	Predicted	Predicted end	
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NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			PRFELILEMNVQSVRSTDPQRLGGLDTRPHYITRRYAEFSSALV
1	İ		SINQTIPNERTMQLLGQLQVEVENFVLRVAAEFSSRKEQLVFLI
1	1		NNYDMMLGVLM\E*ERAADDSKEVESFQQLLNARTQEFIEELLS
	1		PPFGGLVAFVKEAEALIBRGQAERLRGEEARVTQLIRGFGSSWK
	•		SSVESLSQDVMRSFTNFRNGTSIIQGALTQLIQ\LYHRFHRV\L
1			SQPQLRALPARAELINIHHLMVELKKHKPNF
5883	2	1374	EFPGRRFRAVMBAGAGAGAGAGWSCPGPGPTVTTLGSYEASEG
1			CERKKGQRWGSLERRGMQAMEGEVLLPALYEEBEEEEEEEEE
1	ı		EEEEQVQKGGSVGSLSVNKHRGLSLTETELEELRAQVLQLVAEL
ĺ			BETRELAGQHEDDSLELQGLLEDERLASAQQAEVFTKQIQQLQG
ŀ	1		ELRSLREEISLLEHEKESELKEIEQELHLAQAEIQSLRQAAEDS
1			ATEHESDIASLQEDLCRMQNELEDMERIRGDYEMEIASLRAEME
	Ì		MKSSEPSGSLGLSDYSGLQEELQELRERYHFLNEEYRALQESNS
1			SLTGQLADLESERTQRATERWLQSQTLSMTSAESQTSEMDFLEP
			DPEMQLLRQQLRDAEEQMHGMKNKCQELCCELEELQHHRQVSEE
1			EQRRLQRELKCAQNEVLRFQTSHS\SPSHPLPPIPPSSPCLL*A
	1		LVVISALLWCWWAETSS
5884	4261	2522	GVLARASARLRVPLTGVRACAEPEVGAEPAKVAGAAEPDEDGGR
1		•	SRLRDCGDYTPSERLGPKGAMLWFQGAIPAAIATAKRSGAVFVV
•	}		FVAGDDEQSTQMAASWEDDKVTEASSNSFVAIKIDTKSEACLQF
l	1		SQIYPVVCVPSSFFIGDSGIPLEVIAGSVSADELVTRIHKVRQM
ľ	}		HLLKSETSVANGSQSESSVSTPSASFEPNNTCENSQSRNAELCE
i	! !		IPSTSDTKSDTATGGESAGHATSSQEPSGCSDQRPAEDLNIRVE
İ	[ ]		RLTKKLEERREEKRKEEEQREIKKEIERRKTGKEMLDYKRKQEE
l	[		BLTKRMLBERNREKAEDRAARERIKQQIALDRAERAARFAKTKE
	ł l		EVEAAKAAALLAKQAEMEVKRESYARERSTVARIQFRLPDGSSF
ļ	ĺ		TNQFPSDAPLEEARQFAAQTVGNTYGNFSLATMFPRREFTKEDY
1			KKKLLDLELAPSASVVLLP/ALFINF*AGRPTASIVHSSSGDIW
			TLLGTVLYPFLAIWRLISNFLFSNPPPTQTSVRVTSSEPPNPAS
			SSKSEKREPVRKRVLEKRGDDFKKEGKIYRLRTQDDGEDENNTW
			NGNSTQQM
5885	900	467	AAGGGRRSRLSRSWPTGPSKSPSGVRCCG\RR\AWEDKDEFLDV
	1		IYWFRQIIAVVLGVIWGVLPLRGFLGIAGFCLINAGVLYLYFSN
	1		YLQIDEEEYGGTWELTKEGFMTSFA/IVHGHLDHLLHCHPL*LM
			VYSSQVLPIQSKGPS
5886	86	1341	PFRGRALTLKKQPRPGVAPPSLGTCHKSDPGRPAAQSQPPSPGS
	1		GTFGLLSFRMVRTKTWTLKKHFVGYPTNSDFELKTSELPPLKNG
	ļ		EVLLEALFLTVDPYMRVAAKRLKEGDTMMGQQVAKVVESKNVAL
			PKGTIVLASPGWTTHSISDGKDLEKLLTEWPDTIPLSLALGTVG
	ĺ		MPGLTAYFGLLEICGVKGGETVMVNAAAGAVGSVVGQIAKLKGC
	ł		KVVGAVGSDEKVAYLQKLGFDVVFNYKTVESLEETLKKASPDGY
			DCYPDNVGGEFSNTVIGQMKKFGRIAICGAISTYNRTGPLPPGP
			PPEIGIYQELRMEAFVVYRWQGDARQKALKDLLKWVLELPYFVI
			D*LQANTLVYKSMKSAKPSLEYISEKLVSG\KIQYKEYIIEGFE
5887	1937		NMPAAFMGMLKGDNLGKTIVKA
3087	133/	104	APGCRGCRATRCPCRGPRWDSLGDEAARSPAAPGGAPGLLGLRE
			RPDRCHPGGDDRGPQLHRGSPG/SFSELSRRPGPPGLPGLQGPP
	-		PAPGLPQSRTL/PVLCVCDLSPAQCDINCCCDPDCSSVDFSVFS
i			ACSVPVVTGDSQFCSQKAVIYSLMFTANPPQRVFELVDQINPSI
ł	1		FCIHITN\*NLHYPLLIQKYL/NENNFDTLMKTSDGFTLNAESY
ļ	1		VSFTTKLDIPTAAKYEYGVPLQTSDSFLRFPSSLTSSLCTDNNP
i	j	1	AAFLVNQAVKCTRKINLEQCEEIEALSMAFYSSPEILRVPDSRK
	ļ		KVPITVQSIVIQSLNKTLTRREDTDVLQPTLVNAGHFSLCVNVV
	]	ł	LEVKYSLTYTDAGEVTKADLSFVLGTVSSVVVPLQQKFEIHFLQ
	[	ſ	ENTOPVPLSGNPGYVVGLPLAAGFQPHKGSGIIQTTNRYGQLTI
ľ		ł	LHSTTEQDCLALEGVRTPVLFGYTMQSGCKLRLTGALPCQLVAQ
1		-	KVKSLLWGQGFPDYVAPFGNSQGP/ADMLDWVPIHFITQSFNRK
1		j	DSCQLPGALVIEVKWTKYGSLLNPQAKIVNVTANLISSSFPEAN
-		!	SGNERTILISTAVTFVDVSAPAEAGFRAPPAINARLPFNFFFPF
			V

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
į.	to first	amino acid	
Į	amino acid		P=Proline, Q=Glutamine, R=Arginine,
i		residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
5888	375	2302	LLCRTPGVAMQRADSEQPSKRPRCDDSPRTPSNTPSAEADWSPG
1	1	ľ	LELHPDYKTWGPEQVCSFLRRGGFEEPVLLKNIRENEITGALLP
1	Ī		CLDESRFENLGVSSLGERKKLLSYIQRLVQIHVDTMKVINDPIH
1			GHIELHPLLVRIIDTPOFORLRYIKOLGGGYYVFPGASHNRFEH
1		ł	SLGVGYLAGCLVHALGEKQPELQISERDVLCVQIAGLCHDLGHG
1		i	PFSHMFDGRFIPLARPEVKWTHEQGSVMMFEHLINSNGIKPVME
	i	1	QYGLIPEEDICFIKEQIVGPLESPVEDSLWPYKGRPENKSFLYE
1	i	1	IVSNKRNGIDVDKWDYFARDCHHLGIQNNFDYKRFIKFARVCEV
		l	DNELRICARDKEVGNLYDMFHTRNSLHRRAYQHKVGNIIDTMIT
1	1		
l	i		DAFLKADDYIEITGAGGKKYRISTAIDDMEAYTKLTDNIFLEIL
ı	1	ŀ	YSTDPKLKDAREILKQIEYRNLFKYVGETQPTGQIKIKREDYES
1	İ		LPKEVASAKPKVLLDVKLKAEDFIVDVINMDYGMQBKNPIDHVS
1	İ	1	FYCKTAPNRAIRITKNQVSQLLP\EXFAEQ\LIRVYCKKVDRKS
1	1		LYA\ARQYFVQW\CADR\NFT\KPQDGRCY*PPTP*HPQKKGW\
		ł .	NDSTFSPKIPTRLPRRLPKSRV\QLFKDDPM
5889	1831	731	LPAACGRPVTARPRQAPEGRSGRPRDLDPYPPQVFPPRPDRVAI
•			VTGGTDGIGYSTAKHLARLGMHVIIAGNNDSKAKQVVSKIKEET
1			LNDKET*VLLCCPGWLCLWNSSDPPTSASRGAGTTGVHHHFLLK
1	1		FGIFIL\DLASMTSIRQFVQKFKMKKIPLHVLINNAGVMMVPOR
			KTRDGFEEHFGLNYLGHFLLTNLLLDTLKESGSPGHSARVVTVS
1	i i		SATHYVAELNMDDLQSSACYSPHAAYAQSKLALVLFTYHLQRLL
	<b>!</b>		AAEGSHVTANVVDPGVVNTDLYKHVFWATRLAKKLLGWLLFKTP
1	1		DEGAWTSIYAAVTPELEGVGGRYLYNKKETKSLHVTYNOKLOOO
			LWSKSCEMTGVLDVTL
5890	1322	200	FRRGWSAAGRAVPVAFCSRISASSPRRPRGAVRLOSGTEAACRS
1 3030	1 -522	200	GRPDPRPASAAGGHAGERMSQRDTLVHLFAGGCGGTVGAILTCP
į			
i	ĺ		LEVVKTRLQSSSVTLYISEVQLNTMAGASVNRVVSPGPLHCLKV
İ	i i		ILEKEGPRSLFRGLGPNLVGVAPSRAIYFAAYSNCKEKLNDVFD
Į.	<b>[</b>		PDSTQVHMISAAMAGFTAITATNPIWLIKTRLQL*/SQGTAGKR
	Į.		RMGAFECVRKVYQTDGLKGFYRGMSASYAGISETVIHFVIYESI
İ			KQKLLEYKTASTMENDEESVKEASDFVGMMLAAATSK\LVATTI
			AYPHEVVRTRLREEGTKYRSFFQTLSLLVQEEGYGSLYRGLTTH
			LVRQIP\NTAIMMATYELVVYLLNG
5891	1322	200	FRRGWSAAGRAVPVAFCSRISASSPRRPRGAVRLQSGTEAACRS
1 .			GRPDPRPASAAGGHAGERMSQRDTLVHLFAGGCGGTVGAILTCP
1			LEVVKTRLQSSSVTLYISEVQLNTMAGASVNRVVSPGPLHCLKV
1			ILEKEGPRSLFRGLGPNLVGVAPSRAIYFAAYSNCKEKLNDVFD
			PDSTQVHMISAAMAGFTAITATNPIWLIKTRLQL*/SQGTAGKR
1			RMGAFECVRKVYQTDGLKGFYRGMSASYAGISETVIHFVIYESI
1			KQKLLBYKTASTMENDEESVKEASDFVGMMLAAATSK\LVATTI
			AYPHEVVRTRLREEGTKYRSFFQTLSLLVQEEGYGSLYRGLTTH
1			LVRQIP\NTAIMMATYELVVYLLNG
5892	1764	379	VVLRVCGRLSVNSAVSSRTGGWSAGLTCAMORLOVVLGHLRGPA
			DSGWMPQAAPCLSGAPHASAADVVVVHGRRTAICRAGRGGFKDT
1			TPDELLSAVMTAVLKDVNLRPEQLGDICVGNVLQPGAGAIMARI
1			AQFLSDIPETVPLSTVNRQCSSGLQAVASIAGGIRNGSYDIGMA
1			·· —
1	j		CGVESMSLADRGNPGNITSRLMEKEKARDCLIPMGITSENVAER
			FGISREKQDTFALASQQKAARAQSKGCFQAEIVPVTTTVHDDKG
1			TKRSITVTQDEGIRPSTTMEGLAKLKPAFKKDGSTTAGNSSQVS
1	j		DGAAAILLARRSKAEELGLPILGVLRSYAVVGVPPDIMGIGPAY
			AIPVALQKAGLTVSDVDIFEINE\AFASQAAYCVEKLRLPP*EG
			*TPLGGASGP*GHPLGLHWGHVQVITLAQ*S*SARGKRAYRSGC
			PCAIGSWNGSPLPVFEYPWGT
5893	3	1653	ILSKRRCQKAKTKELMAKKVAVIGAGVSGLISLKCCVDEGLEPT
{		. 1	CFERTEDIGGVWRFKENVEDGRASIYQSVVTNTSKEMSCFSDFP
	1		MPEDFPNFLHNSKLLEYFRIFAKKFDLLKYIQFQTTVLSVRKCP
1 1			DFSSSGQWKVVTQSNGKEQSAVFDAVMVCSGHHILPHIPLKSFP
			GMERFKGQYFHSRQYKHPDGFEGKRILVIGMGNLGSDIAVELSK
J f	1		NAAQVFISTRHGTWVMSRISEDGYPWDSVFHTRFRSMLRNVLPR
1	1		TAVKWMIEQOMNRWFNHENYGLEPONKYIMKEPVLNDDVPSRLL
]	į		CGAIKVKSTVKELTETSAIFEDGTVEENIDVIIFATGYSFSFPF
			THE THE TAXABLE PROPERTY OF THE TAXABLE PROPERTY OF THE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
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ĺ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
İ	residue of		
		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	•		LEDSLVKVENNMVSLYKYIFPAHLDKSTLACIGLIQPLGSIFPT
		ļ	AELQARWVTRVFKGLCSLPSERTMMMDIIKRNEKRIDLFGESQS
1		ĺ	QTLQTNYVDYLDELALEIGAKPDFCSLLFKDPKLAVRLYFGPCN
	İ	1	SY*YRLVGPGQWEGARNAIFTQKQRILKPLKTRALKDSSNFSVS
		1	FLLKILGLLAVVVAFF\CQLQWS
5894	174	1673	RYSPKKVLONKESSLKLGMATALVSAHSLAPLNLKKEGLRVVRE
			DHYSTWEQGFKLQGNSKGLGQEPLCKQFRQLRYEETTGPREALS
	1		RLRELCOOWLOPETHTKEHILELLVLEOFLIILPKELOARVOEH
1	1	l .	HPESREDVVVVLEDLQLDLGETGQQVDPDQPKKQKILVEEMAPL
		1	KGVQEQQVRHECEVTKPEKEKGEETRIENGKLIVVTDSCGRVES
1	ł		SGKISEPMEAHNEGSNLERHQAKPKEKIEYKCSEREQRFIQHLD
-	1		LIEHASTHTGKKLCESDVCQSSSLTGHKKVLS*ERKVIQC\HGV
	ļ		LGKAFQRSSHLVRHQKIHLGEKPYQCNECGKVFSQNAGLLEHLR
i			IHTGEKPYLCIHCGKNFRRSSHLNRHQRIHSQEEPCBCKECGKT
1	1		FSQALLLTHHQRIHSHSKSHQCNECGKAFSLTSDLIRHHRIHTG
	1		EKPFKCNICQKAFRLNSHLAQHVRIHNEEKPYQCSECGEAFRQR
L			SGLFQHQRYHHKDKLA
5895	2967	86	HPSLLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE
1	1		MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT
	1		RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW
1			EATELOPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS
İ			RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW
			FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSFA
ł			EGKGLSPIEPESEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ
1	ł i		NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS
i	1		RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA
i			DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD
ł			TVEQLRCEHCARF\LADRFVEGVCFFCGYEEARGDQCDKCGKLI
			NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL
1			1
1	<b>}</b>		PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E
			GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ
ſ	[		FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG
	1		K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA
1			FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV
			LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH
1	[		GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML
1	1		QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP
	}		LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA
]	j i		LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG
			KPPBAPKGKKKK
5896	2967	86	HPSLLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE
Į.			MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT
1			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW
]			EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS
1			RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW
1			FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA
1			BGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ
1			NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS
1			RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA
]			DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD
]			TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI
]			NAVELKKPOCKVCRSCPVVOSSOHLFLDLPKLEKRLEEWLGRTL
į i			PGSDWTPNAOFITPFFGFRENPSKPRWO*TRDLK\WGNPGTP*E
1			
	±	·	GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ
{	ĺ		FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG
1			K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA
1 1			FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV
			LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH
1 .			GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML
1 1			QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP
			LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA

Deginning   nucleotide   location   corresponding   correspo	SEQ	Predicted	Predicted end	l Amino and d
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corresponding to first to first amino acid amino acid sequence service of amino acid sequence	NO:			Glutamia Daid E Phonesia - Deaspartic Acid, E=
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maino acid cesidue of amino acid amino acid amino acid sequence  PATTYPICOPHAN, X-Tyrosine, X-Unknown, *=Stop Codom, /=possible nucleotide deletion, Codom, /=possible nucleotide deletion, Codom, /=possible nucleotide deletion, X-DERADOR COMM, /=possible nucleotide deletion, X-DERADOR COMM, /=possible nucleotide deletion, X-DERADOR COMM, /=possible nucleotide deletion, X-DERADOR COMM, /=possible nucleotide deletion, X-DERADOR COMM, /=possible nucleotide deletion, X-DERADOR COMM, /=possible nucleotide deletion, X-DERADOR COMM, /=possible nucleotide deletion, X-DERADOR COMM, /=possible nucleotide deletion, X-DERADOR COMM, /=possible nucleotide deletion, X-DERADOR COMM, /=possible nucleotide deletion, X-DERADOR COMM, /=possible nucleotide deletion, X-DERADOR COMM, /=possible nucleotide deletion, X-DERADOR COMM, /=possible nucleotide deletion, X-DERADOR COMM, /=possible nucleotide nu	J	corresponding	, -	La Leucine M-Methioning N. America
Segrine, T-Threenine, V-Valine, sequence  sible nucleotide deletion, \_possible nucleotide deletio			amino acid	P=Proline. O=Glutamine P=Arginine
#### #################################		amino acid	residue of	S=Serine, T=Threonine, V=Valine
Sequence    Codon, /=possible nuclectide deletion,    -possible nuclectide insertion    -possible nuclectide insertion     LMDEVINGGRIVEELKAQIKADNEVARLEVAKLIDLKKQLAVAEC     KPERAYKKKKK     KPERAYKKKKK     MELEVBOYRCLEVELANGKARGRAEVILISTVOEPEDCVVPIT     REKVPULQIDSGRYIPFIPPLYLEMSKRESHIPINGGRIGE     RELEVBOYRCLEVELANGKARGRAEVILISTVOEPEDCVVPIT     REKVPULQIDSGRYIPFIPPLYLEMSKRESHIPINGGRIGE     RELEVBOYRCLEVELANGKARGRAEVILISTVOEPEDCVVPIT     REKVPULQIDSGRYIPFIPPLYLVOKKKKE GEVULAR NYLUKGKOPOFPA     RETAIN	İ	residue of	amino acid	Wallytophan Yalvosine Yallytophan taken
Appossible nucleotide insertion	İ		sequence	Codon, /=possible nucleotide deletion
S897  86  HPSLICALPFYPPESSPWEPLLINNSHKKSHFFINGGTIRGE RLEVEDGYGCLPVLAAAGRAGKAULSTVECVUPFLT REXUPULQLDSGMYLPSTSAICRYFFLLISGMEDDLYNGMEN EATELQFTLSAALTYTL/VQGKGKGEVLGSVERTHTHIDHSLS RQ\NCPFLAGSTESLADIVLMGALYPLLQDPAYLPSELSALISW FOTTSTQ\EPCOL AARRILLKOK QGVLIALSVERTLGPGPSPA SGKGLSPISFBEBLATLSEELIAMAVTAWEKGLESLPPLEPG DIYAMENSTYLTLGGTDEYGTATETKAL\ERGLIPGEICKYHIHIHA DIYAMENSTYLTLGGTDEYGTATETKAL\ERGLIPGEICKYHIHIHA DIYAMENSTYLTLGGTDEYGTATETKAL\ERGLIPGEICKYHIHIHA DIYAMENSTYLTLGGTDEYGTATETKAL\ERGLIPGEICKYHIHIHA DIYAMENSTYLTGGTDEYGTATETKAL\ERGLIPGEICKYHIHIHA RAVELKKPQGKYCKGSCVVGSSGMILHILDHELEKELBEMLGRIL RAVELKKPQGKYCKGSCVVGSSGMILHILDHELEKELBEMLGRIL RAVELKKPQGKYCKGSCVVGSSGMILHILDHELEKELBEMLGRIL RAVELKKPQGKYCKGSCVVGSSGMILHILDHELEKELBEMLGRIL RAVELKKPQGKYCKGSCVVGSSGMILHILDHELEKELBEMLGRIL RAVELKKPQGKYCKGSCVVGSSGMILHILDHELEKELBEMLGRIL RAVELKKPQGKYCKGSCVVGSSGMILHILDHELEKELBEMLGRIL RAVELKKPQGKYCKGSCVVGSSGMILHILDHELEKELBEMLGRIL RAVELKKPQGKYCHANADGKAURTGTOMARHAUCHTUNGHLIATEYLINYEDG ARANTYTOMARHAUCHTUNGALTYTCMRRWAWARDGVILYAM RAVELKARDGACHAUCHTUNGALTYTCHANANTALLISMM RAVELKARDGACHAUCHTUNGALTYTCHANANTALLISMM RAVELKARDGACHAUCHTUNGALTYTLANANTALLISMM RAVELKARDGACHAUCHTUNGALTYTLANANTALLISMM RAVELKARDGACHAUCHTUNGALTYTLANANTALLISMM RAVELKARDGACHAUCHTUNGALTYTLANANTALLISMM RAVELKARDGACHAUCHTUNGALTYTLANANTALLISMM RAVELKARDGACHAUCHTUNGALTYTLANANTALLISMM RAVELKARDGACHAUCHTUNGALTYTLANATALLISMM RAVELKARDGACHAUCHTUNGALTYTLANATALLISMM RAVELKARDGACHAUCHTUNGALTYTLANATALLISMATALLISMA RAVELKARDGACHAUCHTUNGALTYTLANATALLISMATALLISMATAL RAVELKARDGACHAUCHTUNGALTYTLANATALLISMA		sequence		\=possible nucleotide insertion)
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NAVELKEPOCKVCRSCPVVGSSORIPELDIPELEKRIEBMLGRTI POSSWITHNAQFITPFFGFREWPSKPRGY*TRUK\\GMPGGTP*E GFEK\\PYVWPDATIGYLSITANDTOWERWW\KNPEQUDLYQ GFEK\\PYVWPDATIGYLSITANDTOWERWW\KNPEQUDLYQ FW\AKONVPFHSUVPPSSALGABNYTU\UVHLIATEYLINYDDG K\FSKSRGVGVPRM\AHDTGTPPISFTYL\LYIPPEK\DSA FEWTDLLKNMS\ELLANLGNPINRA\GMFVSKFGG\YVPEMW LTPDDQRLLA\HVTLELQHYHQ\LLEKYRIRDALBSILITS\RH GNQYI\QVWEPW\KRIKGSEADQRAGTVTGLAWIAALLSVML LFPODQRLLA\HVTLELQHYHQ\LLEKYRIRDALBSILITS\RH GNQYI\QVWEPW\KRIKGSEADQRAGTVTGLAWIAALLSVML LFPODQRLLA\HVTLEQHYHQ\LLEKYRIRDALBSILITS\RH GNQYI\QVWEPW\KRIKGSEADQRAGTVTGLAWIAALLSVML LFPOTLENQITSTALGYPPPSSSPWPPLYLFWNSHKKSRHFINQRGIHGE KPPEAPKGKKKK  HPSLLGAIPFYPPPSSSPWPPPLYLFWNSHKKSRHFINQRGIHGE RATELQPTLSAALYTL\VVQGKKG\EDVLGSVRRTLTHIDHSIS RQ\\CYPLEVAGEREVLITSTALGTYGOPSDEVVPPTJ RPKVPVLOLDGGNVLPFSAICTSTALGTVLGVGRQDDLTNQMLEW RATELQPTLSAALYTL\VVQGKKG\EDVLGSVRRTLTHIDHSIS RQ\\CYPLEVAGERVLITSTALGTVLGWPGAYLFELSALHSW RQ\NCOPLAGERTENLITSTALGTVLGWRGQLENAPHYDE RGKGLSPIEPBEERLATLSEEEIAMAVTAWEKGLESJPPLRPQQ NPULFVAGERVLITSTALGTVLGWRGYLETYLDYBARYS RLEQWNTLYLCGTDEYGTATETKAL\GEGLTPOBICOKYMITHA DIY\RWFNISDIPIGRITTPQQ\KTATTYQA\KNEYQTLQD TVRQLRCHCARVLITSTALTYDQVCRW\KNEYQTLQD TVRQLRCHCARVLITSTALTYDQVCRW\KNEYQTLQC RGKGLSPITPFOQ\KTATTYQQ\KNEYLAWREGQLCKCKGCVC RGCYVYVWFDATIGYUSJTHTYQQTERH\KNEYGCYCRC RGYDK\VFYVWFDATIGYUSJTHTYQCYRRTW\KNEYQTLXYBDG K\FSKSCVGVFRMMAHTGISPITSTYNTDQWRRW\KNEYQTDLYQ K\FSKSSCVGVFRMMAHTGISPITSTRYT\LVSELTATETUNXBDG K\FSKSCLVGVFRMMAHTGISPITSTRYT\LVSELTATETUNXBDG K\FSKSCLVGVFRMMAHTGISPITSTRYT\LVSELTATETUNXBDG K\FSKSCLVGVFRMMAHTGISPITSTRYT\LVSELTATETUNXBDG CROYI\QUMPBW\KRIKSSEADRGRAPTGLANTAALLSWML QPYMFTVSATIQAQLQLPPPACSILLTNRICTLARGGIGTVSP LFOKLENDGITSLARGFGGGGGAKTSPKPAVVTVTTTARPQQTQA LMDEVTKGGNIVREBVKRTAGSEADRGRAPTGLANTAALLSWML QPYMTVSATIQAQLQLPPPACSILLINNEYCTLARNQCICAGANTLANTALLISMUL QPYMTYSATIGAGATAVARCATLSWML TLESRIDLSAAKQMPITMALEGGATNRKFPIT SAMSKABEIDAKAGEEPHICKGRLVQTGRLKHMAFIEQ ENYGGLIDKIVVGGLIRLLERVWINVERSKENGGRIKVSN TLESRIDLSAAKQMPITMALEGGATNRKFPIT KANSTVRNPAHIKVLLARRADLLISHAKHITANDLLCIKE KTANTVRPDYWKLGLARADLLISHAKHITANDLLCIKE KTAN			ŀ	TVEOLRCEHCARF\LADREVEGVCDECGVERADGDOCDVCCVYTT
POSSWITPNACHTIPFFOREWSKYNKOMINGWONTON OFENK_VFYVWRDATIGLSITANTYDEKWN\KNBQUDLYQ PM\AKONVPHSUVPSSALGARDNYTL\USHLIATEYLNYEDG K\FSKRGVUPRWN\AHDGIPPISFYL\LYIPPEGK\DS K\FSKRGVUPRWN\AHDGIPPISFYL\LYIPPEGK\DS K\FSKRGVUPRWN\AHDGIPPISFYL\LYIPPEGK\DS LTPDORILLA\NVTIEE_QHHQ\LEKVRITGALNITALSVML UTPDORILLA\NVTIEE_GHHQ\LEKVRITGALNITALSVML QPYMPTVSATIQAQLQLPPPACSILLINFLCTLPRGHQIGTVSS LFOKLENDQIESLRQRTSGGQAKTSPVALVSTVTAKPQOIQA LMDZVIKQONIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPEAPKGKKK  RPSEALGAIFFYPPESSWPPPLYLFMNSHEKSRHFINGRGIHGE MRLFVSDGYPGCLPVLAAAGRARGRAEVLISTVGEDCVVFPLT RPKVPVLQLDSGNNLFSTSAIGRIFF\LIGGWEGDDLTNGMLEW BATELQPTISAALYTL\VVQGKKG\EDVLGSVRRTTHITHSIS RO\NCPTLAGSTESLADIVLMQALYPLLQDPAYLFEELSALHSW FOTLSTO\EPCGR\AARRIVLKO\QGVIALR\PYLGKQPODSDA BEGKGLSPI EPEERBLATLSEEIJAMAVEKGLESLPPLRPQQ NPVLPVAGERSVLITSALPSVNNVPHLGNIIGCULXGDVPARYS RLRQWNTLYLGCTDEVSTATTETKAL\SEGLITPOBICDXYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TXIT\QDIPQCLXRGFVLQD TVEQLCRCHCARP\LADRVESVCPFCGYEBARGQCDCKCGKLI NAVELKKPQCKVCRSCPVQSSQHLEHDRIEKKLEBWIGETL PGSDMTPHAQPITFFGFREWPSKPRQ*TEDLK\KGNPGTT*E GFEDK\UTVETLATTSTATATULSTANTYDCLYNKAKKGRULD K\FSKSRGVYFDM\AHDTOIPPDISRFYL\LYIRPEGK\DSA K\FSKSRGVYFDM\AHDTOIPPDISRFYL\LYIRPEGK\DSA K\FSKSRGVYFDM\AHDTOIPPDISRFYL\LYIRPEGK\DSA K\FSKSRGVYFDM\AHDTOIPPDISRFYL\LYIRPEGK\DSA K\FSKSRGVYFDM\AHDTOIPPDISRFYL\LYIRPEGK\DSA LNDEVTK\GGNIVEBAKGR\GADKWVAREFQGQXTYGFMAY LYPDDQRLLA\HVTLELGHYQ\LLEKVBIRDLANTALSYML QPYMFTVSATIQAQLQLPPPACSILLINFLCTLEAGGIGTVSP LYGKLENDQIESLR\RGFGGGAXTSFKHADARSILTIS\RH GRYT\CVMEPN\KRIKGGGGAXTSFKHYTGANTALAUSML QPYMFTVSATIGAQLQLPPPACSILLINFLCTLEAGGIGTVSP LYGKLENDQIESLR\RGFGGGAXTSFKHYTGANTALVYENC LNDEVTK\GGNIVEBLKAQKADKMEVAAEVAKLLDLKK\LAVAEG KYPEAPKKKKK NCPERSKEFNGVRAFSLFSFLRAMALSDVDVK\QIKHMAFIEQ ENYGGLIDKLUCQGLIRLLERVMIVGCRP\QDLLUCAAVQKAI TLESRIDLSAK\RWPSITRRQAALKVLARRADLISJLSLAKLLBINGDILKK CGVYYPALPQPMPKSLLPLAVHHHTASKSITCAMQQUEDGIFEI KYANTVORTUYPALVRADHCRSASCYNSKHRYRSJULKLAVLAUCHR KYANTVORTUYNADHCRSASCYNSKHRYSSTORDLKUYND TLESRIDLSAK\RWPSITRRGALKKFLQNFLLKYSLOTAVKLOL KYANTVORTUYNADHCRSASCYNSKHRYSSTORDLKUYND TLESRIDLSAK\RWPSITRRGAL	1	į.		NAVELKKPQCKVCRSCPVVOSSOHLFLDLPKLEKRLEEWIGPTY.
GFEXKVFYWPDATIGYLSITANTOWERWW\KNPEQUDLYQ FM\AKDMVPFHSLUPPSSALGAEDYTI\VSHLIATPELINYEDG K\FSKRGVGVPFMM\AIDTGIPDISFYI\LYIPBGK\DSA FSWTDLILKNINS\ELIKULGNISFYIL\VSHLIATPELINYEDG K\FSKRGVGVPFMM\AIDTGIPDISFYI\LYIPBGK\DSA FSWTDLILKNINS\ELIKULGNISFYEL\KSHKAYBERYGFGG\YVFEMV LTPDDQRLLA\UTTLE:QHHMQ\LLEKVRIRDALRSILTIS\RH GMYYI\QVFEMY\KRIKGSEADRQRAGTYTGLMYAIAALLSVML LFQDQRLLA\UTTLE:QHHMQ\LLEKVRIRDALRSILTIS\RH GMYYI\QVFEMY\KRIKGSEADRQRAGTYTGLMYAIAALLSVML LFQXLENDQIBELRQRFGGGGAKTSPKRAVVETYTTAKFQQIGA KDPSTKGCNIVREIKAGRADKRVEARBVALISTVGFBDCVVPFLIF LFQXLENDQISEGLEPYBFSSPWPPLYLFWNSHRKSRHFINGRGIHGE MRLFVSDGYPGCLPVLAAAGRARGRAEVLISTVGFBDCVVPFLIF RPKVPVLQDLSGNN\LFSTSGICYRFYLGSMCDDLINGWLEW EATELQPTLSAALYTL\VVOGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWQALYPLLQDFXYLFBELSALHSW FOTLSTO\EPCQR\AARRILVLQ\UTTLAGREGDDLINGWLEW EATELQPTLSAALYTL\VVOGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWQALYPLLQDFXYLFBELSALHSW FOTLSTO\EPCQR\AARRILVLQ\UTTLAGREGDDLINGWLEW EATELQPTLSAALYTL\VVOGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWQALYPLLQDFXYLFBELSALHSW FOTLSTO\EPCQRTVALTTSALFYNNOYHEINIGIICCVLSADVPARYS RLKQMNTLYLCGTDEYGTATETKAL\GEGLTPOBECKKYHIHA DIY\RWFNISTDIFGRTTTPQO\KTYTLKGNICCVLSACVPYQSQALLTHGNICCVLSACVPYLOP TVSQLRCEHCARF\LADRFVESVCPFCGVERRAGOQCCKCKGILI NAPUSKKPCCVCRSCOVYQSQALLTHGNICCVLSACVPYLOP PGSBWYPHAQPITPFFGFEWPSXPRO*TRDLK\KGNPGTF*E GFSBK\VYTVWFDATIGYLSITANYTDQWERW\KREGVTLO FM\AKDNVPFSLVFPSSALGAEDNYTLVSHLIKATEXHYDG K\FSKSRCVGYFRDM\AHDTGIPPDISRYTL\LVIREGK\DSA K\FSKSRCVGYFRDM\AHDTGIPPDISRYTL\LVIREGK\DSA K\FSKSRCVGYFRDM\AHDTGIPPDISRYTL\LVIREGK\DSA K\FSKSRCVGYFRDM\AHDTGIPPDISRYTL\LVIREGK\DSA K\FSKSRCVGYFRDM\AHDTGIPPDISRYTL\LVIREGK\DSA K\FSKSRCVGYFRDM\AHDTGIPPDISRYTL\LVIREGK\DSA K\FSKSRCVGYFRDM\AHDTGIPPDISRYTL\LVIREGK\DSA K\FSKSRCVGFRGGGAXTSKERFRQVTYTTAKPQQIQA LMDEVTKGGIIVERLAQADALSAALLLASIVEND CKYLLISTITANYTDQUERVK\CLSAVLAGEGATINGKTETQ LLMBETTKGGIIVERLAQADALSAALLLASIVEND TLESRLDLSAKKOMPETRMALFGCATNIKFFI  KYANTORPDYWIKSLERALDLSAKHARISTICHHHRACHILKHHRACHILK KYANTORPDYWIKGHLARADDLICHE KYANTORPDYWIKGHLARADDLICHE KYANTORPDYWIKGHLARADDLICHE KYANTORPD			ł	PGSDWTPNAQFITPFFGFREWPSKPRWO*TRDLK\WGNPGTP*R
PM\AKONVPFISLVPPSSALGAEDNYTL\USHLIATEYLAYEDG  K\FSKRGUVUPRGM\AIDTGIT pPSGYL\DSA FSWTDLLLKNNS\ELLINLGMFINRA\CMFVSKPFGG\YVDEMV LTPDOGELLA\HYTLELGHYHG\\LLEKVRIRDALRSILITS\RH GNQYI\QVNEPBW\KRIKGSEADRQRAGTYTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLINELCTLPRGRQIGTVSP LFQCKLENDQIESLRGCRAFTGGAANTAKPQQIQA LMDSVTKQGNIVRELKAQKADKWEVAREVAKILDLKKQLAVAEG KPPSAPKGKKKK  KPPSAPKGKKKK  RPSLLGAIPFYPPPSSPWPPPLYLFWNSHKKSRHFINGRGIHGE MRLSVSDGVPGLPULAAAGRARGAEVLISTVGBEDCVVPPLT RPKVPVLQLDSGNYLFSTSAICRYPF\LLSWNEDDLTNQMLEW RASSOGVPGLPVDFLAAAGRARGAEVLISTVGBEDCVVPPLT RPKVPVLQLDSGNYLFSTSAICRYPF\LLSWNEDDLTNQMLEW GRALSPIFSERSADIVLWGALYPLLQPPAYLFELSALHSW FQTISTQ\EPCQR\AARRLVLKQ\QQVLALK\PYLQRQPQSPSA EGKALSPIFSERSADIVLWGALYPLLQPPAYLFELSALHSW FQTISTQ\EPCQR\AARRLVLKQ\QQVLALK\PYLQRQPQSPSA EGKALSPIFSERSADIVLWGALYPLLQPPAYLFELSALHSW FQTISTQ\EPCQR\AARRLVLKQ\QQVLALK\PYLQRQPQSPSA REKUNTILYLGCTBSTATTSREIXAMTWRKGLESIPPLRPQO NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVPARYS RLQWNTLYLLGCTBYGTATTETAL,EGLTPQBELOXHYII HAD DIY\RWFNISPDIFGRTTTPQQ\TXIT\QDIFQQLXRGFVLQD TVPQLCEHCARF\LADRFVCGVCVCSSQHLFLDLFRELEEWLGRTL PGSDWTPRAQFITFFFOFREWSERPRQ*TEDLK\RGNPGTF*E GFBK\VYTVVWFDAITGYLSITATUT\USERVM\CNNGTT*E GFBK\VYTVVWFDAITGYLSITATUT\USERVM\CNNGTT*E GFBK\VYTVVWFDAITGYLSITATUT\USERVM\CNNGTT*E GFBK\VYTVVWFDAITGYLSITATUT\USERVM\CNNGTT*E GFBK\VYTVVWFDAITGYLSITATUT\USERVM\CNNGTT*E GFBK\VYTVVWFDAITGYLSITATUT\USERVM\CNNGTT*E GFBK\VYTVVWFDAITGYLSITATUT\USERVM\CNNGTT*E GFBK\VYTVVWFDAITGYLSITATUT\USERVM\CNNGTT*E GFBK\VTVVYFDAITGYLSITATUT\USERVM\CNNGTT*E GFBK\VTVYFDAITGYLLAHVT\USERVM\CNNGTT*E GFBK\VTVYFDAITGYLLAHVT\USERVM\CNNGTT\USERVM\CNNGTT*E GFBK\VTVYFDAITGYLLAHVT\USERVM\CNNGTT\USERVM\				GFEDK\VFYVWFDATIGYLSITANYTDOWERWW\KNPEOVDLYO
FSWIDLLKNINS\ELINBLGNFINRA\GMFUSKFFGG\YUPEMV LTPDOGRLIA\HTLEGHYHQ\LTPLGTHYBQLTUTS\RIN GNQYI\QVREPW\KRIKGSRADRQRAGTUTGLAVNIAALLSYML QPYMPTVSATIQAQLQLPPPACSILITR\LTPLATHAGOIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVETYTTAKPQQIQA LMDEVTKQRNIVRELKAQKADKWEVAREWAKILDLKKQLAVARG KPESAPKGKKKK  RPESAPKGKKKK  HPSILGAIFYPFPSSPWPPPLYLFWNSHRKSRHFINGGGIHGE MRLFVSDGVPGCLPVLAAAGRARGREVLISTVGPEDCVVPPLT RPKVPVLQLDSGNYLFSTSAICEYPF\LLSGWGDDDITNOMLEW ARGUNGPTLSAALTYL\VVQGKKGVULGSVRRTLTHIDHSLS RO\\CPPLAGETESLADIVLMGALYPLLQDPAYLPEELSALHSW FOTLSTO\EPCQR\ARRILLKQ\GQVLALK\PYLGQPQPSPA EGKGLSPIFPEEESLADIVLMGALYPLLQDPAYLPEELSALHSW RLGWMTLYLGGTESVATMSTEKLFLSBEIAMATWAKGLESLFPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLQWMTLYLGGTESVATTAFTEKLFLSBEIAMATWAKGLESLFPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLQWMTLYLGGTESVATTAFTEKLFLSBEIAMATWAKGLESLFPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLQWMTLYLGGTESVATTAFTEKLFLSBEIAMFULKY RLGWMTLYLGGTESVATTAFTEKLFLSBEIAMFUNGTULD TVRQLECHCARF\LARGFVGSYCGSYBARGQQCDKCGKLI NAVELKKPQCXVCRSCPVQSSQHLFLDLFRCLERRLERHIGRTL PGSDMTFNAGFITPFFGFREWSERPRWG\TTDLK\KGNRGTTF*E GFSDK\VFYVWFDATIGVISTIATNTDQWERW\KNRGTESVHQFT FM\AKUNVPFISLVFPSSALGAEDMYTL\VSHLIATEYLNYEDG K\FSKSRCGVFFRM\AHDTG\PPSFYL\L\XINTEGK\LDSHL\ K\FSKSRCGVFFRM\AHDTG\PPSFYL\L\XINTEGK\LDSHL\XINTEGHYL\XINTEGK\ GNQYI\QVNEPW\KRIKGSEADRGATGVTGLAVNIAALLSUML QPYMPTVSATIQAQLQLPPPACSILLITNFLCTLPAGGIGTVVSP LDFQKLENDQIESLRGFGGGGAXTSPKAVVETVTTRKQQIQA LDDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKQLAVAEG KPPEAPKKKK  CQKXILMSTMRQARIKVLRARNDLISDLLSEAKURLSRIUED BVYGGLLDKLULOGLLRLLEPVMTVCREPQDLLKMYEKKEQIE QVXILLMSTMRQARIKVLRARNDLISDLLSEAKURLSRIUED BVYGGLLDKLULOGLLRLLEPVMTVCREPQOLLEVEAAVQKAI FSYMTISCHUEV\QIDKAFALKAGRADTWRELSHLHSRLQDLLK KAARGBEGLEFFCEGCGVSSHLDGERMWFRLSHLHSRLQDLLK KAARGBEGLEFFCEGCGVSSHLDGERMYRLSHLHSRLQDLLK KYANTVARFYDVURLRDHCRSASCVNSKTIGRGBLTDASVDLCIKR KYNTVARFYDVURLRDHCRSASCVNSKTIGRGBLTDASVDLCIKR KYNTVARFYDVURLRDHCRSASCVNSKTIGRGBLTDASVDLCIKR KYNTVARFYDVURLRDHCRSASCVNSKTIGRGBLTDASVDLCIKR KYNTVARFYDVURLRDHCRSASCVNSKTIGRGBLTDASVDLCIKR KYNTVARFYDVURLRDHCRSASC				FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLTATEVLNVEDG
LTPDORELA\HTTLEIGHYO\LEKURIRDALRSILITS\RH GNQVI\QVNEBW\KRIKGSEADRGAGTATUGLAVUNTAALLSVML QPYMPTVSATIQAQLQLPPACSILLTNFLCTLPAGHQITVSP LFQKLENDQIESLEXGRFGGGAXTSPKPAVVETVTTAKEQQIQA KPESARGKKK KPESARGKKKK  FPESARGKKKK  APSLICATIFYPPPSSPWPPPLYLFWNSHRKSRHFINGRGIHGE MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVOPBDCVVPPLT RPKVPVLQLDSGNVLFSTRAICFPYLLSGNEDDDLTNQMLEW EATELQPTLSAALYYL\VVQKKKG\EDVLGSVRRTLTHDHSLS RO\NCPFLAGETESLADVLWGALYPLLQPAYLFBELSALHSW FOTISTO\PPCQR\AARRULKQ\QGVLARK\PYLGKQPOPSPA BGKSLSPIFPEEBLATLSEESIAMAVTAAGKGLESLPPLRQQ NPVLPVAGERNVLITSAAPVUNPLGNIIGCUSADVPARVS RLRQWNILVLGCTDEYGTATETKAL\EGGITPQBLCDKYHIIHA DIY\RWPNISPDIFGRTTTPQQ\TXIT\QDLKEKRLEKBULGRTL DIV\RWPNISPDIFFGTRENFRQ\TTC\DIFQULKRGFVLQD TVEQLRCEHCARF\LADRFVEGVPFGYBEARGOCOKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLKLEKRLEKBLGRTL GFBDK\VFYVWEDATIGLISITANYTDQWERW\KNPEQVDLYQ FM\AKINVPFHSLAVPPSSALGAEDNYTL\VSHLIATETLNVEDG K\FSKSRGVGVFRDM\AHDTGIPDLISRFYL\LYTRPBGK\DSA FSWTDLLKNNS\ELLNNLGNFINRA\GWFUSKFTGG\YVDEMV LTPDDQRLLA\HUTVLELQHHYQ\LLEKVRIDALBSILTIS\RH GRQYI\QVNEPW\KRIKGSRDRQRAGTYTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLINNELCTLPAGFQIGTVSP LFGKLENDQLESLRQRFGGGQAKTSPKPAVVETVTTARPQQIQA LMDEVTKQGNIVRBLKAQRADKNEVAABVAKLLDLKKQLAVAGE KPPEAPKKKKK NCPESKEPNOYAPSLLSCHVQTQRLKMENYEKKEKQIE QQKKLLMSTMENQARLKVLRANDLISDLLSGAKURISRIVEDD EVYQGLLDKLVQICKEALAVECSWEVWEVYSKOKKVEN TLESSLDLSAKQKMPBIRMALFGANTINKFII SAARGEBDAKKAREDDAKRAEBPNIEKGRUQTQRLKMENYEKKEKQIE QQKKLLMSTMENQARLKVLRANDLISDLLSGAKURISRIVEDD EVYQGLLDKLVQICKEALAVECSWEVWEVYSKOKKVEN TLESSLDLSAKQKMPBIRMALFGANTINKFII KAARGEDGEGEFGEFCLVSSHDLJGREMWYHELSHLHSBRLQDLLK CGVYYPALPQDPNFKSLLPLAVHHHTASKSLTCAWQQHEDHFEL KYANTVMR FDYVWLRHDGCNSASCYNSKTHGRLHGSRLQDFRIL KYANTVMR FDYVWLRHDGCNSASCYNSKTHGRLHGSRLDFREIL KYANTVMR FDYVWLRHDGCNSASCYNSKTHGRLHGSRLDFREIL KYANTVMR FDYVWLRHDGCNSASCYNSKTHGRLDFREILYGRIVGRUNDYPRIL LWNAEIYQQQVPSUCQSFLETINGSLKKFQNGVLYQPRI LWNAEIYQQQVPSUCQSFLETINGSLKKFQNGVLYQPRI LWNAEIYQQQVPSTDGCSFREDTAYTKLA	i		ı	K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA
GNOYT (QVNBEW) KRIKGSEADRQRAGTYTULAVNIALLSVMI.  QPYMPTVSATIQA(LOLPPPACSILLITHICLTLAGHQIGTUS) LFOKLENDOIESLRQRFGGGAKTSPKBAVVETVTTAKPQQIQA LMDZVYKOGNIVYBEKAKKAKDKNEVAAEVAKILDLKKQLAVAEG KPPEAPKGKKKK  HPSILGAIPFYPEPSSPWPPPLYLFWNSHRKSRHFINGRGIHGE RGLYSUGDVGGUPVLANAGRARGRAEVLISTVOPEDCVVPPLT RPKVPVLQLDSGNYLFSTSAIGTYFF\LLSGNEQDDLTNQWLEW ARLFYSDGVYGGLPVLANAGRARGRAEVLISTVOPEDCVVPPLT RPKVPVLQLDSGNYLFSTSAIGTYFF\LLSGNEQDDLTNQWLEW FOTLSTQ\FPCQR\ARRIVLKQ\QGWLAUR\PYLQKQPOSPA RGKGLSPIPPEEBELATLSEELFAMTYAKGKLESIPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVPARYS RLRQWNTLYLCGTBEYGTATETKALLEGLIPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVPARYS RLRQWNTLYLGGTBEYGTATETGQ\TKKIT\QDIFQGLXRGFVLQD TVEQLRCERCAFF\LADRFVEGVCPFGGYRBARGQCCNCGKLI NAVELKKPQCKVCRSCPVVQSSQHIFLDLPKLEKKLBSVLGRTL PGSDWTFNAQFITPFFGFREWPSKPRNO*TRDLK\WGNPGIP*E GFSDK\VFYVWFDATIGYLSITANYTUPERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\LYSHLATEYLNVEDG K\FSKSRGUVGFND\ARDGTIPPDIGRFWI\LYSHLATEYLNVEDG K\FSKSRGUVGFND\ARDGTIPPDIGRFWI\LYSHLATEYLNVEDG K\FSKSRGUVGFND\ARDGTIPPDIGRFWI\LYSHLATEYLNVEDG K\FSKSRGUVGFND\ARDGTIPPDIGRFWI\LYSHLATEYLNVEDG K\FSKSRGUVGFND\ARDGTIPPDIGRFWI\LYSHLATEYLNVEDG K\FSKSRGUVGFND\ARDGTIPPDIGRFWI\LYSHLATEYLNVEDG K\FSKSRGUVGFND\ARDGTIPPDIGRFWI\LYSHLATEYLNYBDG K\FSKSRGUVGFND\ARDGTIPPDIGRFWI\LYSHLATEYLNYBGG K\FSKSRGUVGFND\ARDGTIPPDIGRFYIL\LYTTREGK\DSA PSWTDLLLKNNS\GGGGGAKTSFKPAVVSTVTTAKPQOIQA LDBEVTYGGNIVTRSIKAQKADKNEVAREVAKLLDLKKQLAVAEG KPPEAPKGKKKK  PPEAPKGKKKK  NCPKKEFNGVRAFSLFSPLRAMALSDUVKKQIKHMMAFIEQ EANNEKABEIDAKABEEPNIEKGRLVQTGRLKIMEYYEKEKGQIE QVKKILMSTMNOARLSVLRARNDLTSDLLSEAKLRJSRTVEDD EYVGGLIDKLIVLQLIKLEFVNICRP\QDLLKVEAN PEYMTISOKHVEV\QIDKAB*LAVEGNETWYRISHHSRLGDLLK GGVYYPALFQONFKSLLPLAVHWHITASKSLTCAWQOHEDHFEL KXANTVMRFDVYWLRDHCRSASCYNSKTHORSLDTASVOLCIRR KTIRLDETTLFFWPDGHTKKLUGNIVKNSYEGGKGKVIQPRI LWRBEIVQOAQVPSUCOSFIETINBGLKKFLQNFLLYGIPPAL	ł			FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV
GPYMPTVSATIGAQLOLPPPACSILLITMFLCTLPAGHQIGTUSPS LFQKLENDQIESLEQRFEGGGATSPERAVVETUTAKPQQIQA LMDZVTKQGNIVRELKAQKADKNEVAAEVAKI,LDLKKQLAVAEG KPPEAPKGKKK  S898 2967 86 HPSILGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVOPBDCVVPPLT RPKVPVLQLDISGNVLFSTSAI CFPF\LLSGNEQDDLTNQMLEW RPKVPVLQDLSGNVLFSTSAI CFF\LLSGNEQDDLTNQMLEW RPKVPVLQDLSGNVLFSTSAI CFF\LLSGNEQDDLTNQMLEW RPKVPVLQDLSGNVLFSTSAI CHQPAYLFEELSALHSW RQ\NCCPFLAGETTSLADIVLWGALYPLLQPAYLFEELSALHSW RQ\NCCPFLAGETSLADIVLWGALYPLLQPAYLFEELSALHSW RQ\NCCPFLAGETSLADIVLWGALYPLUGNCDPSPA BGKSLSPI EPEEERLATISEE IAMAVTAWEKGLESL PPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNI IGCVLSADVFARYS RLRQWNTLYLCGTDBYGTATETKAL\CEGGLTPQEICDKYHI IHA DIY\RWFNISFDIFGRTTTPQQ\TXIT\QDIFQXLKRGFVLQD TVSQLKCEHCARF\LADRFVSCPGYBEARGQCDXCGKLI NAVELKEPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGGKL PGSDWTPNAQFITPFFGYFEEPSERPRQ*TNDLK\WGNPGTF*E GFBDK\VFVWFDATIGYLSITANYTOWERWW\NFPESUDLYQ FM\AKDNVPFHSLVPPSSALGAEDNYTL\VSHLLATEYLNYEDG K\FSKSCGVGVFRDM\AHDTGIPPSIRFYL\LYHTPEGK\DSA K\FSKSCGVGVFRDM\AHDTGIPPSIRFYL\LYHTPEGK\DSA K\FSKSCGVGVFRDM\AHDTGIPPSIRFYL\LYHTPEGK\DSA K\FSKSCGVGVFRDM\AHDTGIPPSIRFYL\LYHTPEGK\DSA LTPDDQRLLA\HVTLEQHHQ\LLEKVBIRDALBSILTIS\RH GNCYI \QVNEPW\KRIKGSBARGATYTGLKWIAALLSUML QPYMPTVSATIQAQLQLPPPACSILLITNFLCTLPAGHQIGTVSP LFQKLENDQIESLRQRFGGGQATTSFKPAVVSTVTTARPQOIQA KPPEAPKGKKKK QQXXLLMSTMNQARLKVLRARNDLISULLKQLAVAEG KPPEAPKGKKKK  SPEAPKGKKKK  SPEAPKGKKKK  CQXXLMSTMNQARLKVLRARNDLISULLKQLAVAEG KPPEAPKGKKKK  NCPKSKEENGVFADSLEBPIRGAMMALSDUDVKKQIKHMMAFIEQ EANEKAEEIDAKAEEEPNIEKGRLVQTQRLKKGLKVSN TLESRLDLSAKQNDEIRMALFGANTINKFFI  SANEKAEEIDAKAEEPNIEKGRLVQTQRLKKEYEKKEQIE GCYYTPALFQONFKSLDFLAVHWHITAGKSLTCAWQOHEDHFEL KXANTVARPDYVAURDHCRSASCYNSKTHQRSLDTASVULCIKP KTIRLDETTLFFTWPDGHTKLAGHCANKTHQRSULDIKGQKKVLQPRI LWNAEIVQAQVPSUDCOSFTETNISGLKKFQUFLLYGIUTGILK KXANTVARPDYVAURDHCRSASCYNSKTHQRSLDTASVULCIKP KTIRLDETTLFFTWPDGHTKLARRIGULTKGUNYTTSGREGGTAYTKLA				GNOVI OWNERWY PROCESS PROPERTY OF THE CHARGE TO THE CHARGE
LFOKLENDQIESLRORFGGGGAKTSPRPAVVETVITAKFQQIQA LMDZVTKQGNIVREIKAQKADKNEVAABVAKILDLKKQLAVAEG KPPZAPKSKKKK  HPSLLGAIFFYPPDSSPWPPDLYLFWNSHRKSRHFINORGIHGE MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGGEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNEGODLTNQMLEW ARLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGGEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNEGODLTNQMLEW FOTLSTQ\EPGCARAYYI\VVQGK\G\EDUGSVRFTLTHIDHSLS RQ\NCPFLAGETSSLADIVLMGALYPLLQDFAYLFELSALHSW FOTLSTQ\EPGCARAYYI\VVQGVALRK\PYLQKOPQDSPA RGKGLSPIFPEBELATLESETIAMAVTAWEKGLESIPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLLGGTDGYSTATKAL\EBGLTPOEICDKYHIIHA DIY\RWFNISPDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCAFF\LADRFVEGVCPFCGYERARGDQCKCGKLI NAAVELKKPQCKVCRSGPVVGSSQHLFLDIPKLEKRLEBWLGRTL PGSDWTPNAQFTTPFFGFREWSSKPRNQ*TRDLK\MGNPGTP*E GFBLX\VFYVWFDATIGYLSTATYTDQWERWW\KNPEQVDLYQ FM\AKNNVPFHSLVPPSSALGAENNYTL\VSHLIATEYLNYEDG K\FSKSRGGVSVFRDM\AHNTGIPPDISFYI\LYIRPBGK\DSA FSWTDLLLKNNS*LELINNIGNFINRA\GMFVSKFFGG\YVVEMV LTPDDQRLLA\HVTLELGHYHQ\LLEKYIRDALRSILTIS\RH GNQYI\QVMEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQIQLDFPPACSILLTNFLCTLFAGEGIGTVSP LFQKLENDQIESLRQRFGGGGAKTSPKPAVVETVITAKPQQIQA LMDEVTKQGNIVRELKAQKADKNEVAABEVAKLLDLKKQLAVABG KPPEAPKGKKKK OCPKSKEPNGVRAFSLFSPLRAMALSDUDVKKQIKHMMAFIEQ QKKILMSTMRNQARLKVLRARNDLISDLSEAKLRISRIVEDD EVYGGLIDKLVLQGLIRLLEPWITYGCRP\QDLLLVEAAVOKAI PEYMTISQKHVEV\QIDKEA*LAVECSWEVWEYYSGNQRKVSN TLESRLDLSARQNOPEIHMALFGANTMKFFI SANSKABEIDAARGEPHIERGRLQQTQRLKIMSYYEKKEKQIE GGVIYPALPQONFKSLLPLAVHWHTLSHLHIBRLQDLLK KYANTVRRFDYWLQGLRLLBEPMITYGRNDTASSUDLCIKR KYANTVRRFDYWLRDHCRSASCYNSKTHQRSLDTASVDLCIKR KTIRLDETTLFFTWPDGHTYKKYDLNWYRTSSGGQCKVQRRI LWNAEIYQQAQVPSVDCQSFLETNEGLKKFLQNFLLIGTAFVEN VPPTGEHTEKLABRISLIRETISGREDHINGERGDFRGGGRKYTQRRI LWNAEIYQQAQVPSVDCQSFLETNEGLKKFLQNFLLYGTAFVEN VPPTGEHTEKLABRISLIRETISGRENYFTGRGGDFRGGDFRGFRGCHXTQTAFVEN VPPTGEHTEKLABRISLIRETISGREDFRGFRGFRGFRGFRGFRGFRGFRGFRGFRGFRGFRGFRGF	1			OPYMPTVSATIONOLOLDEDACSILLTMEN OF DAGGOTOR
S898  2967  86  HPSLIGAT PFYPPSSPWPPLYLFNNSHRKSRHFINQRGTHGE MRLFYSDGYPGCLPYLAAAGRARGRAGTAVULSTVUEPDCVYPFLT RPKYPVLQLDSGYVLSTSSTATICKYFY\LLSGWEDDCVYPFLT RPKYPVLQLDSGYVLSTSATICKYFY\LLSGWEDDCVTPPLT RPKYPVLQLDSGYVLSTSATICKYFY\LLSGWEDDCVTQWLEW EATELQPTLSRALYTL\VVQGKKG\EDVLGSVRFTLTHIDHSLS RQ\NCPFLAGETSLADIVLWGALYPLLQDFAYLPEELSALHSW FOTLSTQ\EPCQR\AARRLVLKQ\GGVLALR\PYTLQDFAYLPEELSALHSW FOTLSTQ\EPCQR\AARRLVLKQ\GGVLALR\PYTLQKQPQPSPA EGKKLSPIFPEEERLATLEEESIAMAVTAWEKGLESIPPLRPQQ NPVLPVAGERUNVITSALPVYPHICMICGVLSADVYPARYS RLRQWNTLYLCGTDEYGTATTETKAL\EBGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TXIT\QDIFQCLLKRGFVLQD TVEQLRCEHCARF\LADRYCGVCPFCGYBERRGPQCKXCKGLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEREWLGRTL PGSDWTPNAQFTTPPFGFPEEWPKRPWQ*TRDLK\WGNPGTI**E GFEDK\VFYVWFDATIGYLSTANTYDCWERW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDMYTL\VSHLIATEVLNYEDG K\FSKSRGVGVSFDM\AHDTGIPDISFYL\VITREGK\DSA K\FSKSRGVGVSFDM\AHDTGIPDISFYL\VITREGK\DSA K\FSKSRGVGVSFDM\AHDTGIPDISFYL\VITREGK\DSA K\FSKSRGVGVSFDM\AHDTGIPDISFYL\VITREGK\DSA K\FSKSRGVGVSFDM\AHDTGIPDISFYL\VITREGK\DSA CRQYI\QVMEPY\KRIKGSEADRQRAGTYTGLAVNIAALLSVML QPYMFVSATIQAOLQJPPACSILLITHFLCTLPAGFGIGTVSP LFOKLENDQIESLRQRFGGGGAKTSPKPAVVVETVTTAKPQOIQA LMDEVTKQGNIVRBLKAQKADKNEVAABVAKLLDLKKQLAVAGE KPPEAPKGKKKK  OCKYLKGNIVRBLKAQKADKNEVAABVAKLLDLKKQLAVAGE KPPEAPKGKKKK  OCKYLKGNIVRBLKAQKADKNEVAARALLSDLVKKGIKHMAFIQ ENYGGLLDKLVLQCLIRLLEPUTVCRP\QDLLLVEAAVQKAI PSYMTISGKHVEV\QIDKEA*LAVECSFEWWYYSGNQRIKVSN TLESSLDLSAKQKMPEIRMALFGANTNKFFI  SAMERAEBIDAKAEBIDAKACHPHTASKSLTCAWQOHEDHFEL KYANTVKFPYVWIRDHCRSASCVNKTTHQRSLDTASVDLCIKK KYANTVKFPYVWIRDHCRSASCVNKTTHQRSLDTASVDLCIKK KYANTVKFPYVWIRDHCRSASCVNKTTHQRSLDTASVDLCIKK KTIRLDETTLFFTWPDGHVTKYDLINUKNSYSGQCKYVQRRI LWNAEIYQQAQVPSVDCQSFLETMEGLKKFLONFLLYGIAFVEN VPPTGEHTEKLARBISLIRTIYGRMWYFTSDFRGDTAYTKLA				LFQKLENDOIESLRORFGGGOAKTSPKPAUVETUTTA VECCION
S898  2967  86  HPSALGATPFYPPSSDWPPPLYLFWNSHRKSRHFINGRGIHGE MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEGDDLTNQWLEW EATELQFTLSAAALYYL\VVQKK\SUVGSVRFTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDFAYLFELSAHSW FOTLSTQ\FEBERLATLSEBIAMAVTAWEGLESLPPLERQDL RGKGLSDIFPEBERLATLSEBIAMAVTAWEGLESLPPLERQDL RGKGLSDIFPEBERLATLSEBIAMAVTAWEGLESLPPLERQDL NPVLPVAGERNVLITSALPYVNNVPHLGNIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EGGLTPGBLTCDKYHIIHA DIY\RWNISFDIFGRTTTPQQ\TKIT\QDIPQCLKRGFVLQD TVRQLRCGHCARF\LADRFVEGVCPFCGYBEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHIFLDLPKLEKRLBEWLGRTL PGSDWTPNAQFITPFFGFREWBSKPRMQ*TRDLK\WGNPGTP*E GFBDK\VFTVWFDATIGYLSITANTYDOWERWN\KNPEQVDLYQ FM\AKNOVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LITREGK\DSA FFWHTOLLKNNS\ELLNNLGHFINRA\GMFYSKFFGG\YVPEMV LTPDDQRLLA\HVTLEQGHYHQ\LLEKVRIRDALBSILTIS\RH GNQYI\QVMEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQFPAGSILLTHFLCTLPAGFGIGTVSP GNGYI\QVMEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQFPAGSILLTHFLCTLPAGFGIGTVSP LFCKLENDQLISSLRQRFGGGGGKTSPKPAVVETVTTAKPQOIQA LMDEVTKQONIVRELKAQKADKNEVAAEVAKLLDLKKQLAVABG KPPEAPKGKKKK  SPEYMTISKHVEV\QIDKEA*LAVECSWEWWEYSGNGIKKVSN TLESSLDLSAKQKMPEIRMALFGANTNRKFFI FYYMGLLDKLHVQCGLLELLEPVMIVRCRP\QDLLLVEAAVGKAI FEYMTISKHVEV\QIDKEA*LAVECSWEWWEYSGNGIKKVSN TLESSLDLSAKQKMPEIRMALFGANTNRKFFI GGVIYPALPQPNFKSLLPLAVHWHHTASKSLTCAWQOHEDHFFL KYANTVMFFDYWILDHCRASTONSKHTHGRSLDTASVDLCIKK KTIRLDETTLFFTWPDGHVTKYDLNWVRRJCHTSRUDTASVDLCIKK KTIRLDETTLFFTWPDGHVTKYDLNWVRNSYEGQRQKVQRRI LWNAEIYQQAQVPSVDCQSFLETNEGLKKRJONFLLYGIAFVEN VPPTOEHTEKLARGRISLIRETIGGMWYTKSPRGROTTKLA	i		•	LMDEVTKQGNIVRELKAQKADKNEVAARVAKIJDIKKOLAVARG
MRI-VSGSVPGCLPVILAAGRARGRAEVLISTVGEBDCVVPELT RPKVPVLQLDSGNYLFSTSAICRYEF\LLSGNEQDDLTNQWLEW RPKVPVLQLDSGNYLFSTSAICRYEF\LLSGNEQDDLTNQWLEW RPKVPVLQLDSGNYLFSTSAICRYEF\LLSGNEQDDLTNQWLEW RPKVPVLQLDSGNYLFSTSAICRYEF\LLSGNEQDDLTNQWLEW RPKVPVLQLDSGNYLFSTSAICRYEF\LLSGNEQDDLTNQWLEW RPKVPVLQLDSGNYLFSTSAICRYEF\LLSGNEQDDLTNQWLEW RPKVPVLQLDSGNYLFSTSAICRYEF\LLSGNEQDDLTNQWLEW RPKVPVLQLDSGNYLFSTSAICRYEF\LLSGNEQDDLTNQWLEW RPKVPVLQLDSGNYLFSTSAICRYEF\LLSGNEQDDLTNQWLEW RPOLLSGNEGSTSLAINVLKQ\QQVLALR\PYLQKQDQPSPA EGKELSPIEPBERLATLSEETIMAWTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNYPHLGNIIGCVLSADVFRRYS RLRQWNTLYLCGTDEYGTATETKAL\EGGITPQBICDKYHIIHA DIIY\RWENISPDIEPGRTTTQQ\XXIY\DIFQGLKREFVLQD TVRQLRCEHCARF\LADRFVEGVCPFCGYBEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVGSQRHILDLEKLERLBEWLGRTI PGSDWTPNAQFITPFFGFRWPSRPRQCTDLEK\RUMPGTP*E GFBDK\VFYVWFDAITGYLSITANYTDOWERWN\KNPEQVDLYQ FM\AKDNVPHSLVFPSSAIGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVSVFRDM\AHDTGIPPDISRFT\\YVTIPAGK\DISP\CHAP\CHAP\CHAP\CHAP\CHAP\CHAP\CHAP\CHA	Fano			KPPEAPKGKKKK
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		L		LDRHTDTTYFQEPCGIQVFHCLKHEGTGGRTLLVDGFYAAEQVL

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
		1	QKAPEEFELLSKSAI\KHEYIEDVGECHQPHDWDWAQS*ISTHG
1		ľ	/YKELYLIRYNNYDRAVINTVPYDVVHRWYTAHRTLTIELRRPE
1			NEFWVKLKPGRVLFIDNWRVLHGRECFTGYRQLCGCYLTRDDVL
			NTARLLGLQA
5901	1	2121	VAIEQTSLKMMQAVGGAPARPTGEYICNQCGAKYTSLDSFQTHL
			KTHLDTVLPKLTCPQCNKEFPNQESLLKHVTIHFMITSTYYICE
1			SCDKQFTSVDDLQKHLLDMHTFVFFRCTLCQEVFDSKVSIQLHL
ľ			\AVKHSNEKKVYRCTSCNWDFRNETDLQLHVKHNHLENQGKVHK
			CIFCGESFGTEVELQCHITTHSKKYNCKFCSKAFHAIILLEKHL
			REKHCVFETKTPNCGTNGASEQVQKEEVELQTLLTNSQESHNSH
			DGSEEDVDTSEPMYGCDICGAAYTMETLLQNHQLRDHNIRPGES
•			AIVKKKAELIKGNYKCNVCSRTFFSENGLREHMQTHLGPVKHYM
			CPICGERFPSLLTLTEHKVTHSKSLDTGNCRICKMPLOSEEBFL
			EHCQMHPDLRNSLTGFRCVVCMQTVTSTLELKIHGTFHMOKTGN
			GSAVQTTGRGQHVQKLYKCASCLKEFRSKQDLVKLDINGLPYGL
j			CAGCVNLSKSASPGINVPPGTNRPGLGQNENLSAIEGKGKVCGL
İ			KTRCS*LATFKF*VLKVELPEPHPKPFHRGVSRPDSNSTOLKTP
			QVSPMPRISPSQSDEKKTYQCIKCQMVFYNEWDIQVHVANHMID
] ;			EGLNHECKLCSQTFDSPAKLQCHLIEHSFEGMGGTFKCPVCFTV
1			FVQANKLQQHIFSAHGQEDKIYDCTQCPQKFFFQTELQNHTMTQ
5902	712	200	HSS
3302	1 /12	209	LKNRRRSRPSIRQSIGSTSVSRWLTSLFTYLDHTADVQ*V*REF
			IPLXPRQ*ED*MFQSWLHAWGDTLEEAFEQCAMAMFGYMTDTGT
1 1			VEPLQTVEVETQGDDLQSLLFHFLDEWLYKFSADEFFIP\GWGE
5903	2106	735	BFSLSKHPQGTEVKAITYSAMQVYNEENPEVFVIIDI
1000		133	DTPGPSLPSTTAPFSLRSLSFPSRPSYLLPGDPQPLQGRGLPTT
			PALFALSAVPGGAASPMPPSGLRLLPLLLPLLWLLVLTPGRPAA GLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGEVPPGP
			LPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVET
1.			HNEIYDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRL
			KLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEWLSFDVTGVV
]			RQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFTTGR\RGDL
1 1	1		ATIHGMNRPFLLLMATPLERAQHLQS\SRHRQAL\DTNY\CFSF
1 1	]		HGGRNCLRC/VHC*HLIFRKDL\GW\KWI\HE\PKGYHANFC\L
1			GPCPYIWSLDTQYSKVLALYNQ\HKPG\ASAAP\CCVPQALEP\
			LPIVYY\VGRKPKVEQLSNMIVRSCKCS
5904	3	1126	MMEETENAINTFKEEQRLIYEELIKEEKTTNNELSAISRKIDTW
			ALGNSETEKAPRAISSKVPVDKVTPSTLPEEVLDFEKFLOOTGG
1	İ		RQGAWDDYDHQNFVKVRNKHKGKPTFMEEVLEHLPGKTODEVOO
1 1			HEKWYQKFLALEERKKESIQIWKTKKQQKREEIFKLKEKADNTP
1			VLFHNKQEDNQKQKEEQRKKQKLAVEAWKKOKSIEMSMKCASOL
1 1			KEEEEKEKKHQKERQRQFKLKLLLESYTOOKKEOEEFLRLEKEI
1 [			REKAEKAEKRKNAADEISRFQERDLHKLELKILDROAKEDEKSO
1			KQRRLAKLKEKVENNVSRDPSRLY/NTHQRLGRTNQKDRTNRLW
5905			ATSTYPT*GYSNLETRNTEKSMR
3,03	287	2912	MASFPPRVNEKEIVRLRTIGELLAPAAPFDKKCGRENWTVAFAP
1 1	1		DGSYFAWSQGHRTVKLVPWSQCLQNFLLHGTKNVTNSSSLRLPR
1			QNSDGGQKNKPREHIIDCGDIVWSLAFGSSVPEKQSRCVNIEWH
1		i	RFRFGQDQLLLATGLNSGRIKIWDVYTGKLLLNLVDHTGVVRDL
		i	TFAPDGSLILVSASRDKTLRVWDLRDDGN\MMKVLRGHQNWVY\
[ ]	1	İ	SCAFSPDSSMLCSVGASKAVVAAILV*LRLCWHHSHTGATMVLS
	1		WAERVASLATGLGATFTIG*SNLAFVLQGVLYVHRCWSMSTFCF
]		j	SFFLFFFFKVISPTVKYH*LLSKLIFQFYGIGSLTSETNLM*SI
1 1			WLSNGFSVLFFGILSDSRDILRL*FNLKFVLIFF*K*CIVSVQK
1			KKKPKRIALLQEERLS*DKPPSSHLI*QTEVNIRILFRAILHS*
]	į	l	LLIFRI*NCI*TYS*IIDPFYIQMTYDRG*FGKNKMVKF*FIEM *LYYFHKIAFSFCNVV*HPCCLPKKFHLAVNILFACSICFSS*A
} i	1	ľ	QVGDPSLL*TSDYLKGRCQWSNNLLTLRFLSVYFFKNLVVSGKK
}			REGGL*YLTLFISVYFS*LVFGINGFQYSFVVKLHCLYFMFRLI
	ļ		FKLTFNRNI*NRICMSALINLKTDFNLTMTLSIFFKLLIIYNA*
			YNLN*I*QF*YKMCHFVLCMSE*SYNICLFIAGF\LWNMDKYTM

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
	beginning		
ID		nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
		sequence	
	sequence	<u> </u>	\=possible nucleotide insertion) .
-	İ		IRKLEGHHHDVVACDFSPDGALLATASYDTRVYIWDPHNGDILM
1	1	İ	EFGHLFPPPTPIFAGGANDRWVRSVSFSHDGLHVASLADDKMVR
İ	i		FWRIDEDYPVQVAPLSNGLCCAFSTDGSVLAAGTHDGSVYFWAT
1	1	1	PROVPSLQHLCRMSIRRVMPTQEVQELPIPSKLLEFLSYRI
5906	146	2038	REGAGSGRMASGA\YNPYIEIIEOPRORGMRFRYKCEGRSAGSI
1 3300	140	2030	
1			PGEHSTDNNRTYPSIQIMNYYGKGKV\RITLVTK\NDPYKPHPH
i			DLVGKDCRD\GYYEAEFGQE\RRP\LFFQN\LGIRCVKKKEVKE
1	1	ł	A\IITR\IKAGINPFDVP*KQLNDIEDCDLDVVRLWFRVFLPDG
]	1		HGNL\TTALPPV\VSSPIYDNRAPNTAELRVCRVNKNCGSVRGG
	i		DEIFLLCDKVQKDDIEVRFVLNDWEAKGIFSQADVHRQVAIVFK
	ŀ		
1			TPPYCKAITEPVTVKMQLRRPSDQEVSESMDFRYLPDEKDTYGN
İ			KAKKQKTTLLFQKLCQDHVETGFRHVDQDGLELLTSGDPPTLAS
1	1		QSAGITVNFPERPRPGLLGSIGEGRYFKKEPNLFSHDAVVREMP
		1	TGVSSQAESYYPSPGPISSGLSHHASMAPLPSSSWSSVAHPTPR
	1		SGNTNPLSSFSTRTLPSNSQGIPPFLRIPVGNDLNASNACIYNN
	!		ADDIVGMEASSMPSADLYGISDPNMLSNCSVNMMTTSSDSMGET
1	i		DNPRLLSMNLENPSCNSVLDPRDLRQLHQMSSSSMSAGANSNTT
	1		VFVSQSDAFEGSDFSCADNSMINESGPSNSTNPNSHVFVODSQY
1			SGIGSMONEQLSDSFPYEFFOV
5007			
5907	99	1873	TYLLSSWSS**NLDTKIKSQVKV/RKGHKKISWPYPQPAKQNGK
	j		KATSKVPSAPHFVHPNDHANREAELKKKWVEEMREKQQAAREQE
			RQKRRTIESYCQDVLRRQEEFEHKEEVLQELNMFPQLDDEATRK
i			AYYKEFRKVVEYSDVILEVLDARDPLGCRCFQMEEAVLRAQGNK
1		}	KLVLVLNKIDLVPKEVVEKWLDYLRNELPTVAFKASTOHOVKNL
1	1		NRCSVPVDQASESLLKSKACFGABNLMRVLGNYCRLGEVRTHIR
			VGVVGLPNVGKSSLINSLKRSRACSVGAVPGITKFMQEVYLDKF
i			· · · · · · · · · · · · · · · · · · ·
			IRLLDAPGIVPGPNSEVGTILRNCVHVQKLADPVTPVETILQRC
			NLBEISNYYGVSGFQTTEHFLTAVAHRLGKKKKGGLYSQEQAAK
1	J		AVLADWVSGKISFYIPPPATHTLPTHLSAEIVKEMTEVFDIEDT
1			EQANEDTMECLATGESDELLGDTDPLEMEIKLLHSPMTKIADAI
i .			ENKTTVYKIGDLTGYCTNPNRHQMGWAKRNVDHRPKSNSMVDVC
1			SVDRRSVLQRIMETDPLQQGQALASALKNKKKMQKRADKIASKL
			SDSMMSALDLSGNADDGVGD
5908	247	975	HCGIKKRGEGSGSPSPASGGFOLGCQIPEPSLPSEEETHPHTRA
****		2.3	
			HTRTLRATLTRRPPRSHSTRLRFPMPLDGDGGLASWK/PMRER*
1 ' '			GWRRPAKAAGASLGVAATGKRGCRMSKRYLQKATKGKLLIIIFI
1			VTLWGKVVSSANHHKAHHVKTGTCEVVALHRCCNKNKIEERSQT
1	]		VKCSCFPGQVAGTTRAAPSCVDASIVEQKWWCHMQPCLEGEECK
1			VLPDRKGWSCSSGNKVKTTRVTH
5909	1	5002	PATPGSTIIWAPGSHSAARADGRHGSLPSOSOAPGALCGARAPP
'	[	,	SSNLRADRSMICAQARAGKNLYHNRFLGLAAMAFPSRNSQSLRR
			CKEPIRYSYNPDOFHNMDLRGGPHDGVTIPRSTSDTDLVTSDSR
]			STLMGRSSYYSIGHSQDLVIHWDIKEEVDAGDWIGMYLIDEVLS
			ENFLDYKNRGVNGSHRGQIIWKIDASSYFVEPETKICFKYYHGV
1			SGALRATTPSVTVKNSAAPIFKSIGADETVQGQGSRRLISFSLS
1			DFQAMGLKKGMFFNPDPYLKISIQPGKHSIFPALPHHGQERRSK
1			IIGNTVNPIWQAEQFSFVSLPTDVLEIEVKDKFAKSRPIIKRFL
		1	GKLSMPVQRLLERHAIGDRVVSYTLGRRLPTDHVSGQLQFRFEI
1			TSSIHPDDEEISLSTEPESAQIQDSPMNNLMESGSGEPRSEAPE
] ]			SSESWKPEQLGEGSVPDRPGNOSIELSRPAEEAAVITEAGDOGM
] [			
]			VSVGPEGAGELLAQVQKDIQPAPSAEELAEQLDLGEEASALLLE
			DGEAPASTKEEPLEEEATTQSRAGREEBEKEQEEEGDVSTLEQG
ļ .	Į.		EGRLQLRASVKRKSRPCSLPVSELETVIASACGDPETPRTHYIR
			IHTLLHSMPSAQGGSAAEEEDGAEEESTLKDSSEKDGLSEVDTV
, i			AADPSALEEDREEPEGATPGTAHPGHSGGHFPSLANGAAQDGDT
			HPSTGSESDSSPRQGGDHSCEGCDASCCSPSCYSSSCYSTSCYS
			SSCYSASCYSPSCYNGNRFASHTRFSSVDSAKISESTVFSSODD
, 1			
j 1			EEEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER
			SPEGLESPVAGPSNRREGECPILHNSQPVSQLPSLRPEHHHYPT
			IDEPLPPNWEARIDSHGRVFYVDHVNRTTTWQRPTAAATPDGMR
<u> </u>		İ	RSGSIQQMEQLNRRYQNIQRTIATBRSEEDSGSQSCEQAPAGGG
	<del></del>		

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	U-Vistiding Total angles W. Yari
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	i	L=Leucine, M=Methionine, N=Asparagine,
1		amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ŀ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence	1	\=possible nucleotide insertion)
			GGGGSDSEABSSQSSLDLRREGSLSPVNSQKITLLLQSPAVKFI
j			TNPEFFTVLHANYSAYRVFTSSTCLKHMILKVRRDARNFERYQH
1	ĺ	[	NRDLVNFINMFADTRLELPRGWEIKTDQQGKSFFVDHNSRATTF
1	!		
ł	ļ	l ·	IDPRIPLONGRLPNHLTHROHLORLRSYSAGEASEVSRNRGASL
			LARPGHSLVAAIRSQHQHESLPLAYNDKIVAFLRQPNIFEMLQE
1	į.	1	RQPSLARNHTLREKIHYIRTEGNHGLEKLSCDADLVILLSLFEE
			EIMSYVPLQAAFHPGYSFSPRCSPCSSPQNSPGLQRASARAPSP
ļ	1	l	YRRDFEAKLRNFYRKLEAKGFGQGPGKIKLIIRRDHLLEGTFNQ
	1	i	VMAYSRKELQRNKLYVTFVGEEGLDYSGPSREFFFLLSQELFNP
ļ	ļ		YYGLFEYSANDTYTVQISPMSAFVENHLEWFRFSGRILG\LALI
	i	ł	HQYLLDAFFT\RPFYKALL\RLPC\D\LSDLEYLDEEFHQSLQW
			MKDNNITDILDLTFTVNEEVFGQVTERELKSGGANTQVTEKNKK
1	ł		EYIERMVKWRVERGVVQQTEALVRGFYEVVDSRLVSVFDARELE
I	1		LVIAGTAEIDLNDWRNNTEYRGGYHDGHLVIRWFWAAVERFNNE
ĺ	i		QRLRLLQFVTGTSSVPYEGFAAPPWEPMGLRRFLP*KKWGKITS
_			LPPRG\HTCLQPDWDLPTVSPRTPMLYEK\LLTA\VEETSTFGT
5910	1526	446	VAEFAAMEPGRTQIKLDPRYTADLLEVLKTNYGIPSACFSQPPT
1	1		AAQLLRALGPVELALTSILTLLALGSIAIFLEDAVYLYKNTLCP
1			IKRRTLLWKSSAPTVVSVLCCFGLWIPRSLVLVEMTITSFYAVC
			EVIIMIMM/PCPCCVPANTEM PROPROMETERS CONTROL
Į.	}		FYLLMLVMVEGFGGKEAVLRTLRDTPMMVHTGPCCCCCPCCPRL
	1		LLTRKKLQ\R*CWALSNTPS*R*R*PWWACFSSPTASMTQQTFL
1	1		RGAÇLYGSTLSSA/CSTLLALWTLGIISRQARLHLGEQNMGAKF
1			ALFQVLLILTALQPSIFSVLANGGQIACSPPYSSKTRSQVMNCH
1	i i		LLILETFLMTVLTRMYYRRKDHKVGYETFSSPDLDLNLKALRWM
<u> </u>			AWTMKGCCTH
5911	109	595	QDPLAPCIQGKGLEMRSPKPQSFIIRSSHSGAGLLVKNPSTPVF
			CGHRRGGAAFKYKPTPVVGPEQRPTGQKHMRGGVSLLSPRLECS
1			GTISAHCNLRLPSSSNSPAPAS*LAGITGVCHHAQLIFVFLVET
			GFHHVGQAGLELL/NVVIHLPRPPKVLGLQA
5912	924	277	MILNKALMLGALALTTVMSPCGGEDIVADHVASYGVNLYQSYGP
			SGQYSHEFDGDEEFYVDLERKETVWQLPLFRRFRRFDPQFALTN
1 .	l		IAVLKHNLNIVIKRSNSTAATNEVPEVTVFSKSPVTLGQPNTLI
l i			CLVDNIFPPVVNITWLSNGHSVTEGVSETRPSSPKSDHFILQDQ
			VTSPSFPFE**DL*TAKVEQLGAWFEPLLKHWGAEIPTTL
5913	46	1198	QLRMAGAEGAAGRQSELEPVVSLVDVLEEDEELENEACAVLGGS
		4630	DSEKCSYSQGSVKRQALYACSTCTPEGEEPAGICLACSYECHGS
1 1			
			HKLFELYTKRNFRCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN
1	1		FFGLYCICKRPYPDPEDEIPDEMIQCVVCEDWFHGRHLGAIPPE
1	]		SGDFQEMVCQACMKRCSFLWAYAAQLAVTKIST\GMMDWCGTLM
1 1	. 1	·	E*/DDQEVIKPENGEHQDSTLKEDVPEQGKDDVREVKVEQNSRP
] !	1		CAGSSSESDLQTVFKNESLNAESKSGCKLQELKAKQLIKKDTAT
1	1		YWPLNWRSKLCTCQDCMKMYGDLDVLFLTDEYDTVLAYENKGKI
F 501			AQATORSDPLMDTLSSMNRVQQVELIC/GIQ*FED
5914	960	124	NLGGSELPPEEALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN
1	• 1		ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG
] [			GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS
1 1	į		IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE
<u> </u>			SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP
1 1	1		KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH
1 <i>i</i>	1		PHRHLPGLCRPAATS
5915	1604	703	FPGRPTRPLKLGRRRKRARI IQAPHCHSPRPRTCPPGALQAPEA
1 1			PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT
			PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS
<u> </u>		1	
		ļ	KPPPGFSGLLPSPHP\PVSPAPPPPPPQK/RPRLLPAP/PGLPS
] [	,		PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS
F			PVLQELPGPAGGEFPEGL**AAGPAAH
. 5916	256	633	SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR
j 1			TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH
<u> </u>			PTRLILQ*NQATADKNN*TTALLQPHQRL\VSPRMAEA
5917	1343	827	AHQILTYLEP/ICLVVNYNKILTVFLTKSVLEI*KFIHTPQTYR

PCT/US00/34263 WO 01/53312

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
i	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
-	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			F*NDFFGIKEVYVSRRLRKTSF/RLAVTFLEQAVVSKECVPVDQ
l			FMEHLLPSLLSLASDPVPNVRVLLAKALRQMLLEKAYFRNAGNP
			HLEVIEETILALQSDRDQDVSFFAALEPKRRNIIDTAVLEKQN
5918	13	1247	EGAQVARRRSRRQWRAGRCGRGRGGRRAERTGGRGPPGRPRPLP
į		ļ	PGPARRGRRRMETPFYGDEALSGLGGGASGSGGTFASPGRLFPG
1			APPTAAAGSMMKKDALTLSLSEQVAAALKPAPAPASYPPA\ADG
1			APSAAPPDGLLASPDLGLLKLASPELERLIIQSNGLVTTTPTSS
1			QFLYPKVAASEEQEFAEGFVKALEDLHKQNQLGAGRAAAAAAA
			AGGPSGTATGSAPPGELAPAAAAPEAPVYA\NLSSY\AGGCRGL
			RGGAAT\VAFAAEPVPFPPPPPPGALGPRRP/RLALQGRRPQTV
			PDVP\SFGESP\PLSPIET\DTPRRI\KAKRKRL\RNPQIRAPK
1 1			PASRKLGAQSRALERESEDPS*SPEHGSLASTASLLREQVAQLK
70.0			QKVLSHVNSGCQLLPQHQVPAY
5919	1	4254	TSVQGDSQGTPTSSQGSINMRHWISQAIHGSTTSTTSSSSTQSG
1 1			GSGAAHRLADVMAQTHIENHSAPPDVTTYTSEHSIQVERPQGST
, I			GSRTAPKYGNAELMETGDGVPVSSRVSAKIQQLVNTLKRPKRPP
			LREFFVDDFEELLEVQQPDPNQPKPEGAQMLAMRGEQLGVVTNW PPSLEAALQRWGTISPKAPCLTTMDTNGKPLYILTYGKLWTRSM
			KVAYSILHKLGTKOEPMVRPGDRVALVFPNNDPAAFMAAFYGCL
			LAEVVPVPIEVPLTRKDAGSQQIGFLLGSCGVTVALTSDACHKG
!!!			LPKSPTGEIPQFKGWPKLLWFVTESKHLSKPPRDWF\PHIKDAN
			NDTAYIEYKTCK\DGSVLGVTVTRTALLTHCQALTQACGYTEAE
1 1			TIVNVLDFKKDVGLWHGILTSVMNMMHVISIPYSLMKVNPLSWI
			QKVCQYKAKVACVKSRDMHWALVAHRDORDINLSSLRMLIVADG
1 1	Ì		ANPWSISSCDAFLNVFQSKGLRQEVICPCASSPEALTVAIRRPT
			DDSNQPPGRGVLSMHGLTYGVIRVDSEEKLSVLTVQDVGLVMPG
1			AIMCSVKPDGVPQLCRTDEIGELCVCAVATGTSYYGLSGMTKNT
! )	Į		PEVFAMTSSGAPISEYPFIRTGLLGFVGPGGLVFVVGKMDGLMV
}			VSGRRHNADDIVATALAVEPMKFVYRGRIAVFSVTVLHDERIVI
1 1			VAEQRPDSTEEDSFQWMSRVLQAIDSIHQVGVYCLALVPANTLP
}			KTPLGGIHLSETKQLFLEGSLHPCNVLMCPHTCVTNLPKPRQKQ
1			PEIGPASVMVGNLVSGKRIAQASGRDLGQIEDNDQARKFLFLSE
] [			VLQWRAQTTPDHILYTLLNCRGAIANSLTCVQLHKRAEKIAVML
] ]			MERGHLQDGDHVALVYPPGIDLIAAFYGCLYAGCVPITVRPPHP
1 1			CNIATTLPTVKMIVEVSRSACLMTTQLICKLLRSREAAAAVDVR
1			TWPLILDTDD*PKKRPAQICKPCNPDTLAYLDFSVSTTGMLAGV
1 1			KMSHAATSAFCRSIKLQCELYPSREVAICLDPYCGLGFVLWCLC
i !			SVYSGHQSILIPPSELETNPALWLLAVSQYKVRDTFCSYSVMEL
ł i			CTKGLGSQTESLKARGLDLSRVRTCVVVABERPRIALTQSFSKL FKDLGLHPRAVSTSFGCRVNLAICLQGTSGPDPTTVYVDMRALR
i i			HDRVRLVERGSPHSLPLMESGKILPGVRIIIANPETKGPLGDSH
; 1			LGEIWVHSAHNASGYFTIYGDESLOSDHFNSRLSFGDTOTIWAR
		-	TGYLGFLRRTELTDANGERHDALYVVGALDEAMELRGMRYHPID
			IETSVIRAHKSVTECAVFTWTNLLVVVVELDGSEQEALDLVPLV
]			TNVVLEEHYLIVGVVVVVDIGVIPINSRGEKQRMHLRDGFLADQ
!!	1		LDPIYVAYNM
5920	1381	1499	QLGAVAHAGVSRIPP+LFPPLHPTFLSLWCLHHKLP/HPPGASM
j l	1	ļ	VRPPVVPRRPPAHISSVRQASTQVPRTVPHTQRVANIGTQTTGP
{	l		SGVGCCTPGRPLLPCKCSSAAHSTYRVQEPAVHIPGQEPLTASM
	ĺ	ļ	LAAAPLHEQKQMIGERLYPLIHDVHTQLAGKITGMLLEIDNSEL
			LLMLESPESLHAKIDEAVAVLQAHQAMEQPKAYMH
5921	727	157	VCPGTGGE*GLWGQLGGLPKETPLKPMDAFTGSGLKRKFDDVDV
			GSSVSNSDDEISSSDSADSCDSLNPPTTASFTPTSILKRQKQLR
	ł		RKNVRFDQVTVYYFARRQGFTSVPSQGGSSLGMAQRHNSVRSYT
		. 1	LCEFAQEQEVNHREILREHLKEEKLHAKKMKLTKNGTVESVEAD
1	1		GLTLDDVSDEDIDVENVEVDDYFFLQPLPTKRRRALLRASGVHR
			IDAEEKQELRAIRLSREECGCDCRLYCDPEACACSQAGIKCQVD
	ļ		RMSFPCGCSRDGCGNMAGRIEFNPIRVRTHYLHTIMKLELESKR
	1		Q\GAAQQPQ\*GALPDCQLQPDRSTGL*DPSWIGSKGLSFTGKG
5023	2425	405	AAATHLIILRVIENRGAEGKRK
5922	2475	495	SYSNWGLFPSVFIQVPRSRTGNLKPIFLFYSYYE\CMETLKG\T
			401

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	l .	Whichiding T. Taplouring, Gaglycine,
İ	•	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ŀ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	!	\=possible nucleotide insertion)
			CLYNATQYKVCSPRNDRPDACYNPSEPAATTVFEIRTGLLLGDT
1			SKIITRTBEKEIPKQITLRFDACAAINSKKLEIGCGSLN*ERS*
Ì	1		RVENKYVCHESGVCKNCAYWPCVI*AT*KKNKNDSVYLQKGEAN
1	i	ļ	
ì	ì		PSCAAGHCNPLELIITNPLDPHWKKGERVTLGINRTGLKPQVVI
			LIKGEVHKCSPKPVFQTFYEELNLPAPELLKKTKNLFLQLAENV
	ŀ		IFLLNGTSCYVRGGTTIGDRWPWEA*ELVPTDPAPDIIPI*KAE
j			ASNF*VLKTSIIRQYCIAREGKDFIIPVGKPNCIGQKLYNSTTK
1			TIT**DLNHTEKNPFSKFSKLKTA*AHAESH*DWTVPSGLY*IC
	i		RHRAYFRLPNKWADSCVIGTIKPSFFLLPIKMGELLGFSVYASR
}			EKKGIVIGNWKDNEWPRERIIQYYGPATWAQDGSWGYR/TP/VY
	j i		MLNWIIRLQAILEIISNETGRALTVLAWQETQMRNAIYQNRLAL
	i		DYLLVAEGGVCRKFNLTNCCLQINDQGQVVKNIVRDMTKLAHVP
1			IQVWHKFDPESLFGKWFPAIGGFKTLIVGVLLVIRTCLLLPCVL
İ	(		PLLFQMIKGIVATLVHQKTSAHVNYMNHYRSISQRDSKSEDESE
1	<u> </u>		NSH
5923	137	638	
3323	137	936	QLCGRRGQRFRTSIKRMHPI*RTCPNTNL/IILLSQENTQIRDL
			QQENRELWISLEEHQDALELIMSKYRKQMLQLMVAKKAVDAEPV
		•	LKAHQSHSAEIESQIDRICEMGEVMRKAVQVDDDQFCKIQEKLA
			QLELENKELRELLSISSESLQARKENSMDTASQAIK
5924	274	2146	EKGKVKDAGAEQWISLSLSCKGSWETQFSNHLNSLTPPTSVRRM
			PLITTVTLLKMVARHHMKLLCSKAFSTQLQQKIFLHSQMGIHHQ
			SVCMKLKPNTSHIISILMGQPMALVQLETLAPLTIIIQKFQTQD
			HMKFWKNLPLHSHHLTPSVPQTVIPKKTGSPEIKLKITKTIONG
1			RELFESSLCGDLLNEVQASE\Q*NQSIESRKEKRKKSNKHDSSR
1			SEERKSHKIPKLEPEEQNRPNERVDTVSEKPREEPVLKEGSPSS
			ANTIFCSNNGSVHW\FKFQVGDLVWSKVGTYFWWPCMVSSDPOL
	i		
1			EVHTKINTRGAREYHVQFFSNQPERAWVHEKRVREYKGHKQYEE
1			LLAEATKQASNHSEKQKIRKPRPQRERAQWDIGIAHAEKALKMT
1			REERIEQYTFIYIDKQPEEALSQAKKSVASKTEVKKTRRPRSVL
1 1			NTQPEQTNAGEVASSLSSTEIRRHSQRRHTSAEEEEPPPVKIAW
1			KTAAARKSLPASITMHKGSLDLQKCNMSPVVKIEQVFALQNATG
			DGKFIDQFVYSTKGIGNKTEISVRGQDRLIISTPNQRNEKPTQS
			VSSPEATSGSTGSVEKKQQRRSIRTRSESEKSTEVVPKKKIKKE
			QVGFLHVES
5925	216	1911	MMTAESREATGLSPQAAQEKDGIVIVKVEEEDEEDHMWGQDSTL
1			QDTPPPDPEIFRQRFRRFCYQNTFGPREALSRLKELCHQWLRPE
1 1	1		INTREQILELLVLEQFLSILPKELOVWLQEYRPDSGEEAVTLLE
1 1			DLELDLSGQQVFGQVHGPEMLARGMVPLDPVQESSSFDLHHEAT
]		:	QSHFKHSSRKPRLLQSRALPAAHIPAPPHEGSPRDQAMASALFT
1 1			ADSQAMVKIEDMAVSLILEEWGCQNLARRNLSRDNRQENYGSAF
į l		İ	PQGGENRNENEESTSKAETSEDSASRGETTGRSQKEFGEKRDQE
	ļ		
<u> </u>			GKTGERQQKNPEEKTRKEKRDSGPAIGKDKKTITGERGPREKGK
1 1			GLGRSFSLSSNFTTPEEVPTGTKSHRCDECGKCFTRSSSLIRHK
j			IIHTGEKPYECSECGKAF\SLNS\NLVLHQRI\HTGEKPHECNE
	1		CGKAFSHSSNLILHQRIHSGEKPYECNECGKAFSQSSD\LTKHQ
1	1		RIHTGEKPYECSECGKAFNRNSYLILHRRVHTREKPYKCTKCGK
I			\AFTRSSTLTLHHRIHARERASEYSPASLDAFGAFLKSCV
5926	2	233	DRCLMLKQGSQPGSPPAT/CEPPAPPVYQAPCQSCPEPPGAHEP
			SDSPHHTPVHPPPEHSAACPAPATCCPPPRSSMS
5927	4146	1248	KHFSKFGSQALYQLKRPASGONSISVMPAQKITKPAAKYGIPLA
-	1.5		
1	ŀ		YKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR
1 1	į		KRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREQG
	ì	ļ	WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQ
1 1		l	MQQQRAEDNEAKWKREIYGRGLPERQKGQLAVERAKQVEEFLQR
j 1			KREAMQNKARAEGHMGILQNLAAMYGGRPSSSRGGKPRNKEEEV
[		i	YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM
, 1		İ	RRKK\IESLKAHANARAAVLKEQLERKRKEAYEREKKVWEEHLV
	·	]	AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS
		ł	SLTDTRETSEEMQKTNNAISSKREILRRLNENLKAQEDEKGKQN
]	1		LSDTFEINVHEDAKEHBKEKSVSSDRKKWEAGGQLVIPLDELTL
1			DTSFSTTERHTVGEVIKLGPNGSPRRAWGKSPTDSVLKILGEAE
<u> </u>			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1			LQLQTELLENTTIRSEISPEGEKYKPLITGEKKVQCISHEINPS
1			AIVDSPVETKSPEFSEASPQMSLKLEGNLEEPDDLETEILQEPS
Į.			GTNKDE\SLPCTITDVWISEEKETKETQSADRITIQENEVSEDG
į			VSSTVDQLSDIHIEPGTNDSQHSKCDVDKSVQPEPFFHKVVHSE
İ			HLNLVPQVQSVQCSPEESFAFRSHSHLPPKNKNKNSLLIGLSTG LFDANNPKMLRTCSLPDLSKLFRTLMDVPTVGDVRQDNLEIDEI
ļ	ļ		EDENIKEGPSDSEDIVFEETDTDLQELQASMEQLLREQPGEEYS
1			EEEESVLKNSDVEPTANGTDVADEDDNPSSESALNEEWHSDNSD
ŀ			GEIASECECDSVFNHLEELRLHLEQEMGFEKFFEVYEKIKAIHE
			DEDENIEICSKIVQNILGNEHQHLYAKILHLVMADGAYQEDNDE
5928	4146	1248	KHFSKFGSQALYQLKRPASGQNSISVMPAQKITKPAAKYGIPLA
1			YKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR
1	į į		KRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREQG
			WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQ
1			MQQQRAEDNEAKWKREIYGRGLPERQKGQLAVERAKQVEEFLQR
1			KREAMQNKARAEGHMGILQNLAAMYGGRPSSSRGKPRNKEEEV
			YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM RRKK\IESLKAHANARAAVLKEQLERKRKEAYEREKKVWEEHLV
1			AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS
			SLTDTRETSEEMQKTNNAISSKREILRRLNENLKAQEDEKGKQN
1			LSDTFEINVHEDAKEHEKEKSVSSDRKKWEAGGQLVIPLDELTL
1			DTSFSTTERHTVGEVIKLGPNGSPRRAWGKSPTDSVLKILGEAE
			LQLQTELLENTTIRSEISPEGEKYKPLITGEKKVQCISHEINPS
1			AIVDSPVETKSPEFSEASPQMSLKLEGNLEEPDDLETEILQEPS
į į			GTNKDE\SLPCTITDVWISEEKETKETQSADRITIQENBVSEDG
1			VSSTVDQLSDIHIEPGTNDSQHSKCDVDKSVQPEPFFHKVVHSE HLNLVPQVQSVQCSPEESFAFRSHSHLPPKNKNKNSLLIGLSTG
1			LFDANNPKMLRTCSLPDLSKLFRTLMDVPTVGDVRQDNLEIDEI
]			EDENIKEGPSDSEDIVFEETDTDLQELQASMEQLLREQPGEEYS
			EEEESVLKNSDVEPTANGTDVADEDDNPSSESALNEEWHSDNSD
] [			GEIASECECDSVFNHLEELRLHLEQEMGFEKFFEVYEKIKAIHE
5020			DEDENIEICSKIVQNILGNEHQHLYAKILHLVMADGAYQEDNDE
5929	3	1558	LDFSMTTQLPAYVAILLFYVSRASCQDTFTAAVYEHAAILPNAT
			LTPVSREEALALMNRNLDILEGAITSAADQGAHIIVTPEDAIYG
			WNFNRDSLYPYLEDIPDPEVNWIPCNNRNRFGQTFVQERLSCL\ AKNNSIYVVANIGDKKPCDTSDPQCPPDGRYQYNTDVVF\DSQG
) /	1		KLVARYHKQNLFMGENQFNVPKEPEIVTFNTTFGSFGIFTCFDI
	į		LFHDPAVTLVKDFHVDTIVFPTAWMNVLPHLSAVEFHSAWAMGM
	İ		RVNFLASNIHYPSKKMTGSGIYAPNSSRAFHYDMKTEEGKLLLS
1			QLDSHPSHSAVVNWTSYASSIEALSSGNKEFKGTVFFDEFTFVK
1			LTGVAGNYTVCQKDLCCHLSYKMSENIPNEVYALGAFDGLHTVE
1 1			GRYYLQICTLLKCKTTNLNTCGDSAETASTRFEMFSLSGTFGTQ
			YVFPEVLLSENQLAPGEFQVSTDGRLFSLKPTSGPVLTVTLFGR
5930	113	6082	LYEKDWASNASSGLTAQARIIMLIVIAPIVCSLSW RGNCFWIVPFTMAORTGLEDPERYLFVDRAVIYNPATOADWTAK
	***	0002	RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLVWIPSERHGFEAASIKEERGDEVMVBLAENGKKAMVNKDDIO
] [			KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF
1 1			CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM
1			LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN
			IPGE\LERQLLQANFILESFGNARTVQNDNSSRFGKFIRINFDV
1			TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL
ł !	}		KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG
1 1			FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL
j l			CHLLGMNVMEFTRAILTPRIKVGRDYVÇKAQTKEQADFAVEALA
1	1	f	KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN
1		j	SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEO
1	ľ	j	GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND
1 [		1	NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT
	1		KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK
			LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
	eedneuce	-	\=possible nucleotide insertion)
			NAIPKGFMDGKQACBRMIRALELDPNLYRIGQSKIFFRAGVLAH
1			LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR
		}	NCAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVK
i			BKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETBLFAEAEEM
1			RARLAAKKQELEEILHDLESRVEEEEERNQILQNEKKKMQAHIQ
ł			DLEEQLDEEEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF
-			IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE
1			RLKKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL
l			AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES
1			EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE
1			QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR
			FKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKLDAQV
i			QELHAKVSEGDRLRVELAEKASKLQNELDNVSTLLEEAEKKGIK
1			FAKDAASLESQLQDTQELLQEETRQKLNLSSRIRQLEEEKNSLQ
1			EQQEEEEEARKNLEKQVLALQSQLADTKKKVDDDLGTIESLEEA
1	}		KKKLLKDAEALSQRLEEKALAYDKLEXTKNRLQQELDDLTVDLD
1	ĺ		HQRQVASNLEKKQ\KKFDQLLAEEKSISARYAEERDRAEAEARE
			KETKALSLARALEEALEAKEEFERQNKQLRADMEDLMSSKDDVG
1			KNVHELEKSKRALEQQV\EEMRTQLEELEDBLQATEDAKLRLEV
l	i i		NMQAMKAQFERDLQTRDEQNEEKKRLLIKQVRELEAELEDERKQ
			RALAVASKKKMEIDLKDLEAQIEAANKARDEVIKQLRKLQAQMK DYQRELEEARASRDEIFAQSKESEKKLKSLEAEILQLQEELASS
ľ			ERARRHAEQERDELADEITNSASGKSALLDEKRRLEARIAQLEE
			ELEEBQSNMELLNDRFRKTTLQVDTLNAELAAERSAAQKSDNAR
			QQLERQNKELKAKLQELEGAVKSKFKATISALEAKIGQLEEQLE
			QEAKERAAANKLVRRTEKKLKEIFMQVEDERRHADQYKEQMEKA
			NARMKQLKRQLEBAEEEATRANASRRKLQRELDDATEANEGLSR
}			EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK
L			TSDVNETQPPQSE
5931	113	6082	RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK
]			KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ
1			KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF
1			CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM
1 1	1		LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN
			IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL
į l	i		KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHING
1			FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL
1			CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA
			KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFBLN
1 1		•	SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL
			DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ
			GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND
( 1	ł	-	NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT
j <b>i</b>		!	KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK
[			LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP
; 1		İ	NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH
į [		1	LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR
1 1			NCAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVK
			EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM
]			RARLAAKKQELEEILHDLESRVEEEEERNQILQNEKKKMQAHIQ
, .	ļ		DLEEQLDEEEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF
1	1		IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE
) l	į	[	RLKKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES
	1	•	EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE
	į	ŀ	QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR
ļ j	Ī	ļ	FKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKLDAQV
	}	Ì	QELHAKVSEGDRLRVELAEKASKLONELDNVSTLLEEABKKGIK
		i	- The state of the
	I		FAKDAASLESQLQDTOELLOEETROKLNLSSRIROLEERKNGLO
			FAKDAASLESQLQDTQELLQEETRQKLNLSSRIRQLEEEKNSLQ EQQBEEEEARKNLEKQVLALQSQLADTKKKVDDDLGTIESLEEA

Deginning   Cocation	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
No:   nucleotide   corresponding to first   mino acid   feed due of   fe				
L-Loucing, M-Mothioning, N-Asparagine, saino acid residue of smino acid residue of smino acid sequence   P-Proling, Q-Glutamine, R-Arginine, S-Serine, T-Threonine, V-Valine, sequence   Codon, /=possible nucleotide deletion, V-possible nucleotide sequence   NKKLLKDARALSGKLEEKKLATPKLEKTNNELQGELDDLTVLDL	NO:			
L-Leucing, M-Methioning, N-Asparagine, samino acid residue of maino acid residue of maino acid sequence   P-P-P-Coling, Q-Giltamine, R-Aspainne, samino acid sequence   S-Serine, T-Threonine, V-Vallne, samino acid sequence   Codon, /=possible nucleotide deletion, V-possible nucleotide sequence   NKKLLKOARALSGKLEEKOLATYKLEKINSKLOGELDDLTVDLD   KKKLLKOARALSGKLEEKOLATYKLEKINSKLOGELDDLTVDLD   KKKLLKOARALSGKLEEKOLATYKLEKINSKLOGELDDLTVDLD   KKKLLKOARALSGKLEEKOLATYKLEKINSKLOGELDDLTVDLD   KKKLLKOARALSGKLEEKOLATYKLEKINSKLOGELDDLTVDLD   KKKLLKOARALSGKLEEKOLATYKLEKINSKLOGELDDLTVDLD   KKKLLKOARALSGKLEEKOLATYKLEKINSKLOGELDDLTVDLD   KKKLLKOARALSGKLEEKOLATYKLEKINSKLOGELDDLTVDLD   KKKLLKOARALSGKLEEKOLATYKLEKINSKLOGELDDLTVDLD   KKKLLKOARALSGKLAKINGKANALOGELDBLTKANALOGELDBLAKKEN   KKTALSGKLAKINGKANALOGELBEARASGKANALOKINGKANALOGELBEARASGKANALOKINGKANALOGELBEARASKANALOKINGKANALOGELBEARASKANALOKINGKANALOGELBEARASKANALOKINGKANALOGELBEARASKANALOKINGKANALOGELBEARASKANALOKINGKANALOGELBEARASKANALOKINGKANALOGEBEARASKANALOGEBEARASKANALOKINGKANALOGEBEARASKANALOKINGKANALOGEBEARASKANALOKINGKANALOGEBEARASKANALOKINGKANALOGEBEARASKANALOKINGKANALOGEBEARASKANALOKINGKANALOGEBEARASKANALOKINGKANALOGEBEARASKANALOKINGKANALOGEBEARASKANALOKINGKANALOGEBEARASKANALOKINGKANALOGEBEARASKANALOKINGKANALOGEBEARASKANALOKINGKANALOGEBEARASKANALOKINGKANALOKINGKANALOKINGKANALOGEBEARASKANALOKINGKANALOKINGKANALOKINGKANALOKINGKANALOKINGKANALOKINGKANALOKINGKANALOKINGKANALOKINGKANALOKINGKANALOKINGKANALOKINGKANALOKINGKANALOKINGKANALOKINGKANALOKINGKANALOKI			P. Control of the con	
to first amino acid residue of amino acid sequence  sequence  #TYPTODIAIR, Y=TYTOSIRE, X=UNIKNOWN, *=Stop codon, /=possible nucleotide insertion)  **RYKLKDARAISGNEERKALTANKEERKINKEAGGELDDLTVDLD HQRQVASNLERKQ\KKPOLLABERSISARYABERDERABERER KEYALSIARALBERISHERKGYLKROLGADELDDLTVDLD HQRQVASNLERKQ\KKPOLLABERSISARYABERDERABERER KEYALSIARALBERISHERKGYLKROLGADELDDLTVDLD HQRQVASNLERKQ\KKPOLLABERSISARYABERDERABERER KEYALSIARALBERISHERKGYLKROLGADELDDLTVDLD HQRQVASNLERKQ\KKPOLLABERSISARYABERDERABERER KEYALSIARALBERISHERKGYLKROLGADELDDLTVDLD HQRQVASNLERKQ\KKPOLLABERSISARYABERDERABERER KEYALSIARALBERISHERKGYLKROLGADELDDLTVDLD HQRQVASNLERKQ\KKPOLLABERSISARYABERDERABERER KEYALSIARALBERISHERKGYLKROLGADELDDLTVDLD HQRQVASNLERKQ\KKPOLLABERSISARYABERDERABERER KEYALSIARALBERISHERGERKGATANABERISHINGYHLERABLEDBEKG RALAWSKKKNMSIDLKUBGAQISTARANABERSICQUELDSENGELABER DOBBERSHERABANASHELABEITINGYHLERABLEDBEKG RALAWSKKKNMSIDLKUBGAQISTARANABERSICQUELDSENGELABEIT CORRESPONDER HANDEN GERMEN GE	1	corresponding		L-Leucine, M-Mcthionine, N-Asparagine,
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LCPERSVF  5934  1  3190  GTRKLKMADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGPSD  SDMPSRTRPKSPRKHNYRNESARESLCDSPHQNLSRPLLENKLK  AFSIGKMSTAKRTLSKKEQEELKKKEDEKAAAEIYEEFLAAFEG  SDGMKVKTFVRGGVVNAAKEEHETDEKEGKIYKPSSRFADQKNP  PNQSSNERPPSLLVIETKKPPLKKGEKEKKKSNLELFKEELKQI  QEERDERHKTKGRLSRFEPPQSDSDGQRRSMDAPSRRNRSSGVL  DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLKKCCCQEFGRFGP  LASVKIMWPRTDEERARERNCGFVAPMNRDAERALKNLNGKMI  MSFEMKLGWGKAVPIPPHPTYIPPSMBEHTLPPPPSGLPFNAQP  RERLKNPNAPMLPPPKNKEDFEKTLSQAIVKVVIPTERNLLALI  HRMIEFVVREGPMFEAMIMNREINNPMFRFLFENQTPAHVYYRW  KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPPLHPYLHGMSEEQ  ETEAFVEEPSKKGALKEEQRDKLEEILRGLTPRKNDIGDAMVFC  LNNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA  KVANASYYRKFFETKLCQIFSDLNATTRTIQGHLQSENFKQRVM  TCFRAWEDWAIYPEPFLIKLQNIFLGLVNIIEEKETEDVPDDLD				
5934  1 3190 GTRKLKMADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGPSD SDMPSRTRPKSPRKHNYRNESARESLCDSPHQNLSRPLLENKLK AFSIGKMSTAKRTLSKKEQEELKKKBDEKAAAEIYEEFLAAFEG SDGNKVKTFVRGGVVNAAKEEHETDEKRGKIYKPSSRFADQKNP PNQSSNERPPSLLVIETKKPPLKKGEKEKKKSNLELFKEELKQI QEERDERHKTKGRLSRFEPPQSDSDGQRRSMDAPSRRNRSSGVL DDYAFGSHDVGDPSTT\NFYLGNI\NPQMNLKKCCQEFGRFGP LASVKIMWPRTDEERARERNCGFVAFMNRRDAERALKNLNGKMI MSFEMKLGWGKAVPIPPHPIYIPPSMMEHTLPPPPSGLPFNAQP RERLKNPNAPMLPPFKNKEDFEKTLSQAIVKVVIPTERNLLALI HRMIEFVVREGPMFEAMIMNREINNPMFRFLFENQTPAHVYYRW KLYSILQGDSPTKWRTEDFRMFKNGSFFRPPPLNPYLHGMSEEQ ETEAFVEEPSKKGALKEEQRDKLEELLRGLTPRNDIGDAMVFC LNNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSGLNATTRTIQGHLQSENFKQRVM TCFRAWEDWAIYPEPFLIKLQNIFLGLVNIIEEKETEDVPDDLD				
SDMPSRTRPKSPRKHNYRNESARESLCDSPHQNLSRPLLENKLK AFSIGKMSTAKRTLSKKEQEELKKKBDEKAAAEIYEEFLAAFEG SDGNKVKTFVRGGVVNAAKEEHETDEKRGKIYKPSSRFADQKNP PNQSSNERPPSLLVIETKKPPLKKGEKEKKKSNLELFKEELKQI QEEKDERHKTKGRLSRFEPPQSDSDGQRRSMDAPSRRNRSSGVL DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLKKCCCQEFGRFGP LASVKIMWPRTDEERARERNCGFVAFMNRRDAERALKNLINGKMI MSFEMKLGWGKAVPIPPHPIYIPPSMMEHTLPPPPSGLPFNAQP RERLKNPNAPMLPPPKNKEDFEKTLSQAIVKVVIPTERNLLALI HRMIEFVVREGPMFEAMIMNREINNPMFRFLFENQTPAHVYYRW KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPPLNPYLHGMSEEQ ETEAFVEEPSKKGALKEEGRDKLEELIRGLTPRKNDIGDAMVFC LNNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM TCFRAWEDWAIYPBPFLIKLQNIFLGLVNIEEKETEDVPDDLD	5934	1	3190	
AFSIGKMSTAKRTLSKKEQEELKKKEDEKAAAEIYEEFLAAFEG SDGNKVKTFVRGGVVNAAKEEHETDEKRGKIYKPSSRFADQKNP PNQSSNERPPSLLVIETKKP PLKKGEKEKKKSNLELFKEELKQI QEERDERHKTKGRLSRFEPPQSDSDGQRRSMDAPSRRNRSSGVL DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLKKCCCQEFGRFGP LASVKIMWPRTDEERARERNCGFVAFMNRRDAERALKNLINGKMI MSFEMKLGWGKAVPIPPHPIYIPPSMMEHTLPPPPSGLPFNAQP RERLKNPNAPMLPPPKNKEDFEKTLSQAIVKVVIPTERNLLALI HRMIEFVVREGFMFEAMINNREINNPMFFFFENOTPAHVYYRW KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPPLNPYLHGMSEQ ETEAFVEEPSKKGALKEEQRDKLEEILRGLTPRKNDIGDAMVFC LNNAEAAEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM TCFRAWEDWAIYPBPFLIKLQNIFLGLVNIIEEKETEDVPDDLD		<b>,</b>	3130	
SDGNKVKTFVRGGVVNAAKEEHETDEKRGKIYKPSSRFADQKNP PNQSSNERPPSLLVIETKKPPLKKGEKEKKKSNLELFKEELKQI QEEKDERHKTKGRLSRFEPPQSDSDGQRSMDAPSRRNRSSGVL DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLKKCCQEFGRFGP LASVKIMWPRTDEERARERNGGFVAPMNRRDAERALKNLNGKMI MSFEMKLGWGKAVPIPPHPIYIPPSMMEHTLPPPPSGLPFNAQP RERLKNPNAPMLPPPKNKEDFEKTLSQAIVKVVIPTERNLLALI HRMIEFVVREGFMFEAMIMNREINNPMFRFLFENQTPAHVYYRW KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPPLMFYLHGMSEEQ ETEAFVEEPSKKGALKEEQRDKLEEILRGLTPRKNDIGDAMVFC LNNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM TCFRAWEDWAIYPBPFLIKLQNIFLGLVNIIEEKETEDVPDDLD	1		!	) ·
PNQSSNERPPSLLVIETKKPPLKKGEKEKKKSNLELFKEELKQI QEERDERHKTKGRLSRFEPPQSDSDGQRSMDAPSRRNRSSGVL DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLKKCCQEFGRFGP LASVKIMWPRTDEERARERNCGFVAFMNRDAERALKNLNGKMI MSFEMKLGWGKAVPIPPHPTYIPPSMMEHTLPPPPSGLPFNAQP RERLKNPNAPMLPPPKNKEDFEKTLSQAIVKVVIPTERNLLALI HRMIEFVVREGPMFEAMIMNREINNPMFRFLFENQTPAHVYYRW KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPPLHPYLHGMSEEQ ETEAFVEEPSKKGALKEEQRKLEEILRGLTPRKNDIGDAMVFC LNNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM TCFRAWEDWAIYPEPFLIKLQNIFLGLVNIIEEKETEDVPDDLD	]			<u> </u>
QEERDERHKTKGRLSRFEPPQSDSDGQRRSMDAPSRRNRSSGVL DDYAPGSHDVGDPSTT\NFYLGNI\NPQNNLKKCCQEFGRFGP LASVKIMPRTDEERARERNCGFVAFMNRRDAERALKNLNGKMI MSFEMKLGWGKAVPIPPHPIYIPPSMMEHTLPPPPSGLPFNAQP RERLKNPNAPMLPPPKNKEDFEKTLSQAIVKVVIPTERNLLALI HRMIEFVVREGPMFEAMIMNREINNPMFRFLFENQTPAHVYYRW KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPPLNPYLHGMSEEQ ETEAFVEEPSKKGALKEEQROKLEEILRGLTPRNNDIGDAMVFC LNNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSGLNATTRTIQGHLQSENFKQRVM TCFRAWEDWAIYPEPFLIKLQNIFLGLVNIIEEKETEDVPDDLD	1			f == ===
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LASVKIMWPRTDEERARERNCGFVAPMNRRDAERALKNLNGKMI MSFEMKLGWGKAVPIPPHPIYIPPSMMEHTLPPPPSGLPFNAQP RERLKNPNAPMLPPPKNKEDFEKTLSQAIVKVVIPTERNILALI HRMIEFVVREGPMFEAMIMNREINNPMFRFLFENQTPAHVYYRW KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPPPLNPYLHGMSEEQ ETEAFVEEPSKKGALKEEQRDKLEEILRGLTPRKNDIGDAMVFC LNNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM TCFRAWEDWAIYPBPFLIKLQNIFLGLVNIIEEKBTEDVPDDLD				
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HRMIEFVVREGPMFEAMIMNREINNPMFRFLFENQTPAHVYYRW KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPPLNFYLHGMSEEQ ETEAFVEEPSKKGALKEEQRDKLEEILRGLTPRINDIGDAMVFC LINNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM TCFRAWEDWAIYPBPFLIKLQNIFLGLVNIIEEKETEDVPDDLD	1	]	i	MSFEMKLGWGKAVPIPPHPIYIPPSMMEHTLPPPPSGLPFNAQP
KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPPLNPYLHGMSEEQ ETEAFVEEPSKKGALKEEQRDKLEEILRGLTPRKNDIGDAMVFC LNNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM TCFRAWEDWAIYPBPFLIKLQNIFLGLVNIIEEKETEDVPDDLD		ļ		RERLKNPNAPMLPPPKNKEDFEKTLSQAIVKVVIPTERNLLALI
ETEAFVEEPSKKGALKEEQRDKLEEILRGLTPRKNDIGDAMVFC LNNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM TCFRAWEDWAIYPBPFLIKLQNIFLGLVNIIEEKETEDVPDDLD	Į			
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KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM TCFRAWEDWAIYPBPFLIKLQNIFLGLVNIIEEKBTEDVPDDLD	1			
TCFRAWEDWAIYPEPFLIKLQNIFLGLVNIIEEKETEDVPDDLD	]			
1	1			
GAPIEEELDGAPLEDVDGIPIDATPIDDLDGVPIKSLDDDLDGV	1			
				GAPIEEELDGAPLEDVDGIPIDATPIDDLDGVPIKSLDDDLDGV

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
l	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
•	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
<b>l</b>	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
			PLDATEDSKKNEPIFKVAPSKWEAVDESELEAQAVTTSKWELFD
l	Ì	ł.	OHEESEEEENQNQEEESEDEEDTQSSKSEEHHLYSNPIKEEMTE
		j	SKFSKYSEMSEEKRAKLREIELKVMKFQDELESGKRPKKPGQSF
i	1	į.	QEQVEHYRDKLLQREKEKELBRERERDKKDKEKLESRSKDKKEK
	1		DECTPTRKERKRRHSTSPSPSRSSSGRRVKSPSPKSERSER
	i		SHKESSRSSSHKDSPRDVSKKAKRSPSGSRTPKRSRSRSRSP
İ	1	<b>:</b>	KKSGKKSRSQSRSPHRSHKKSKGKTNTGRKFFKKAVTYWKCDLF
Į	i	į	
<u></u>			LCPERSVF
5935	3	4493	SYMLSGWRLSRPPRQFWAGWRGIGRFGTMAPVHGDDCEIGASAL
	Ī	, -	
1	1	J	TGVYEEVDEEQYSKLVQARQDDDWIVDDDGIGYVEDGREIFDDD
	[	1	LEDDALDADEKGKDGKARNKDKRNVKKLAVTKPNNIKSMFIACA
1		}	GKKTADKAVDLSKDGLLGDILQDLNTETPQITPPPVMILKKKRS
l	Į.		IGASPNPFSVHTATAVPSGKIASPVSRKEPPLTPVPLKRAEFAG
			DDVQVESTEEEQESGAMEFEDGDFDEPMEVEEVDLEPMAAKAWD
}		1	KESEPAEEVKQEADSGKGTVSYLGSFLPDVSCWDIDQEGDSSFS
ł		1	VQEVQVDSSHLPLVKGADEEQVFHFYWLDAYEDQYNQPGVVFLF
ĺ	1	]	GKVWIESAETHVSCCVMVKNIERTLYFLPREMKIDLNTGKETGT
1	1	1	PISMKDVYEEFDEKIATKYKIMKFKSKPVEKNYAFEIPDVPEKS
	İ	1	EYLEVKYSAEMPOLPODLKGETFSHVFGTNTSSLELFLMNRKIK
	1		GPCWLEVKKSTALNQPVSWCKVEAMALKPDLVNVIKDVSPPPLV
		1	VMAFSMKTMQNAKNHQNEIIAMAALVHHSFALDKAAFKPPFQSH
1		i	FCVVSKPKDCIFPYAFKEVIEKKNVKVEVAATERTLLGFFLAKV
ļ	1		HKIDPDIIVGHNIYGFELEVLLQRINVCKAPHWSKICRLKRSNM
]		i	
1		1	PKLGGRSGFGERNATCGRMICDVEISAKELIRCKSYHLSELVQQ
	1		ILKTERVVIPMENIQNMYSESSQLLYLLEHTWKDA\KFILQIMC
ļ		1	ELNVLPLALQITNIAGNIMSRTLMGGRSERNBFLLLHAFYENNY
1	ŀ	İ	IVPDKQIFRKPQQKLGDEDEEIDGDTNKYKKGRKKGAYAGGLVL
ŀ			DPKVGFYDKFILLLDFNSLYPSIIQEFNICFTTVQRVASEAQKV
!	ļ	j,	TEDGEQEQIPELPDPSLEMGILPREIRKLVERRKQVKQLMKQQD
[	1		LNPDLILQYDIRQKALKLTANSMYGCLGFSYSRFYAKPLAALVT
<b>)</b> .	ł	ł	YKGREILMHTKEMVQKMNLEVIYGDTDSIMINTNSTNLEBVFKL
1			GNKVKSEVNKLYKLLEIDIDGVFKSLLLLKKKKYAALVVEPTSD
,		l .	GNYVTKQELKGLDIVRRDWCDLAKDTGNFVIGQILSDQSRDTIV
1		1	ENIOKRLIEIGENVLNGSVPVSQFEINKALTKDPQDYPDKKSLP
İ		1'	HVHVALWINSQGGRKVKAGDTVSYVICQDGSNLTASQRAYAPEQ
1	1		LOKODNLTIDTOYYLAQQIHPVVARICEPIDGIDAVLIATGWEL
1			\DPTQFKVHHYHKDEENDALLGGPAQLTDEEKYRDCERFKCPCP
		1	TCGTENIYDNVFDGSGTDMEPSLYRCSNIDCKASPLTFTVQLSN
ì		1	KLIMDIRRFIKKYYDGWLICEEPTCRNRTRHLPLQFSRTGPLCP
1			ACMKATLQPEYSDKSLYTQLCFYRYIFDAECALEKLTTDHEKDK
			LKKQFFTPKVLQDYRKLKNTAEQFLSRSGYSEVNLSKLFAGCAV
		<u> </u>	KS
5936	1124	139	RGEEQFDAEFRRFACLGFGERLQEFSRLLRAVHRSRAWTCYLAI
			RMLMATCCPSPTTTACTGPWQRAPPLRLLVQKREADSSGLAFAS
1			NSLCRRKKGLLLRPVAPLRTRPPLLISLPQDFRQVSSVIDVDLL
J			PETHRRVRLHKHGSDRPLGFYIRDGMSVRVAPQG\LERVPGIFI
1			SRLVRGGLAESTGLLAVSDEILEVNGIEVAGKTLNQVTDMMVAN
1			SHN\LIVTVKPANQRNNVVRGASGRLTGPPSAGPGPAEPDSDDD
			SSDLVIENROPPSSNGLSQGPPCWDLHPGCRHPGTRSSLPSLDD
			OEQASSGWGSRIRGDGSGFSL
5937	31	1600	PTSLLKSTVQLMCRLLQDKRYQCVYSLAEIFKVLASFYVILVIL
233/	1 31	1 1000	YGLTSSYSLWWMLRSSLKQYSFEALREKSNYSDIPDVKNDFAFI
1	1	Į.	LHLADQYDPLYSKRFSIFLSEVSENKLKQINLNNEWTVEKLKSK
1	}		
1	İ	1	LVKNAQDKIELHLFMLNGLPDNVFELTEMEVLSLELIPEVKLPS
			AVSQLVNLKELRVYHSSLVVDHPALAFLEENLKILRLKFTEMGK
1			IPRWVFHLKNLKELYLSGCVLPEQLSTMQLEGFQDLKNLRTLYL
1	1		KSSLSRIPQVVTDLLPSLQKLSLDNEGSKLVVLNNLKKMVNLKS
İ			LELISCOLERIPHSIFSLNNLHELDLRENNLKTVEEIISFQHLQ
			NLSCLKLWHNNIAYIPAQIGALSNLEQLSLDHNNIENLPLQLFL
ļ		1	CTKLHYLDLSYNHLTFIPEEIQYL\SNLQYFAVTNNNIEMLPDG

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Į.	to first	3	
		amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
}	residue of	amino acid	W-Tryptophan, Y-Tyrosine, X-Unknown, *=Stop
ŀ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			LFQCKKLQCLLLGKNSLMNLSPHVGELSNLTHREPIG\NYLETL
	t		PPELEGCQSLKRNCLIVEENLLNTLPLPVTERLQTCLDKC
5938	395	1865	YKGEGFFCNQEARGERRKKKKAMSSPNIWSTGSSVYSTPVFSQK
	1		MTVWILLLSLYPGFTSQKSDDDYEDYASNKTWVLTPKVPEGDV
1			TVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGPVNAINME
	!		YTIDIFFAOTWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRN
			SKKADAHWITTPNRMLRIWNDGRVLYSLRLTIDAECQLQLHNPP
1			MDEHSCPLEFSSYGYPREEIVYQWKRSSVEVGDTRSWRLYQFSF
			VGLRNTTEVVKTTSGDYVVMSVYFDLSRRMGYFTIQTYIPCTLI
	. '		VVLSWVSFWINKDAVPARTSLGITTVLTMTTLSTIARKSLPKVS
	ì		YVTAMDLFVSVCFIFVFSALVEYG\TLHYFVSNRKPSKDKDKKK
i	Į ,		·
			KNPAPTIDIRPRSATIQMNNATHLQERDEEYGYECLDGKDCASF
-			FCCFEDCRTGAWRHGRIHIRIAKMDSYARIFFPTAFCLFNLVYW
6020			VSYLYL
5939	66	1404	IRPGYLKEVQENSPGHRAGLEPFFDFIVSINGSRLNKDNDTLKD
1			LLKANVEKPVKMLIYSSKTLELRETSVTPSNLWGGQGLLGVSIR
1			FCSFDGANENVWHVLEVESNSPAALAGLRPHSDYIIGADTVMNE
			SEDLFSLIETHEAKPLKLYVYNTDTDNCREVIITPNSAWGGEGS
			LGCGIGYGYLHRIPTRPFEEGKKISLPGQMAGTPITPLKDGFTE
			VQLSSVNPPSLSPPGTTGIEQSLTGLSISSTP\PAVSSVLSTGV
			PTVP\LLPPQVNQSLTSVPPMESSYLHLPGLNPFTRQGLPNLPQ
1			PSTFNLPR\PTHSWPGVGLYQEFVKPGVLPPLSSMPPRNLPG\I
1	]		APLPLPSEFLPSFPLVPESSSAASSGELLSSLPPTSNAPSDPAT
1	l		TTAKADAASSLTVDVTPPTAKAPTTVEDRVGDSTPVSEKPVSAA
			VDANASESP
5940	145	717	RRSASRSASPRQSAGTAVTTGTRAGGTCLAAAHHRMRWRADGRS
			LEKLPVHMGLVITEVEQEPSFSDIASLVVWCMAVGISYISVYDH
			QGIFKRNNSRLMDEILKQQQELLGLDCSKYSPEFANSNDKDDQV
	ĺ		LNCHLAVKVLSPEDGKADIVRAAQDFCQLVAQKQKRPTDLDVDT
1			LA\VYLVQMVVLILI
5941	13	6147	MCLGRMGASSPRSPEPVGPPAPGLPFCCGGSLLAVVVLLALPVA
1 1			WGQCNAPEW\LPFARPINLTDEFEPPIGTYLNYECRPGYSGRPF
<b>!</b>			SIICLKNSVWTGAKDRCRRKSCRNPPDPVNGMVHVIKGIQFGSQ
	l 1		IKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPP
J j	ļ		TITNGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIY
1	·		CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL
			NEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPPPD
.			VLHAERTORDKDNFSPGOEVFYSCEPGYDLRGAASMRCTPOGDW
			SPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGAKVDFVCDEGF
			QLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTG
1			KPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNG
1		:	VWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYE
			CRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVH
] .		•	VITDIOVGSRINYSCTTGHRLIGHSSAECILSGNAAHWSTKPPI
]		i	CORIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKV
			FELVGEPSIYCTSNDDOVGIWSGPAPOCIIPNKCTPPNVENGIL
			VSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPS
{			The state of the s
1			CSRVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPGYDLRGAA
		i	SMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGA
			KVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSP
1			PVIPNGRHTGKPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTI
1			RCTSDPQGNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASD
[ 1			FPIGTSLKYECRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKT
i			PPDPVNGMVHVITDIQVGSRINYSCTTGHRLIGHSSAECILSGN
1			TAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSVVTYR
ļ		İ	CNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKC
] I	1		TPPNVENGILVSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQA
1 1			LNKWEPBLPSCSRVCQPPPEILHGEHTPSHQDNFSPGQEVFYSC
1 1			EPGYDLRGAASLHCTPQGDWSPEAPRCAVKSCDDFLGQLPHGRV
1 1		i	LFPLNLQLGAKVSFVCDEGPRLKGSSVSHCVLVGMRSLWNNSVP
1	Í		VCEHIFCPNPPAILNGRHTGTPSGDIPYGKEISYTCDPHPDRGM

ID beginning nucleotide   (A=Alanine, C=Cysteing Glutamic Acid, F=Pheny Corresponding to first amino acid   D=Proline, Q=Glutamine   D=Proline, Q=Glutamine   D=Proline, Q=Glutamine   D=Proline, Q=Glutamine   D=Proline, Q=Glutamine   D=Proline, Q=Glutamine   D=Proline, Q=Glutamine   D=Proline, Q=Glutamine   D=Proline, Q=Glutamine   D=Proline, Q=Glutamine   D=Proline, Q=Glutamine   D=Proline, Q=Glutamine   D=Proline, Q=Glutamine   D=Proline, Q=Glutamine   D=Proline, Q=Glutamine   D=Proline, Q=Glutamine   D=Prolin	ntaining signal peptide e, D=Aspartic Acid, E= ylalanine, G=Glycine,
NO: nucleotide location Glutamic Acid, F=Pheny H=Histidine, I=Isoleucorresponding to first L=Leucine, M=Methioning to first amino acid P=Proline, Q=Glutamine	ylalanine, G=Glycine,
location corresponding H=Histidine, I=Isoleucorresponding to first L=Leucine, M=Methioning to first amino acid P=Proline, Q=Glutamine	
corresponding to first L=Leucine, M=Methioning to first amino acid P=Proline, Q=Glutamine	_ 1 . <b>ve =</b> 1
to first amino acid P=Proline, Q=Glutamine	cine, K=Lysine,
	ne, N=Asparagine,
	e, R=Arginine,
amino acid residue of S=Serine, T=Threonine	
	ine, X=Unknown, *=Stop
amino acid sequence Codon, /=possible nuc	
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
1 1	WSSPAPRCELSVRAGHCKTPEQF
1 1	YECRPGYFGKMFSISCLENLVWS
SVEDNCRRKSCGPPPEPFNGM	VHINTDTQFGSTVNYSCNEGFRL
IGSPSTTCLVSGNNVTWDKKA	PICEIISCEPPPTISNGDFYSNN
RTSFHNGTVVTYQCHTGPDGE	QLFELVGERSIYCTSKDDQVGVW
SSPPPRCISTNKCTAPEVENA	IRVPGNRSFFSLTELIRFRCQPG
1 1	PHCSRVCQPPPEILHGEHTLSHQ
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	AASLHCTPOGDWSPEAPRCTVKS
1 1	GAKVSFVCDEGFRLKGRSASHCV
1 1 1 · · · · · · · · · · · · · · · · ·	
1 1	NPPAILNGRHTGTPLGDIPYGKE
	TIRRTSEPHGNGVWSSPAPRCEL
	VSLYLPGMTISYTCDPGYLLVGK
	NCSFPLFMNGISKELEMKKVYHY
] ]	COADDRWDPPLAKCTSRTHDALI
VGTLSGTIFFILLIIFLSWIII	LKHRKGNNAHENPKEVAIHLHSQ
GGSSVHPRTLQTNEENSRVLP	
5942 4509 688 YLYVRMRANPLAYGISHKAYQI	IDPPL\RKHREQ\LVIE\VGRKL
DK\AQMIRFEERTGYFSSTDLC	GRTASHYYIKYNTIETFNELFDA
HKTEGDIFAIVSKAEEPDQIK	VREEEIEELDTLLSNFCELSTPG
GVENSYGKINILLQTYINRGEN	MDSFSLISDSAYVAQNAARIVRA
LFEIALRKRWPTMTYRLINLS	KAIDKRLWGWASPLROFSILPPH
MLTRLEEKKLTVDKLKDMRKDF	BIGHILHHVNIGLKVKQCVHQIP
	IYADFTWNDOVHGTVGEPWWIWV
	ISKEAOLLVFTIPIFEPLPSQYY
1 1	LILPERHPPHTELLDLQPLPITA
1 1 1	I FHTLYHTDCNVLLGAPTGSGKT
1 1 = -	IAPLKALVRERMDDWKVRIEEKL
	DLIVTTPEKWDGVSRSWQNRNYV
	LEVIVSRTNFISSHTEKPVRIVG
	LFNFRPSVRPVPLEVHIQGFPGQ
1 1	PAKPVLIFVSSRRQTRLTALELI
·	NIIATVRDSNLKLTLAFGIGMHH
1 1	/LIATSTLAWGVNFPAHLVIIKG
	MGRAGRPQFDDQGKAVILVHDI
1 1	/LSDHLNAEIAGGTITSKQDALD
1	OVSHDSVNKFLSHLIEKSLIELE
	ASYYYLKHQTVKMFKDRLKPEC
	inedhmnselakclpiesnphsf
DSPHTKAHLLLQAHLSRAMLPC	PDYDTDTKTVLDQALRVCQAML
DVAANQGWLVTVLNITNLIQMV	/IQGRWLKDSSLLTLPNIENHHL
HLFKKWKPIMKGPHARGRTSIE	CLPELIHACGGKDHVFSSMVES
ELHAAKTKQAWNFLSHLPEINV	GISVKGSWDDLVEGHNELSVST
1 1	QVSLQRVHFGFHKGKPESCAVT
	LIALKRVGYIRNHHVASLSFYT
	OOYD/NLSORYTSESFCTGOHO
GL	
<u> </u>	PVGDGELWOTWLPNHVVFLRLR
	PPPOLLTRNVVFGLGGELFLWD
1 1 : : : : : : : : : : : : : : : : : :	
1 1 '	ALSQYQRLLCINPPLFEIYQVL
	KRWGKNSEFEGGKSTVNCSTTP
	EILDPHVVLLTSDNVIRIYSLR
1 1 7	KGRAYTASLGETAVAFDFGPLA
1	LYENGETFLTYISLLHSPGN/I
	CAVLCLPCVPNILVIATESGML
	RIDLIPSLYVFECVELELALKL
	KCPSRYHCTHEAGVHSVGLTWI
	BOKCFVEHILCTKPLPCROPAP
IRGFWIVPDILGPTMICITSTY	BCLIWPLLSTVHPASPPLLCTR
	HIRSILQRSVANPAFLKASEKD
i i	YILKODLAKEEIORRVKLLCDQ
	ERLADKYEEAKEKQEDIMNRMK
1 ***********************************	

SEQ	Predicted	Predicted end	Amino acid coment containing cional popula-
_	1 .		Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
j.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	L	
		sequence	Codon, /=possible nucleotide deletion,
1	sequence	1	\=possible nucleotide insertion)
			KLLHSFHSELPVLSDSERDMKKELQLIPDQLRHLGNAIKQVTMK
	li .	]	
		i	KDYQQQKMEKVLSLPKPTIILSAYQRKCIQSILKEEGEHIREMV
}		1	KQINDIRNHVNF
5944	167	3428	FSIATFTDEPEVLTEPPSATTTTTIGISATWTTLAGSHGKRNNT
1			ITTTSSKRKNRKNKITPENVQIIFDDPLPISYSQPEKVNGESKS
	i		
		Í	SSTSESGDSDNMRISSCSDESSNSNSSRKSDNHSPAVVTTTVSS
		1	KKOPSVLVTFPKEERKSVSGKASIKLSETISEGTSNSLSTCTKS
1		\$	GPSPLSSPNGKLTVASPKRGOKREEGWKEVVRRSKXVSVPSTVI
1		1	<del>-</del>
l l	1	1	SRVIGRGGCNINAIREFTGAHIDIDKQKDKTGDRIITIRGGTES
1	i	l	TROATOLINALIKOPOKBIDELIPKNRLKSSSANSKIGSSAPTT
1	!	l	TAANTSLMGIKMTTVALSSTSQTATALTVPAISSASTHKTIKNP
1	i	,	· ·
1	1	1	VN\NVRPGFPVSFP\LAYPPPQFAHALLAAQTFQQIRPPRLPMT
ŀ	1	í	HFGGTFPPAQSTWGPFPVRPLSPARATNSPKPHMVPRHSNQNSS
1	1	1	GSQVNSAGSLTSSPTTTTSSSASTVPGTSTNGSPSSPSVRRQLF
1	I	[	
I	1	I	VTVVKTSNATTTTVTTTASNNNTAPTNATYPMPTAKEHYPVSSP
	1	i	SSPSPPAQPGGVSRNSPLDCGSASPNKVASSSEQEAGSPPVVET
1	I		TNTRPPNSSSSSSSSSAHSNQQQPPGSVSQEPRPPLQQSQVPPP
	1	I	EVRMTVPPLATSSAPVAVPSTAPVTYPMPQTPMGCPQPTPKMET
	İ	ŀ	1
	l		PAIRPPPHGTTAPHKNSASVQNSSVAVLSVNHIKRPHSVPSSVQ
1	İ		LPSTLSTQSACQNSVHPANKPIAPNFSAPLPFGPFSTLFENSPT
i	l		SAHAFWGGSVVSSQSTPESMLSGKSSYLPNSDPLHQSDTSKAPG
1			1-
1			FRPPLQRPAPSPSGIVNMDSPYGSVTPSSTHLGNFASNISGGQM
1			YGPGAPLGGAPAAANFNRQHFSPLSLLTPCSSASNDSSAQSVSS
	1	!	GVRAPSPAPSSVPLGSEKPSNVSODRKVPVPIGTERSARIROTG
1	1		TSAPSVIGSNLSTSVGHSGIWSFEGIGGNQDKVDWCNPGMGNPM
1	1	}	_
1	1		IHRPMSDPGVFSQHQAMERDSTGIVTPSGTFHQHVPAGYMDFPK
1			VGGMPFSVYGNAMIPPVAPIPDGAGGPIFNGPHAADPSWNSLIK
			MVSSSTENNGPQTVWTGPWAPHMNSVHMNQLG
5945	1461	197	GVTHLFLFGKRKLRNGIAEDLKGQADFFFLLVSEAVVATGSPRA
			I
			WLTCLILPLPGIIFSVLPKAMSRPLLITFTPATDPSDLWKDGQQ
	ļ		QPQPEKPESTLDGAAARAFYEALIGDESSAPDSQRSQTEPARER
	i l		KRKKRRIMKAPAAEAVAEGASGRHGQGRSLEAEDKMTHRILRAA
1	1		QEGDLPELRRLLEPHEAGGAGGNINARDAFWWTPLMCAARAGQG
i i	1		
	1		AAVSYLLGRGAAWVGVCELSGRDAAQLAEEAGFPEVARMVRESH
	1		GETRSPENRSPTPSLQYCENCDTHFQDSNHRTSTAHLLSLSQGP
1			QPPNLPLGVPISSPGFKLLLRGGWEPGMGLGPRGEGRANPIPTV
1			LKRDQEGLGYRSAPQPRVTHFPAWDTRAVAGRE\TPPRVATLSW
į l			
			REERRREE\KDRAWERDLRTYMNLEF
5946	541	1666	ILGSYSSIQPEEYS\SVVC\EVVLQDLLA\YVSPK\HSYLRDLP
į i	i		SEGSPORVNSIDFV\EL\EHLQPDVLVHAVLRVVDF/TILTEAV
Ī			YSYRGQKQKKVMLTVEQAQDQHYALVLWGPGAAW\YPQLQRKKG
i			
			YIWEFKYLFVQCNYTLENLELHTTPWSSCECLFDDDIRAITFKA
1			KFQKSAPSFVKISDLATHLEDKCSGVVLIKAQISELAFPITASQ
1	į i		KIALNAHSSLKSIFSSLPNIVYTGCAKCGLELETDENRIYKOCF
1 .	1		SCLPFTMKKIYYRPALMTAIDGRHDVCIRVESKLIEKILLNISA
1 1			
1			DCLNRVIVPSSEITYGMVVADLFHSLLAVSAEPCVLKIQSLFVL
1			DENSYPLOODFSLLDFYPDIVKHGANARL
5947	3	1347	RGIPDRRRRGPIGRVNMDLENKVKKMGLGHEQGFGAPCLKCKEK
3341	] 3	1317	
	ļ		CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDT
	į l		KYTTLIAKLKSDGIPMYKRNVMILTNPVAAKKNVSINTVTYEWA
1			PPVQNQALARQYMQMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD
1			
			QDPSKCHELSPREVKEMEQFVKKYKSEALGVGDVKLPCEMDAQG
1 1			PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEG
Į į	1		DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNBKLYCG
1 1	l i		
			RHYCDSEKPRCAGCDELIFSNEYTQAENQNWHLKHFCCFDCDSI
1			LAGEIYVMVNDKPVCKPCYVKNHAVVCQGCHNAIDPEVQRVTYN
1			NFSWHASTECFLCSCCSKCLIGQKFMPVEGMVFCSVECKKRMS
5948	39	3370	YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDO
1 ~~40	, J.	3310	
1 1			GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQAQRM
{ I	l l		VEIEIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP
			VKIETEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP PVCLRTKRHKNNRVKKKNEALPSAHGTPASASALPEPKVRIVEY

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
•	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ı	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon /-paggible muslestide deletion
	sequence	acquence	Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	) sequence		
1			SPPSAPRRPPVYYKFIEKSAEELDNEVEYDMDEEDYAWLEIVNE
	į.		KRKGDCVPAVSQSMFEFLMDRFEKESHCENQKQGBQQSLIDEDA
i	•		VCCICMDGECQNSNVILFCDMCNLAVHQECYGVPYIPEGQWLC/
i			RAHCLQSRARPADCVLCPNKGGAFKKTDDDRWGHV\VCALW\IP
1	1	}	E\VGFANTVFIEPIDGVRNIPPARWKLT\CNLCKEKGR/VGACI
			QCHKANCYTAFHVTCAQKAGLYMKMEPVKELTGGGTTFSVRKTA
			YCDVHTPPGCTRRPLNIYGDVEMKNGVCRKESSVKTVRSTSKVR
1			KKAKKALAEPCAVLPTVCAPYIPPQRLNRIANQVAIQRKKQ
i	i :		FVERAHSYWLLKRLSRNGAPLLRRLQSSLQSQRSSQQRENDEEM
1	]		KAAKEKLKYWQRLRHDLERARLLIELLRKREKLKREQVKVEQVA
1			MELRLTPLTVLLRSVLDQLQDKDPARIFAQPVSLKEVPDYLDHI
1			KHPMDFATMRKRLEAQGYKNLHEFEEDFDLIIDNCMKYNARDTV
1	ļ		FYRAAVRLRDQGGVVLRQARREVDSIGLEEASGMHLPERPAAAP
1			RRPFSWEDVDRLLDPANRAHLGLEEQLRELLDMLDLTCAMKSSG
1			SRSKRAKLLKKEIALLRNKLSQQHSQPLPTGPGLEGFEEDGAAL
1			GPEAGEEVLPRLETLLQPRKRSRSTCGDSEVEEESPGKRLDAGL
ļ	į į		TNGFGGARSEQEPGGGLGRKATPRRRCASESSISSSNSPLCDSS
1			FNAPKCGRGKPALVRRHTLEDRSELISCIENGNYAKAARIAAEV
1	ĺ		CQSSMWISTDAAASVLEPLKVVWAKCSGYPSYPALIIDPKMPRV
1			PGHHNGVTIPAPPLDVLKIGEHMQTKSDEKLFLVLFFDNKRSWQ
1 1			WLPKSKMVPLGIDETIDKLKMMEGRNSSIRKAVRIAFDRAMNHL
5949	39	2270	SRVHGEPTSDLSDID
3343	39	3370	YRBRYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDQ
.[ ]	.		GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQAQRM
			VEIBIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP
1 1			PVCLRTKRHKNNRVKKKNEALPSAHGTPASASALPEPKVRIVEY SPPSAPRRPPVYYKFIEKSAEELDNEVEYDMDEEDYAWLEIVNE
1			KRKGDCVPAVSQSMFEFLMDRFEKESHCENQKQGEQOSLIDEDA
1			VCCICMDGECQNSNVILFCDMCNLAVHQECYGVPYIPEGQWLC/
			RAHCLQSRARPADCVLCPNKGGAFKKTDDDRWGHV\VCALW\IP
			E\VGFANTVFIEPIDGVRNIPPARWKLT\CNLCKEKGR/VGACI
1			QCHKANCYTAFHVTCAQKAGLYMKMEPVKELTGGGTTFSVRKTA
i i			YCDVHTPPGCTRRPLNIYGDVEMKNGVCRKESSVKTVRSTSKVR
1	'		KKAKKAKKALAEPCAVLPTVCAPYIPPQRLNRIANQVAIQRKKQ
1			FVERAHSYWLLKRLSRNGAPLLRRLQSSLQSQRSSQQRENDEEM
1 1			KAAKEKLKYWQRLRHDLERARLLIELLRKREKLKREQVKVEQVA
1 1			MELRLTPLTVLLRSVLDQLQDKDPARIFAQPVSLKEVPDYLDHI
1 1	•		KHPMDFATMRKRLEAQGYKNLHEFEEDFDLIIDNCMKYNARDTV
1			FYRAAVRLRDQGGVVLRQARREVDSIGLEEASGMHLPERPAAAP
1 1	Į.		RRPFSWEDVDRLLDPANRAHLGLEEQLRELLDMLDLTCAMKSSG
1 1	į		SRSKRAKLLKKEIALLRNKLSQQHSQPLPTGPGLEGFEEDGAAL
1	1		GPEAGEEVLPRLETLLQPRKRSRSTCGDSEVEEESPGKRLDAGL
1			TNGFGGARSEQEPGGGLGRKATPRRRCASESSISSSNSPLCDSS
; !	Ì		FNAPKCGRGKPALVRRHTLEDRSELISCIENGNYAKAARIAAEV
1 1	•		GQSSMWISTDAAASVLEPLKVVWAKCSGYPSYPALIIDPKMPRV
1			PGHHNGVTIPAPPLDVLKIGEHMQTKSDEKLFLVLFFDNKRSWQ
j i	ļ		WLPKSKMVPLGIDETIDKLKMMEGRNSSIRKAVRIAFDRAMNHL
5950	1166	2.55	SRVHGEPTSDLSDID
3930	1166	373	ESRS_TMSTSQPGACPCQGAASRPAILYALLSSSLKAVPRPRSR
; I	ĺ		CLCRQHRPVQLCAPHRTCREALDVLAKTVAFLRNLPSFWQLPPQ
}		ĺ	DQRRLLQGCWGPLFLLGLAQDAVTFEVAEAPVPSILKKILLEEP
į l			SSSGGSGQLPDRPQPSLAAVQWLQCCLESFWSLELSPKE\YACL
j 1			KGPILFNPDVPGLQAASHIGHLQQEAHWVLCEVLEPWCPAAQGR
5951	107	5440	LTRVLLTASTLKSIPTSLLGDLFFRPIIGDVDIAGLLGDMLLLR
3321	143	5449	WNVKPSLLVVQLFKFSDKEEHEQNDSISGKTGETGVEEMIATRK
		į	VEQDSKETVKLSHEDDHILEDAGSSDISSDAACTNPNKTENSLV
f			GLPSCVDEVTECNLELKDTMGIADKTENTLERNKIEPLGYCEDA
] [			ESNRQLESTEFNKSNLEVVDTSTFGPESNILENAICDVPDQNSK
]	1		QLNAIESTKIESHETANLQDDRNSQSSSVSYLESKSVKSKHTKP
] }		ļ	VIHSKONMTTDAPKKIVAAKYEVIHSKTKVNVKSVKRNTDVPES
			QQNFHRPVKVRKKQIDKEPKIQSCNSGVKSVKNQAHSVLKKTLQ

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L-Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion.
1	sequence	,	\=possible nucleotide insertion)
		<del></del>	DOTLVQIFKPLTHSLSDKSHAHPGCLKEPHHPAOTGHVSHSSOK
ļ	1		QCHKPQQQAPAMKTNSHVKEELEHPGVEHFKEEDKLKLKKPEKN
1	}	İ	LQPRQRRSSKSFSLDEPPLFIPDNIATIRREGSDHSSSFESKYM
		1	
ł	1		WTPSKQCGFCKKPHGNRFMVGCGRCDDWFHGDCVGLSLSQAQQM
1			GEEDKEYVCVKCCAEEDKKTEILDPDTLENQATVEFHSGDKTME
		ļ	CEKLGLSKHTTNDRTKYIDDTVKHKVKILKRESGEGRNSSDCRD
1	1		NEIKKWQLAPLRKMGQPVLPRRSSEEKSEKIPKESTTVTCTGEK
	Į.		ASKPGTHEKQEMKKKKV\EKGVLNVHPAASASKPSADQIRQSVR
1	1		HSLKDILMKRLTDSNLKVPEEKAAKVATKIEKELFSFFRDTDAK
I	1		YKNKYRSLMFNLKDPKNNILFKKVLKGEVTPDHLIRMSPEELAS
1	İ .		KELAAWRRRENRHTIEMIEKEQREVERRPITKITHKGEIEIESD
1			APMKEQEAAMEIQEPAANKSLEKPEGSEK\RKEEVDSMSKDTTS
1			QHRQHLFDLNCKICIGRMAPPVDDLSPKKVKVVVGVARKHSDNE
			AESIADALSSTSNILASEFFEEEKQESPKSTFSPAPRPEMPGTV
1			EVESTFLARLNFIWKGFINMPSVAKFVTKAYPVSGSPEYLTEDL
	1		PDSIQVGGRISPQTVWDYVEKIKASGTKEICVVRFTPVTEEDQI
			SYTLLFAYFSSRKRYGVAANNMKQVKDMYLIPLGATDKIPHPLV
1			PFDGPGLELHRPNLLLGLIIRQKLKRQHSACASTSHIAETPESA
			PPIALPPDKKSKIEVSTEEAPEEENDFFNSFTTVLHKQRNKPQQ
	}		NLQEDLPTAVEPLMEVTKQEPPKPLRFLPGVLIGWENQPTTLEL
	,		ANKPLPVDDILQSLLGTTGQVYDQ\AQSVMEQNTVKEIPFLNEQ
			TNSKIEKTDNVEVTDGENKEIKVKVDNISESTDKSABIETSVVG
1 :			SSSISAGSLTSLSLRGKPPDVSTEAFLTNLSIQSKQBETVESKE
			KTLKRQLQEDQENNLQDNQTSNSSPCRSNVGKGNIDGNVSCSEN
i i			LVANTARSPQFINLKRDPRQAAGRSQPVTTSESKDGDSCRNGEK
1			HMLPGLSHNKEHLTEQINVEEKLCSAEKNSCVQQSDNLKVAQNS
			PSVENIQTSQAEQAKPLQEDILMQNIETVHPFRRGSAVATSHFE
1			VGNTCPSEFPSKSITFTSRSTSPRTSTNPSPMRPQQPNLQHLKS
1	,		SPPGFPFPGPPNFPPQSMFGFPPHLPPPLLPPPGFG\FA\QNPM
1	į		VPWPPVV\HLP\GQPQRMMGPLSQASRYIGPQNFYQVKDIRRPE
1	1		RRHSDPWGRQDQQQLDRPFNRGKGDRQRFYSDSHHLKRERHEKE
1 1			WEQESERHRRDRSQDKDRDRKSREEGHKDKERARLSHGDRGTD
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}			QTKVLKKRHTKEKVLRRAKRRWAPIPCSMLENSLGPFPLFLQQV
1 1			QSDTAQNYTIYYSIRGPGVDQEPRNLFYVERDTGNLYCTRPVDR
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1 1			LAQQNLIVSNTEAPGDDXVYSANGFTTQTVGASAQGVCGTVGSG
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WKRCINIARDUGLFGVILDELDASEEEVPEWVKTASGMALALCR WASSLIGSEPPELLARSEELLAEPAGUNSSCLRVPHSHEY NKFAVALLDDSVRVANSSTIVPSLKHILQRNVASLAWKPLGAS VLAVACQSCILIWTLDFISLSTTPSSGCAQVLSHEHGHTVTSLA WARSGGRLISASEVDAAIR WNDVSTETCVPLEWFRGGGVTNLLW SPOOSKILATTPSAVTRVWEAQMWTCERWFILDGGCOTGCWSPD GSRLLFTVLGEPLIYSLSFPERCEGEGGALBUGGCOTGCWSPD GSRLLFTVLGEPLIYSLSFPERCEGEGA(ALBUGGCOTGCWSPD GSRLLFTVLGEPLIYSLSFPERCEGEGA(ALBUGGCOTGCWSPD GSRLLFTVLGEPLIYSLSFPERCEGEGA(ALBUGGCOTGCWSPD GSRLLFTVLGEPLIYSLSFPERCEGEGA(ALBUGGCOTGCWSPD GSRLLFTVLGEPLIYSLSFPERCEGEGA(ALBUGGCOTGCWSPD GSRLLFTVLGEPLIYSSFPERCEGEGA(ALBUGGCOTGCWSPD GSRLLFTVLGEPLIYSSFPERCEGEGA(ALBUGGCOTSCWSPD GSRLLFTVLGEPLIYSSFPERCEGEGA(ALBUGGCOTSCWSPD GSRLLFTVLGEPLIYSSFPERCEGEGA(ALBUGGCOTSCWSPD GSRLLFTVLGEPLIYSSFPERCEGACA) LOWNSIINTLCTUVRVKKRRIRLRRINDCFVSSRAUDVIFSIL LOWNSIINTLCTUVRVKKRRIRLRRINDCFVSSRAUDVIFSIL LOWNSIINTLCTUVRVCQALDDYLRPVTVLTOKKKRT FEDDSCSLVFFTIFDNCDGCLKEMKLVSPARADALFKSDLT KASSLEDLWENLSLKPANSPHVNISATLSPQVINEVMCHSDLT KASSLEDLWENLSLKPANSPHVNISATLSPQVINEVMCHSDLT LALLKTLDESKLSARKKKLLGGFRUFOKFTFITCHV GLLKLLDPGREEFRELLYFWAVAANPEEFRLOKESDNRVVK RIFSKALUDNENLSKGKKKKLLGGFRUFOKFTFITCHV VS\VK\LWAIQNGRDRNRDAGTIVCQRIDQRDYSNMTEKTTODS LIALLKTLDEDSKLSARKKKKLLGGFRUFOKFTFITCHV VS\VK\LWAIQNGRDRNRDAGTIVCQRIDQRDYSNMTEKTTODS LIALLKTLDEDSKLSARKKKKLLGGFRUFOKFTFITCHTV SLKDIKNSKCPBOTKMLIFAGDDFDVTGDYRRIKSLLIDFRG  5957 1479 451 ELQWAVANDTLDBYVKPKKRKRKFLEKREPELMENTKNMLIK CGGNANATYKVLKDVYALKKYPGULVKHDTYFTFTCHDTEFTD SKSGDCSLPMSGSHNKKRPNNLVIGRNYDYHULDMIELGIENFV SLKDIKNSKCPBOTKMLIFAGDDFDVTGDYRRIKSLLIDFRG PTVSNIRLAGLEVULHFTALASKLYFTALWSLLITERPPOTTELBFD  SKSGDCSLPMSGSHNKKRPNNLVIGRNYDYHULDMIELGIENFV SLKDIKNSKCPBOTKMLIFAGAGRAYYCPWBAGGSAQCROIPF DTYNNKRKLLMFPACOARNUTGRPSAVKLLKKSGCCTPRIE LEBWGPSLDVLKRTRUNGTKPBIFFSKNOMFGARYACHANAHGKSCOPTAP LLFTWRNGTKFBIFFSKNOMFGARYACHANAHGKRGCAPAP LLFTWRNGTKFBIFFSKNOMFGARYACHANAHGKGFTAGAQ GELVALTURGKGGGARYACPARASTOGOTYLTUTUMAGNGCHTANGKGFTANTUTUMAGNATYGTHC SDIDNNYGFTUTURGKGGGARYACPWARAFGYTVV VSDVNSDGLDDVAGGFTYNGGARYACPANATGFGANTUTUMAGCAGA GRGVLITURGKGGGARACHAVPRARFFUTGRGGARYACPTUTURG GGGYCALITURGKG	-,,,,		744	
WASSLIGSLEPHLISEREDLIAEPAQVTMWSSCCLRVPANHPHT NEFAVALLDDSVRVVANASTIVEHZQRNVALAWKLEAS VLAVACQSCILIWTLDPTSLSTRPSSGCAQVLSHPGHTPVTSLA WAPSGGRLLSASPVDAAIRWDVSTETCVPLPWRGGGVTNLW SPOSKILATTPSAVFRVMSAQWWTCERMPTLSKGCYGGWSPD GSRLLFTVLGGELIYPSGTPGVWWLCL RQQTRIGWMRGLGGERLTPWSGTPVOWWLCL RQQTRIGWMRGLGGERLTPWSGTPVOWWLCL SPOSK SITATCTGVWWRCHINGAUMYCGALMOV SCORLWQICL RQQTRIGWMRGLGGERLTPWSGTPVOWWLCL TVWSSIINTLGTQUVVKKRHRLHAMDCFVGSEAVDVTFSHL LQWKYGGUDTBPAXVVRVCQALMOV KVFEAVPTKVPGKDKKPT PEDSSCSLYRFTTIPNQDSQLGKENKLYSPAVADALFKSSDIR SASLEDLMENDSLKPANSPHVNISAFLSPQVINSVWGETIGGL LQLVDLPLLDSLLKQQEAVPKIPQFKGGSTWVNSNNLDRGILK AYSDSGDEMUSAJRCSSFLIPDANSPEKYLQKESDIRMVVK ELLFDAIGRYYSSREPLINHISDVHNGTAELLVNGKTETALEAT QLLKKLLDPQNRESFRELLYPMANDEFEKYLQKESDNRMVK RIPSKAIVDNINLSKGKTDLLVLFLVMDHGKUPKTPGTL\HKI VSVKLVAMAIONGBPARDAGYTYCDREDVSNYFEKTYKDB LLALLKTLDEDSKLSAKEKK\LLGQFYKCHPDIFIEHFGD  5957 1479 451 ELQVAVANDTILDEVVKFRYKRAKRFLERKERFKLENENTKNAMLIK GGMANATVRVLKUKVYALKKYPGVYLKKKNITRFFEGOTSLEFF SKKSDCSLFMEGSHNKKRPNNLVIGRMTDYHLDMTELGIENFV SLKDIINSKCPGGTKPMLIFAGDDIVKNIKKNITRFFEGOTSLEFF SKKSDCSLFMEGSHNKKRPNNLVIGRMTDYHLDMTELGIENFV SLKDIINSKCPGGTKPMLIFAGDDIVKLJKKKNITRFFEGOTSLEFF SKKSDCSLFMEGSHNKKRPNNLVIGRMTDYHLDMTELGIENFV SLKDIINSKCPGGTKPMLIFAGDDIVKLJKKNTRFFEGOTSLEFF SKKSDCSLFMEGSHNKKRPNNLVIGRMTDYHLDMTELGIENFV SLKDIINSKCPGGTKPMLIFAGDDIVKLJKKNTRFFEGOTSLEFF SKKSDCSLFMEGSHNKKRPNNLVIGRMTDYHADMTELGIENFV SLKDIINSKCPGGTKPMLIFAGDDIVKLJKKSMMPPALAFPKKKNIGHD TPGTTYGRIHMGKDLSKLOTRRM\KGLKKRPARRITTDHEKKS KRIKKKLMELSQPLLPHCVLLKRIIKHGSQCAPTPHE LEMMGROGALSKLOTRRM\KGLKKRPARRITTDHEKKS KRIKKLMELSQPLLPHCVLLKRIIKHGSQGSVYYCPHAGSAGCGCTPF DTTNNRKIRUNGTETEIPEKSQMGVAYTCPHAGSAGCGCTPF DTTNNRKIRUNGTETEIPEKSQMGVAYCPHAGSPTGNGQQ ELYAGIPRGAGNTGVAINSMALAFFSPCCGNNNADP CGGGCGAGFSLDFYNGGLIVGGGSFYWGGQVITASADDIA NYSFKDILRKLAGEKOTEVAPASYDDSYLGYSVAAGEFTGNSQQ ELYAGIPRGAGNTGVAINSMAMATSAFSPCGNNATHVIN VSDVNSDGLDDVUQAPLFMEREFESSPREVGGIVTLYLQVSSLL FROPQILITGTTSTGRGSAMAHLGDLAQDGOTNAAGLED GGGCCAGSSLDFLVINGNKGTGSTANTUMEVQGL GLAGGIDTGCVPDSMTSSTVSLDERFYNGGSATATUMEVQGL GANNALINNSMGCHTNSLDFRFSUGSTATTUMEVQGL SLKKK	1			,
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VILAVACQSCILIWITLDFISLATRESGCAQUISHEGHTPUTSLA WAPSGGRILIASATPUNDATRIVUMUNTETCVPLPWPRGGGVTNLLW SPDGSKILATTPSAVFRVMEAQMWTCERWPTLSGCQTGCWSPD GSRLLFTUMGGPLIYSISFPERGEGKGALATVOSCQRLMQICL RQQTRIGWMRGLGERITTPWSGTYVCWWWLCL SQTGWGGRARMATVQEKAPALMISALHSPAHRPDGFSVAQKPFGA TYVMSS LIMILGTQVGVKKRHRLHSPHOCPVGSEAVDVIFSHL IONKYFGDVDIPRAKVVRVQQLMDYKVFEAVPTXVPGKDKKFT FEDSSCSLYRFTTIPNQDSQLGKENKLYSPARYADALFKSSDIR SASLEDLWRNISLKARSPHVNISLSPQVINSWWGETIGRL LQLVDLPLLDSLLKQQEAVPKIPQFRGSTMVNSNNLDRGILK AYSDSQDEMUSAALTOCSENLPDVMISTSSFPEOPDRTDLVK ELLFDAIGRYYSSREPLLNHISDVHNGIAELLVNGKTEIALEAT QLLIKLLDPQNRESFRRLLYFMAVAANNESEKQKESDNRMVVK RISSKALVDNKNLSKGKTDLULLFL MDDGKDVFKIPGTL JEHT VS\VK\LMAIONGRDPNRDAGTYYCQRIDQKDVSNNTEKTTKDE LLIALLIKLIDEDSKLSAKEKKLLLLFL MDDGKDVFKIPGTL JEHTGD  5957 1479 451 ELQVAVAMDTLDEVVKDKTKRAKFFLEKREFKLNENTKNBMLIK GGNANATVTKVLKDVYALKKPYGVLYKKKNITRPFEDOTSLEFF SKSDCSLFMGGSINKKRPANNIJGKMTDVHLMELGIRNFV SLKDIKNSKCPEGTKPMLIFAGDDEDVTEDYRRIKSLLLDFFRG PTUSNIFLAGLEVYLHFTALNGKIYFRSYKLLLKKSGCTPPHE LEEMPSSLDLULRTHLASDDLYKLSMMMPKALKFKKKNIGHD TFOTTUGRIHMGKODLSKLQTTRM\GGKRAPABRITEDHEKS KRIKKLMELSQPLLFHCVLLKRIIKHQSIQSFL LFTWRIKTRVGTKEPIEFKSNQWFG\ATVKA\HKGKSGCFVAP LLFTWRIKTRVGTKEPIEFKSNQWFG\ATVKA\HKGKSGCFVAP LLFTWRIKTRVGTKEPIEFKSNQWFG\ATVKA\HKGKSGCFVAP LLFTWRIKTRVGTKEPIEFKSNQWFG\ATVKA\HKGKSGCFVAP LLFTWRIKTRVGTKEPIEFKSNQWFG\ATVKA\HKGKSGCFVAP LLFTWRIKTRVGTKEPIEFKSNQWFG\ATVKA\HKGKSGCFVAP LLFTWRIKTRVGTKEPIEFKSNQWFG\ATVKA\HKGKSGCFVAP LLFTWRIKTRVGTKEPIEFKSNQWFG\ATVKA\HKGKSGCFVAP LLFTWRIKTRVGTKEPIEFKSNQWFG\ATVKA\HKGKSGCFVAP LLFTWRIKTRVGTKEPIEFKSNQWFG\ATVKA\HKGKSGCFVAP LLFTWRIKTRVGTKEPIEFKSNAWHLGDNGYNDIAIGVPFAGKD GRGVLLIYNGNKDGLNTKPPFFCQOWASHAVPSGFGFTLRGD GDGCYCLITGTTFTGFGSAMAHLGDNGYNDIAIGVPFAGKD GDGCYCLITGTTFTGFGSAMAHLGDNGYNDIAIGVPFAGKD GDGCYCLITGTTFTGFGSAMAHLGDNGYNDIAIGVPFAGKD GDGCYCLITGTTFTGFGSAMAHLGDCHVPFAGKD GDGCYCLITGTTFTGFGSAMAHLGDCHVPFAGKD GDGCYCLITGTTFTGFGSAMAHLGDCHVPFAGKD GDGCAYELGFTGNSADAFT EFFFRAKAFFFUNGFYNGFGCFTCYTLATRANTYNFANTVS GARLIVDGSBDNLCVPDLKLSRAPPLVTVAGGLKGGCDFTVYLRD EFFFRAKAFFUNGFNSLDKFFFUNGFGCMASTGCTVFNLOFFTRANTYNFNTUSC QANILV	1			
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TYVWSSIINTLQTQVEVKKRRHRLKRHNDCFVGSEAVOVIFSHL IQNKYFGDVDIPAKVVRVCQALMDYKVFEAVPTKVPGKDKRPT FEDSSCSLVEPTIIPNDGSQLGKNRLTYSPARYADALFKSSDIR SASLEDWENLSLKPANSPHVNISATLSPQVINEVWGETIGRL LQLVDDPLLDSLLKQQEAVPKIPQFKGSTMVNSSNYLDRGILK AYSDSQEDENLSAAIDCSSTLPPQMVVEISSFPEDPDRTDLVK ELLEPDAIGRYYSSREPLLNHLSDVHNGIAELLUNGKTEIALEAT QLLKLLDPQNREEPBRLLYFMAVAANPSEFKLQKESDNRMVVK RIFSKAIVDNKNLSKGKTDLLVLFL\MDEQKDVFKIPGTL\KKI VS\VK\LMAIQNGNDPNRDAGYIYQGRIDQRDYSNNTEKTTKDE LLALLKTLDEDSKLSAKERKKLGGFYKKHPDIFIEHFGD  5957 1479 451 ELQVAVAMDTLDRVVKPKTKRAKRFLEKREPKLNENIKNAMLIK GGNANATVTKVLKDVYALKKPYGVDIYKKKNITRFFEDDTSLEFF SKKSGCSLEMFGSHKKRRPNNLVIGRMYDYHJUNDIELGIBNFV SLKDIKNSKCPBGTKFMLIFAGDDFDVTEDYRRLKSLLIDPFRG PTVSNIRLAGLEYVLHFTALNGKIYFRSYKLLLKKSGCRTPRIE LEEMGPSLDLVLRRTHLASDDLYKLSKKRAKPARENIEDHERKS KRIKKKLMELSOPLLKRRIKKQBOLJKKLSKRAPARENIEDHERKS KRIKKKLMELSOPLLYRRTHLASDDLYKLSKKRYKRKSTENDERKS KRIKKKLMELSOPLHFULUKRIKKQSGVYYCPWPBAGSAQCRQIPF DTTNNRKIKUNGOPLHFULUKRIKKQSGYKGYKAPABRITEDHERKS KRIKKKLMELSOPLHFULUKRIKKQSGVYYCPWPBAGSAQCRQIPF DTTNNRKIKUNTKRPIERFSWMFGATVKAHKGKSGFVAP LLFTWRNFLKPTPEKSPVSTCTVAJQNFSAVAEFSPCONSNADP EGGGYCQAGFSLDPYKNGDLIVGSGVYYCPWPBAGSAQCRQIPF DTTNNRKIKUNTKRPIERFSWMFGATVKAHKGKSGFVAP LLFTWRNFLKPTPEKSPVSTCTVAJQNFSAVAEFSPCONSNADP EGGGYCQAGFSLDPYKNGDLIVGSPGSPYWQGQVITASVADIIA NYSFKDILRKLAGERGTEVAPASYDDSYLGSVAAGEFTGDSQQ ELJAGIPRGAQMFGYSIINSTUMTPIONFTGEQMASTFGTTVV VSDVNSDGLDDVLVQAPLFMREFESNPREVGYTYLTVQSSLL FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLITNGMKDGLINTKPFPFKCQGWASHANPSGFGFTLRGD SDIDKNDYPDLUVGAPFGFKAVYRARPVVYVARAPLVTVINGVSLL FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD URSKYLITNGSLNGALBASTFCRGLEVKPILNYTERUVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDSRNHLMLIINAR NEGEGAYEAELFVNIPSERNYKFGRFGCOPFIVYLRD EFTERROKLSPINISLNYSLDSSTFKEGLEVKPILNYTERUVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDSRNHVNIT RNVVCDLGNPWVSGTNYSLGLRRAVPBLSCTYMSINVT	5956	1705	130	
IONKYFGDVDIPRAKVURVQQALMDYKVPEAUPTKVPGKDKKPT FEDSSCSLYRFTTIPNQDSQLGKENKLYSPARYADALFKSSDIR SASLEDLWEALSLKPANSPHVNISATLSPQVINEWQSETIGRL LQLVDLPLLDSLLKQQEAVPKIPQDKVVEINSFWQDENTIJGK AYSDSQBEMLSAAIDCSBYPQDGKVEINSFPEQDPORTDLVK ELLFDAIGRYYSSREPLLNHLSDVHNGIAELLVNGKTEIALEAT QLLIKLLDFQNRESFRELLYFMAVAANPSEFKLQKESDNRWVK RIPSKAIVDNKNLSKGKTDLLVLEL\MDHQKUVFKIPGTL\HKI VS\VK\LMATQNGRPDRDAGYIYCQRIDQRDYSNNTEKTTKDE LLALLKTLDEDSKLSAKEK\LIGGPYKCHPDIFIEHFGD  5957 1479 451 ELQVAVAMDTLDEVVKPKTRAKRFLEKREFKLNENIKNAMLIK GGANANTVTKVLKUVYALKKPYGYLYKKKNITRFFEDOTSLEFF SKKSDCSLFMFGSHNKKPNLVIGKWYDYHVLLMHIGIENFY SLKDIKNSKCPBGFKPMLIFAGDDEVTEDVRELKSLLIDFFRG PTVSNIRLAGLEYVLHFTALNGKIYFRSYKLLKKSGCRTPRIE LEEMGPSLDLVLRRTHLASDDLVKLSKHMPKALKPKKKNISHD T79TTYGRIHMQKQDLSKLQTRKM\KCLKRPABRITTDHEKKS KRIKKLMBLSQPLLFEVLLKRIIKJRGSFL  5958 1 3138 AAALGMLLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD DTTNNRKIRLNGTKPLEFFSNOWFG\ATVKA\HKGKSCGFVAP LLFTWENFLKDFPBKGPVGTCYVALQNFSAYAEFSPCGNSNADP EGQGYCQAGFSLDFYKNGDLIVGSFFWQQUITASVADIIA NYSFKDILKKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQQ ELVAGIPRGAQNFGVYSINSYDMTFIQNFTGEGMASYFGTTVV VSDVNSDGLDDVLVGAPLFMERFFESNPRVQQIYLYLQVSSLL FRDPQILITGTTFTGRGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRKVLIYMGNKDGLNTKPFPFECQGWASHAVPSGFFTLRGD SDIDKMDYPPLIVURGKALGVAVYARPBVVTVDAGLLHFMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQARNFFPLTVKRQKSQCQDFTVYLRD ETFFRDKLSPHISLNYSLDESTFKBGLEVKPILNYYTRRIVSE QAHILVDCGEDNICVPDLKLSARPDRHQVIIGDENHLMLIINAR NEGGGAYEAELFVMIPEBADVGIERNNKGFRPLSCEYKNENVT RWVCDLGMPWYSGTNYSLGLBFRAVERLEKTMNSINFDLQIRSS	-555	1,03	239	
FEDSSCLYRFTIT PNODSQLGKENKLYSPARYADALFKSSDIR SASLEDLWENLSLKRORADTSPQVINEVWGEETIGRL LQLVDLPLLDSLLKQQEAVEN PQPKRQSTWVNSSNYLDRGILK AYSDSQBDENLSAAIDCSEYLPDQMVWEISRSFPEQPDRTDLVK ELLFDAIGRYYSSREPLINHLSDVHNGIAELLVNGKTEIALEAT QLLKLLDFQNREEFRRLLYFMAVAANPSEFKLQKESDNRWVK RIPSKAIVDNKNLSKGKTDLLVLEI-MDHQKDVFKIPGTL\HKI VS\VK\LMATQNORDPNROJYIVQORIDORDYSNNTEKTYKDE LLNLLKTLDEDSKLSAKEKKK\LLGQPYKCHPDIFIEHFGD  5957 1479 451 ELQVAVAMDTLDRVVKPKTKRAKFLEKREPKLMENIKNAMLIK GGMANATVTKVLKDVVALKHFPKGYLTKKKNITRFFEDGTSLEFF SKKSDCSLFMFGSHNKKRPNNLVIGMYDLWKSLTIFFRG PTVSNIRLAGLEVULHFTALMGKLYFRSYKLLLKKSGCRTFRIE LEEMGPSLDLVLRRTHLASDDLYKLSKMPKALKPKKKNISHD TPGTTYGRIHMQKQDLSKLOTKM\KGLKKRPABRITEDHEKKS KRIKKLMBLSQPLLPHCVLLKRIIKHQSLQSFL ARIASULVGAPKANTSQPLUVEGGAVYXCPPRAESSACQIPF DTTNNRKIRVNGTKEPIEFKSNQWFG\ATVKA\HKGKSCGFVAP LLFTWRNFLKPTEKGPVGTCYVALJONFSAYAEFSPCGNSNADP EGGGYCQAGFSLDFYKNGLUVGGGAVYXCPPRAGSGACQIP TYSPKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQQ ELVAGIFRGAQNFGYVSIINSYDMTEQOTYTKAVADLILKPMIN NYSFKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQQ ELVAGIFRGAQNFGTVSIINSYDMTEQOTYTVOY VSDVNDSGLDDVUKGAPLFWERFFENDRFSGGTLYLVQVSLL FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLIYNGNKGLNTKFPPKFCGGVANSHAVPSGFFTLNCG SDIDKNDYPDLTVGAPGTGKVAVYRARPVVTVDAQLLHMMIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMABVQLD SLKKKGGAIKRTLFLDNHQAHRVPPLVIKRQKSGCQDFIVYILRD ETTERROKASPINISLNYSLDESTFKRGLEVKPILNTYRENIVSE CAHILVDGCGDNLCVPDLKLSARPDRHOVIIGDENHIMLIINAR NEGGGAYEAELFVMIPEBADVVGIERNNKGFRPLSCEYKMENVT RNVVCDLGNPMYSGTNYSLGLHFAVERLEKTMMSINFDLQIRSS	1			
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ELVAGIPRGAQNFGYVSIINSYDMTFIQNFTGEQMASYFGYTVV VSDVNSDGLDDVLVGAPLFMEREFESNPREVGQIYLYLQVSSLL FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLHEMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLINAR NEGEGAYEAELFVMIPEBADYYGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLBKTNMSINFDLQIRSS	1 1	1	ř	
VSDVNSDGLDDVLVGAPLFMEREFESNPREVGQIYLYLQVSSLL FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLIYMGNKDGLNTKPFPKFCQGVMASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLBKTNMSINFDLQIRSS	j l	ļ		
FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVFFAGKD QRGKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYIRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLBKTNMSINFDLQIRSS	j 1	<b>[</b>		
QRGKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDGGDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLBKTNMSINFDLQIRSS	! !	l		
SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKKQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVNIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLBKTNMSINFDLQIRSS	[	[		
LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLMYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGPENHLMLIINAR NEGEGAYEAELFVMIPEBADYYGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLBKTNMSINFDLQIRSS	) l			
SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLBKTNMSINFDLQIRSS	1	ĺ		***************************************
ETEFRDKLSPINISLNYSLDESTFKEGLEYKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLBKTNMSINFDLQIRSS	j			
QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLBKTNMSINFDLQIRSS		İ		
NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLBKTNMSINFDLQIRSS				
RMVVCDLGNPMVSGTNYSLGLRFAVPRLBKTNMSINFDLQIRSS	}		Į.	
	]		İ	
NKDNPUSNFVSLQINITAVAQVEIRGVSHPPQIVLPIHNWEPEE			1	
	L		<u> </u>	NKDNPDSHFVSLQINITAVAQVEIRGVSHPPQIVLPIHNWEPEE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, FaPhenylalanine, G=Glycine,
140:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
}			L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
{	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\=possible nucleotide insertion)
			EPHKEEEVGPLVEHIYELHNIGPSTISDTILEVGWPFSARDEFL
1			LYIFHIOTLGPLOCOPNPNINPODIKPAASPEDTPELSAFLRNS
i	ł	ł	TIPHLVRKRDVHVVEFHRQSPAKILNCTNIECLQISCAVGRLEG
	i	1	_
1	1	I	GESAVLKVRSRLWAHTFLQRKNDPYALASLVSFEVKKMPYTDQP
	1	ļ	AKLPEGSIAIKTSVIWATPNVSFSIPLWVIILAILLGLLVLAIL
	İ	l	TLALWKCGFFDRARPPQEDMTDREQLTNDKTPEA
5959	1	1166	GTSGYAAQQLPSLLKEREFHLGTLNKVFASQWLNHRQVVCGTKC
ł	1		NTLFVVDVQTSQITKIPILKDREPGGVTQQGCGIHAIELNPSRT
1		1	LLATGGDNPNSLAIYRLPTLDPVCVGDDGHKDWIFSIAWISDTM
ĺ	1	Ì	AVSGSRDGSMGLWEVTDDVLTKSDARHNVSRVPVYAHITHKALK
1	ļ		DIPKEDTNPDNCKVRALAFNNKNKELGAVSLDGYFHLWKAENTL
1	1		l .
1	1		SKLLSTKLPYCRENVCLAYGSEWSVYAVGSQAHVSFLDPRQPSY
1	1	}	NVKSVCSRERGSGIRSVSFYEHIITVGTGQGSLLFYDIRAQRFL
1		1	EERLSACYGSKPRLAGENLKLTTG\KGWLNHDETWRNYFSDIDF
	ł	L	FPNAVYTHCYDSSGTKLFVAGGPLPSGLHGNYAGLWS
5960	2853	870	FVWSDGGPRPRRGPAVGAGAAHLSDPWAMTPGTANRATNPLNKE
1	1		LDWASINGFCEQLNEDFEGPPLATRLLAHKIQSPQEWEAIQALT
1	l .	}	VLETCMKSCGKRFHDEVGKFRFLNELIKVVSPKYLGSRTSEKVK
ŀ	1		NKILELLYSWTVGLPEEVKIAEAYOMLKKOG\IVKSDPKLPDDT
1	1	!	TFPLPPPRPKNVIFEDEEKSKMLARLLKSSHPEDLRAANKLIKE
l		İ	MVQEDQKRMEKISKRVNAIEEVNNNVKLLTEMVMSHSQGGAAAG
			SSEDL\MKEL\YQRCERMRPTLFPTGRVDTEDND\EALAEILQA
i		l .	
l	1		NDNLTQVINLYKQLVRGEEVNGDATAGSIPGSTSALLDLSGLDL
-	İ		PPAGTTYPAMPTRPGEQASPEQPSASVSLLDDELMSLGLSDPTP
İ		i	PSGPSLDGTGWNSFQSSDATEPPAPALAQAPSMESRPPAQTSLP
i	1		ASSGLDDLDLLGKTLLQQSLPPESQQVRWEKQQPTPRLTLRDLQ
			NKSSSCSSPSSSATSLLHTVSPEPPRPPQQPVPTELSLASITVP
	i		LESIKPSNILPVTVYDQHGFRILFHFARDPLPGRSDVLVVVVSM
İ	i	ļ	LSTAPOPIRNIVFQSAVPKVMKVKLQPPSGTELPAFNPIVHPSA
Į.	1	1	ITQVLLLANPQKEKVRLRYKLTFTMGDQTYNEMGDVDQFPPPET
		ļ	WGSL
5961	198	3147	SGEPRPEPGNMATCIGEKIEDFKVGNLLGKGSFAGVYRAESIHT
3,01	1 230	314,	GLEVAIKMIDKKAMYKAGMVQRVQNEVKIHCQLKHPSILELYNY
1		ļ	
		<u> </u>	FEDSNYVYLVLEMCHNGEMNRYLKNRVKPFSENEARHFMHQIIT
i	1	İ	GMLYLHSHGILHRDLTLSNLLLTRNMNIKIADFGLATQLKMPHE
	1	i	KHYTLCGTPNYISPEIATRSAHGLESDVWSLGCMFYTLLIGRPP
l	1	i	FDTDTVKNTLNKVVLADYEMPTFLSIEAKDLIHQLLRRNPADRL
			SLSSVLDHPFMSRNSSTKSKDLGTVEDSIDSGHATISTAITASS
	İ		STSISGSLFDKRRLLIGQPLPNKMTVFPKNKSSTDFSSSGDGNS
1	<b>!</b> .	Į	FYTOWGNOETSNSGRGRVIODAEERPHSRYLRRAYSSDRSGTSN
į			SQSQAKTYTMERCHSAEMLSVSKRSGGGENEERYSPTDNNANIF
!			NFFKEKTSSSSGSFERPDNNOALSNHLCPGKTPFPFADPTPQTE
ļ			TVQQWFGNLQINAHLRKTTEYDSISPNRDFQGHPDLQKDTSKNA
1			****
	1		WTDTKVKKNSDASDNAHSVKQQNTMKYMTALHSKPEIIQQECVF
Ì			GSDPLSEQSKTRGMEPPWGYQNRTLRSITSPLVAHRLKPIRQKT
1			KKAVVSILDSEEVCVELVKEYASQEYVKEVLQISSDGNTITIYY
ļ.			PNGG\RGFPLA\DRPPSFT\DNISR\YSF\DNLPEKYWRKYQYA
i	İ		SRFVQLVRSKSPKITYFTRYAKCILMENSPGADFEVWFYDGVKI
1	1		HKTEDFIQVIEKTGKSYTLKSESEVNSLKEEIKMYMDHANEGHR
1			ICLALESIISEBERKTRSAPFFPIIIGRKPGSTSSPKALSPPPS
			VDSNYPTRDRASFNRMVMHSAASPTQAPILNPSMVTNEGLGLTT
l			TASGTDISSNSLKDCLPKSAQLLKSVFVKNVGWATQ\LTSGAVW
l			VOFNDGSQLVVQAGVSSISYTSPNGQ\TTR\YGENEKLPDYIKQ
1			
	<u> </u>		KLQCLSSILLMFSNPTPNFH
5962	20	2447	RVCSSSASTASQAVMADAWEETRRLAADFQRAQFAEATQRLSER
			NCIEIVNKLIAQKQLEVVHTLDGKEYITPAQISKEMRDELHVRG
			GRVNIVDLQQVINVDLIHIENRIGDIIKSEKHVQLVLGQLIDEN
}	Į		YLDRLAEEVNDKLQESGQVTISELCKTYDLPGNFLTQALTQRLG
			RIISGHIDLDNRGVIFTEAFVARHKARIRGLFSAITRPTAVNSL
	j .		ISKYGFQEQLLYSVLEELVNSGRLRGTVVGGRQDKAVFVPDIYS
	]		RTOSTWVDSFFRONGYLEFDALSRLGIPDAVSYIKKRYKTTOLL

Mo:    Mo:	070	Predicted	Predicted end	Amino acid segment containing signal peptide
Not   nucleotide   corresponding to first simino acid residue of sainto acid residue of sainto acid residue of sainto acid sequence   sequenc	SEQ	· ·		
location   cofirst   amino acid   residue of   amino acid   residue of   amino acid   residue of   amino acid   amino acid   residue of   amino acid   amino acid   residue of   residue				
corresponding to first mino acid residue of amino acid residue of amino acid sequence sequenc	NO:	1		
to first amino acid residue of amino acid sequence  #Tryptophan, Y=Tyrosine, K=Unknown, *=Stop coden, Y=possible nucleotide deletion, Coden, Y=possible nucleotide deletion, PLEARCWGGUPUPUSAVERITSESSWTMVLXELLPTSLSVEDA ALLIQOWMRAFSKQASTVVESDTVVVSEKP, INDICTELFRELME  ##Tryptophan, Y=Tyrosine, K=Unknown, *=Stop coden, Y=possible nucleotide insertion)  ##Tryptophan, Y=Tyrosine, K=Unknown, *=Stop coden, Y=possible nucleotide deletion, Coden, Y=possible nucleotide insertion)  ##Tryptophan, Y=Tyrosine, K=Unknown, *=Stop coden, Y=possible nucleotide insertion  ##Tryptophan, Y=Tyrosine, X=Unknown, *=Stop coden, Y=possible nucleotide insertion  ##Tryptophan, Y=Tyrosine, X=Unknown, Y=possible coden, Y=possible nucleotide insertion  ##Tryptophan, Y=Tyrosine, X=Unknown, Y=possible coden, Y=possible nucleotide insertion  ##Tryptophan, Y=Tyrosine, X=Unknown, Y=possible coden, Y=possible nucleotide insertion  ##Tryptophan, Y=Tyrosine, X=Unknown, Y=possible coden, Y=possible nucleotide insertion  ##Tryptophan, Y=Tyrosine, X=Unknown, Y=possible coden, Y=possible nucleotide insertion  ##Tryptophan, Y=Tyrosine, X=Unknown, Y=possible coden, Y=possible nucleotide insertion  ##Tryptophan, Y=Tyrosine, X=Unknown, Y=possible  ##Tryptophan, Y=Tyrosine, X=Unknown, Y=possible  ##Tryptophan, Y=Tyrosine, X=Unknown, Y=possible  ##Tryptophan, Y=Tyrosine, X=Unknown, Y=possible  ##Tryptophan, Y=Tyrosine, Y=possible nucleotide  ##Tryptophan, Y=Tyrosine, Y=possible  ##Tryptophan, Y=Tyrosine, Y=possible  ##Tryptophan, Y=Tyrosine, Y=possible  ##Tryptophan, Y=Tyrosine, Y=possible  ##Tryptophan, Y=Tyrosine, Y=possible  ##Tryptophan, Y=Tyrosine, Y=possible  ##Tryptophan, Y=Tyrosine, Y=possible  ##Tryptophan, Y=Tyrosine, Y=possible  ##Tryptophan, Y=possible nucleotide  ##Tryptophan, Y=possible nucleotide  ##Tryptophan, Y=possible nucleotide  ##Tryptophan, Y=possible  ##Tryptophan, Y=possible  ##Tryptophan, Y=possible  ##Tryptophan, Y=possible  ##Tryptophan, Y=possible  ##Tryptophan, Y=possible  ##Tryptophan, Y=possible  ##Tryptophan, Y=possible  ##Trypto				
amino acid residue of amino acid sequence  Sequence  Ocdon, /~possible nucleotide deletion /~possible nucleotide deletion /~possible nucleotide deletion /~possible nucleotide deletion /~possible nucleotide deletion /~possible nucleotide deletion /~possible nucleotide deletion /~possible nucleotide deletion /~possible			i e	
### ### ### ### ### ### ### ### ### ##	1			
amino acid sequence			. —	
Pequence			amino acid	
PICKANGYGGIUDQVERAYBERATSSGTWUTLAPLISTSLSVEDA AILLIQUWRAFSKORATVYSDTVVYSURFY) INDICTEL FREIMH OKAEKEMKNIPHLITEDLIGISTLSSVSTSKOKKOREREKKA TEBSGSNRGGGGGRAEF VIK KUKKKERKERDDDSDDSSGSSHTÖK KKPETSPRFODE I EDPLIKKHI JODAPEEFI SELABYLI KEPINGTY LEVVRSVPMSSTTSASGTGKRIT KUIO GEFSIKLIVAH KIPKIG MKFFADDTQAALTKHLIJKSVCTDTNLI SPINIASDLAMAVODDPA AITSEIRKKI ISAKLISEKSEEFIKVAJIK KIHASILAKSIAKSI SEDITSCLDSA ABACOIMVKGOKKRERQI LPGHRQALASDLKYTEDPALI LIHLI SVILLFOFSTISMLIHAGRGCVPQI LAF INSKY PEDDHALI LIHLI SVILLFOFSTISMLIHAGRGCVPQI LAF INSKY PEDDHALI LIHLI SVILLFOFSTISMLIHAGRGCVPQI LAF INSKY PEDDHALI LIHLI SVILLFOFSTISMLIHAGRGCVPQI LAF INSKY PEDDHALI LIHLI SVILLFOFSTISMLIHAGRGCVPQI LAF INSKY PEDDHALI LIHLI SVILLFOFSTISMLIHAGRGCVPQI LAF INSKY PEDDHALI LIHLI SVILLFOFSTISMLIHAGRGCVPQI LAF INSKY PEDDHALI LIHLI SVILLFOFSTISMLIHAGRGCVPQI LAF INSKY PEDDHALI LIHLI SVILLFOFSTISMLIHAGRGCVPQI LAF INSKY PEDDHALI LIHLI SVILLFOFSTISMLIHAGRGCVPQI LAF INSKY PEDDHALI LIHLI SVILLFOFSTISMLIHAGRAF LAF INSKY PEDDHALI LAF INSKY MGLPGIQOKKGDKONGGKGI GOKORGRGCH GORGOFOFOPOPOPO GPPGLDGKOPGREFSED FIROVITOVI TRAQLEVILLGSGRIINCOM AKERGKEGPOVRAG FOLGOPOPOPOPOSOPORI ISKEG PRODDALORGOMERIKOFOLGOPOPOPOPOSOPORI ISKEG PRODDALORGOMERIKOFOLGOPOPOPOPOSOPORI ISKEG PRODDALORGOMERIKOFOLGOPOROPORI SVEREC PRODPALORGOMERIKOFOLGOPOROPOROPORI ISKEG PRODDALORGOMERIKOFOLGOPOROPOROPOROPORI ISKEG PRODDALORGOMERIKOFOLGOPOROPOROPOROPORI ISKEG PRODDALORGOMERIKOFOLGOPOROPOROPOROPORI ISKEG PRODDALORGOMERIKOFOLGOPOROPOROPOROPOROPORI ISKEG PRODDALORGOMERIKOFOLGOPOROPOROPOROPOROPOROPOROPOROPOROPOROPO	1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ALLIQQVMRAPSKQASTVYPSDTVWVSEKY INDCTELPREEMED  (KAEKEMANDPHULTEDELQUISTLESSUTSIKKKDERRRKA TESSSSMRGGGGGNARFYKIKVKKGRKDDDSDDSSQSSHTER  (KEPETSPROPEDELEDFLRHIQDAPEET)SELASTLIKPLINETY LEVVRSVWRSSTSASCTGRKTIKDLGEEVSNILVNINIKLPKINETY LEVVRSVWRSSTSASCTGRKTIKDLGEEVSNILVNINIKLPKINETY LEVVRSVWRSSTSASCTGRKTIKDLGEEVSNILVNINIKLPKINETY LEVVRSVWRSSTTASSCTGRKTIKDLGEEVSNILVNINIKLPKINETY LEVVRSVWRSSTTASSCTGRKTIKDLGEEVSNILVNINIKLPKOLDEN ATTSEIRRKILSKLSEETEVALITCHINSLINESSIEDPISCLDEL SVLLOVSTINIKLPGLASCALDECTHILITA SVLLOVSTINIKLPGOPALSTLEUGHAS AEACOTIWVKRGKKKREGOLIDOKRGALAGOLKVTDELGILS SINDUMLKSRKSSTTEE  PHAPPOPPFGRIEGHAN \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	j	sequence		\=possible nucleotide insertion)
OKAEKEMINPHILITEBUKGISTLESUSTLESustlesustl				FLKAACVGQGLVDQVEASVEEAISSGTWVDIAPLLPTSLSVEDA
TBSSSSMRGGGGNAREYKIKKUKKGEKDDBSDBSGSSHTGE KKPETESPROPEDELEDPLENHICOPEEPISLASELASELIKEUNITY LEVVRSVPMSSTTSASCTGRRTIKDLGEEVSNILVNNIKLEUNITY LEVVRSVPMSSTTSASCTGRRTIKDLGEEVSNILVNNIKLEUNITY LEVVRSVPMSSTTSASCTGRRTIKDLGEEVSNILVNNIKLEUNISLA ALPADIOAALTKLLKSVETEVALTKLLHSVETDTLIFPLEABLABLMAVDDPA ATTSEIRKKILSKLSETEVALTKLHNSLEKSIDPISCLGE SPACETORY ALPASTASSASSASSASSASSASSASSASSASSASSASSASSA	1	<b>!</b>	<b> </b>	AILLOOVMRAFSKOASTVVFSDTVVVSEKF\INDCTELFRELMH
TBSSSSMRGGGGNAREYKIKKUKKGEKDDBSDBSGSSHTGE KKPETESPROPEDELEDPLENHICOPEEPISLASELASELIKEUNITY LEVVRSVPMSSTTSASCTGRRTIKDLGEEVSNILVNNIKLEUNITY LEVVRSVPMSSTTSASCTGRRTIKDLGEEVSNILVNNIKLEUNITY LEVVRSVPMSSTTSASCTGRRTIKDLGEEVSNILVNNIKLEUNISLA ALPADIOAALTKLLKSVETEVALTKLLHSVETDTLIFPLEABLABLMAVDDPA ATTSEIRKKILSKLSETEVALTKLHNSLEKSIDPISCLGE SPACETORY ALPASTASSASSASSASSASSASSASSASSASSASSASSASSA	1		1	OKAEKEMKNNPVHLITEEDLKOISTLESVSTSKKDKKDERRRKA
KKPEISPRÖDELEDPLREHIJODAPERISISLEHLIKUNISLEIPEK HKYPADDIOAALTKHLIKSVCTDITHLIFPIKABLEMAVADDA ATTSEIRKKILEKSKJESTKVALIKLINSLEKSIEDISCLOSA ABACDIMWKRGUKKRERGILFORROALBAGUKYTEDPALLIKUL SULLPOPSTINSHLAHPORCYPOILTALISINPIKABIDHAVADDA ATTSEIRKKILEKSKJESTKVALIKHINSLEKSIEDISCLOSA ABACDIMWKRGUKKRERGILFORROALBAGUKYTEDPALLIKUL SULLPOPSTINSHLAHPORCYPOILTALISKINPIDOHALIUWKYC LUYWGLIVJOSKKTOGOBYPIJANELDKEQEDVASTTRKELQELSS SIKDUJUKSKSKSVTEE  PRIPODPFORIEGIMO JOKEGIPP VÕQGIKKGAPGMA (GLUGOS GSPGPOTTOSKORGENGIQGKOENGRGIRFOQTIGHHIO AKGERGKROEPOVAGAIGKEGSOVOLIMOTAGPROQFODPON GSPGLOSKORGENGIGGKOENGRGIRFOQTIGHHIO AKGERGKROEPOVAGAIGKEGSOVOLIMOTAGPROQFODPON GPRILOKORGESTEGOTIRVOUTIARLIPVILLGGRIRMCDI CLAGHISFEI POPPOPIGEGERBRIJGLERGOVOPPOLIVOVAGA GVAGIKKALPORDEKSSOGOTOVARADITARLIPVILLANDERIARDE GVAGIKKALPORDEKSSOGOTOVARADITARLIPVILLANDERIARDE GVAGIKKALPORDEKSSOGOTOVARADITARLIPVILLANDERIARDE RKOPAY  SCATRIGALBELOPPOPIGEGERBRIJGLERGOVAPOLIVOVARADITARLIPVILLANDERIARDE FROPPELIANTELQVASTEVILGERYMTPSDEVORYLIGIKNDNN PRIVOLLAGOVADOVAROLITSVOEPIALPSSU-CAPDSMYTIVAPOP PRIVOLIAGOVADOVAROLITSVOEPIALPSSU-CAPDSMYTIVAPOP PRIVOLIAGOVADOVAROLITSVOEPIALPSSU-CAPDSMYTIVAPOP PRIVOLIAGOVADOVAROLITSVOEPIALPSSU-CAPDSMYTIVAPOP PRIVOLIAGOVADOVAROLITSVOEPIALPSSU-CAPDSMYTIVAPOP PRIVOLIAGOVADOVAROLITSVOEPIALPSSU-CAPDSMYTIVAPOP PRIVOLIAGOVADOVAROLITSVOEPIALPSSU-CAPDSMYTIVAPOP PRIVOLIAGOVADOVAROLITSVOEPIALPSSU-CAPDSMYTIVAPOP PRIVOLIAGOVADOVAROLITSVOEPIALPSSU-CAPDSMYTIVAPOP RKORMANING HAVINASGRILIADISTACHAGADAPALLENGAROLITSVOEPIALISMO ELVIKIYSTILAOTAKOADOVAROLITSVOEPIALPSSU-CAPDSMYTIVAPOR PRIVOLIAGOVADOVAROLITSVOEPIALPSSU-CAPDSMYTIVAPOR PRIVOLIAGOVADOVAROLITSVOEPIALPSSU-ROLITANDOVAROLITSVOEPIALPSSU-ROLITANDOVAROLITSVOEPIALPSSU-ROLITANDOVAROLITSVOEPIALPSSU-ROLITANDOVAROLITSVOEPIALPSSU-ROLITANDOVAROLITSVOEPIALPSSU-ROLITANDOVAROLITSVOEPIALPSSU-ROLITANDOVA	j	<b>§</b>	]	
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SCRTRGLSPLQFREAGSSRGSRASSEPPREGMEEACQVOTTK   RGDPHBLRNIFLQYASTEVDGERYMTPEDFVQKYLGLINNDPNSN     PKIVQLLAGVADQTKOGLISYGCPTLAFESVLCAPDSMFTVAFQL     FDKSGNGSVTFENVKEIFGGTIIHHHIPFNNDCEFIRLHEGHNK     KKHLNYTEFTGPLGPLGLGLEHAGPALKDKISKGMISGLDFSDI     MVTIRSHMLTPFVEENLVSAAGGSISHQVSFSYFNAFNSLLNNM     ELVRKIYSTLAGTRKDAEVTKEERQGSISHQVGATPLEIDILVQ     LADLYMASGRLTLADIERIAPLAEGALPYNLÄELGRQGSFGLGR     PIMIQTAESSAYRFTLGSVAGAVGATAVYPJDLVKTRMQNGRGSG     SVWGELMYNNSPCFKKVLATKEFGQSSALVGAGAGGQSQVIFTNPLEI     VKIRLQVAGEITTGFRVSALMVLRDLGIFGLYKGAKACFLRDIP     FSAIYSPVVAHCKLLLADENGHVGGSLNLLAAGAMAG VPAASLV     TPADVIKTELQVAARAGGTTYSGVIDGFRKIL\RBEGPSAFWKK     TARAVBRSSQPGV-VVLVTYELLGFGYYDFGGKLAGASPFKK     TARAVBRSSQPGV-VVLVTYELLGFGYYDFGGKLAFAGSFFFKK     TARAVBRSSQPGV-VVLVTYELDGFYDFGGKLAFAGSFFFKK     TARAVBRSSQPGV-VVLVTYELDFAPLAGAGSPSISTSASAS     SVGCSCAGAKASLDGKMMGLMCGRRELLRLLGSGRRVHSVAGP     SQWLGKLTTRLLFPAAPCCCRAGFYIDFGKLAFAGSFFKK     GSYCAGAKASLDGKMMGLMCGRRELLRLLGSGRRVHSVAGP     SQWLGKLTTRLLFPAAPCCCRAFYLDLAAGAGHSYYASSEMAL     YQKHGIKLLYRPLLIPAPAPCCRAFIREAKLAGCHLEFYYKASSEMAL     YQKHGIKLLYKPLLIPATOAPIFISFFIAARCTVFARCLIFPILV     GGRFARRIINHIPADIGLFFMWAVLELGAETGVOSSDLQW     MRRVIRMMPLITLPITMHFFTAVFMYMLSINLFSLTQVSCLLIP     AVKTULKIFQRVVHDLDKLPPREGFLESFKKGMKNAEMTROLRE     REQRMNQLELAARGGLRGTFTHNPLLQPGKDNPPNIPSS\SSS     SSKPKSKYPWHDTLG     SSKPMRQUELARAGGLRGTFTHNPLLQPGKDNPPNIPSS\SSS     SSKPKSKYPWHDTLG     SDEFRLRGSSPWQCPVCRSIKKKNTNKQEMGYLTRFUSRML     SDEFRLRGSSPWQCPVCRSIKKKNTNKQEMGYLFRIVERNUK     SDEFRLRGSSPWQCPVCRSIKKKNTNKQEMGYLFRIVERNUK     RAIDLNKKGKDNKHPMYRRLVHSAVDPTIQEKVNEGKYRSYEE     FKADAGLLLHNTVIFYGADSQADALAMLKKDCTCHEL\DELQLC     KNCFYLANARPDNWCYPVCISHKANDAVKDTCHEL\DELQLC     KNCFYLANARPDNWCYPVCISHKANDAVKDTCHEL\DELQLC     KNCFYLANARPDNWCYPVCISHLANARMSGFFFPAKMGKE     DNQVDVFFGHHIQRAWIPSENIODITVNIHRLHVKRSKGMKKA     CDELELHORFIREGRFWKSKNEDRGEEERSSISSTSNEQLKVA     CGEPAKKGRRNQSVEPKKEEEPSTEAVSSSGEPTMOGEKOT	1	1		
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SUSTOTKKLSASSPRILHRSTOTTNDGVCQSMCHRYTKTFNDP KDRNKSDKRRETERVVPELEKLESTBERGADVIKAVANIMGG EMDRICKQVKEKCEFFVEETKKLATOHKOLISOTKKKQMCYNC EERAMYLCKOWTEKCEFFVEETKKLATOHKOLISOTKKKQMCYNC EERAMYLCKOWTEKCENCOWTHAEHKRYCRFKR  5968 81 1288 VRFFREGGAPFTVLTVGRQQGVFLGYGSEPDIPARGOPHEP REVGVSTSAQAQVQPRAMERRILALGLGYCLLAGTSLSVLWVYL ENGLEVSTVPYTYLDCEIPINKLHYKEKPLQPVVWSQYPQPKL LEHRPTQLLTLTDRILAPIVSEGTENNELIYKEKPLQPVVWSQYPQPKL LEHRPTQLLTLTDRILAPIVSEGTENNELIYKEKPLQPVVWSQYPQPKL LEHRPTQLLTLTDRILAPIVSEGTENNELIYKEKPLQPVVWSQYPQPKL LEHRPTQLLTTTBRILAPIVSEGTENNELIYTTINPAAPVEGVPLOPHIL LSSIPIQGHEIMBETSMRRMETISQHTAKRAHREVDTLFCLDUD MVFRIPMWGPFLIGDLUAAH HBYYXVPGPYERRKYSTAFVA DSEGDFYYGGAVFGGQVARVYEFTRGCHMAILADKANGIHAAWR EESHLINRHYISNKSKVLS PEYLMDDRKPQPPSEKKLTRFSTLDK DISCLES  5969 1126 593 DUGFNIKKRCDLDVFLESPRKPSGRRDRAPERGRRIAANKCLC TGVREGEPPS/TTSGXVKEAGRDFTLIVVLPGISITGGLFTTI FKELESSSSSPSKITGRALEKCRSHPEVIGVFGESVKYGGVTVA GREGRUFVRFTEVVKOGLKHTCVKFYTEGSPEKGTOVVAQVYENP GSGEVDFRYIFVSLESYPRRTILIENNSQDD  5970 316 4712 SQNNIGHRLDVAGDATERRVLEVEKEDTEELRGKYVDVKKKATA KALEDLRANFYCELCDKOYQYKONGFTNDHINS VDHAHKQRIKDLK QRFFARNVSSRSKKDEKKQEKALFRIHHELASQHXQARCARGSGP MFXPTTAVAVDEEGGEDDKODESATNSGTGATASCGIGSFSTDKG GPFTAVQITHTTGLAQAGLASQGISFGIRNLETPLQKIGVSF SFAKKARVALESIASVFKOHABERTSEGGTKPDEKSDGGLQKV GDSDGSSNLDGKKEDEDDCOGSLASTIS KLKRKKREGAGATE PSYTHYIPPAHCKVKPNFPFLLWRASEGOMDATHPIKNADES KAGSSFKYKSKCIKAARGCARKTVSSVEROPKETSMTEPSEGS KAGSSKYKSKKIKKRKKKKKKKKKKKKKKKKKKKKKKRESKKALDAFPA GKESSGEGRKFTOFFFUSKDSTALGOLIKQEPGGSFGFB PRENRRAGDDSGRSSLDGKEVETOPLSKDSTALGOLIKQEPGGGSFA PFRENRRAGDDSGRSSLDGKSSTSGNERGEBENGSSSRGHGGE PKKSKVOGEKIVRSSGGRMADARGSANGELLIFTKRAPSISS SKARSGESKSKKRKKKKKKKKKKKKKKKKKKKSKRHEKRANGTESS SKARSGESEEEBEDSGSBRSSLSSRSRSRSHBENDDDSYMS SKARSGESSESSBRSSRSSRSRSRSSRSSSSSSS SCSRSSKRRGRSTTALSWORSRSYSSRSDBASSSSSSSS SCSRSSKRRGRSTTALSWORSRSYSSRSDBASSSSSSSS SCSRSSKRRGRSTTALSWORSRSYSSRSDBASSSSSSSS SCSRSSKRRGRSTTALSWORSRSYSSRSDBASSSSSSSSS SCSRSSKRRGRSTTALSWDSSRSTSTRDBRSTTERSPSQRSSS SCSRSSKRRGRSTTALSWDSSRSTSCDCSSSSSDDGOKKT DDGRDDSKATGPPSQNSNIGTGRGSECDCSPTORTHVLUAPLE LEKRYDHENGTHENGENG	}			
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GKESQEGPKHPTGPFFPVLSKDESTALQWPSELLIFTKAEPSIS YSCNPLYPDFKLSRNKDARTKGTEKPKDIGSSSKDHLQGLDPGE PNKSKEVGGEKIVRSSGGRMDAPASGSACSGLNKQEPGGSHGSE TEDTGRSLPSKKERSGKSHRHKKKKHKKSSAHARTEEK SSKAESGEKSKKRKRKRKKNKSSAPADSBRGPKPEPPGSGSPA PPRRRRAQDDSQRRSLPAEEGSSGKKDEGGGSSSQDHGGRKH KGELPPSSCQRRAGTKRSSRSSHRSQPSSGDEDSDDASSHRLHQ KSPSQYSEEEEEEDGSEHSRGRRHSSHRSSRSYSSSS DASSDQSCYSRQRGYSDDSYSDYSDRSRRHSKRSHDSDDSYAS SKHRSKRHKYSSSDDDYSLSCSQRSRSRSHTRERSRSGRSRS SSCSRSRSKRRSRSTTAHSWQRSRSYSDDSSTRSPSQRSGSR KRSWGHESPEERHSGRDFIRSKIYRSQSPHYFRSGRGEGPGKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEDKNSVTAKLLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPS LGNKPVLPLIGKLPATRKPNKCEESGLERGEEQVESTEEGPP GSSDALFGHQFF\SEETTGPLLDPPPESSKGEVTADHPVAPLG PPAHFDCYLGDPTISHNYLPDPSGNTLESLDSSSQPGPVESSL	1 [	ł		
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PNKSKEVGGEKIVRSSGGRMDAPASGSACSGLNKQEPGGSHGSE TEDTGRSLPSKKERSGKSHRHKKKKKKKKSKSKHKRKHKADTEEK SSKAESGEKSKKRKKRKKKKKKKKKKKHKADTEEK SSKAESGEKSKKRKKRKKKKKKKKSSAPADSERGPKPEPPGSGSPA PPRRRRAQDDSQRRSLPAEEGSSGKDEGGGSSSQDHGGRKH KGELPPSSCQRRACTKRSSRSSHRSQPSSGDEDSDDASSHRLHQ KSPSQYSEEEEEEDGSEHSRSRSRSGRRHSSHRSSRSYSSSS DASSDQSCYSRQREYSDDSYSDYSDRSRRHSKRSHDSDDSDYAS SKHRSKRHKYSSSDDDYSLSCSQSRSRSHTRERSRGRSRS SSCSRSRSKRSRSTTAHSWQRSRSYSRDRSRSTRSPSQRSGSR KRSWGHESPEERHSGRRDFIRSKIYRSQSPHYFRSGREGPGKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEDKNSVTAKLLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGFKLPPS LGNKPVLPLIGHPATRKPNKKCEESGLERGEBQQSETEBGPP GSSDALFGQFF\SEETTGPLLDPPPESSKSGEVTADHPVAPLG PPAHFDCYLGDPTISHNYLPDPSGNTLESLDSSSQPGPVESSL	<b>;</b>	1		GKESQEGPKHPTGPFFPVLSKDESTALQWPSELLIFTKAEPSIS
TEDTGRSLPSKKERSGKSHRHKKKKHKKSSKHKRKHKADTEEK SSKAESGEKSKKRRKKRKKKKKKKKKSKHKRKHKADTEEK SSKAESGEKSKKKRKKRKKKKKKKKKSAPADGERGPKPEPPGGGSPA PPRRRRAQDDSQRRSLPAEEGSSGKKDEGGGSSSQDHGGRKH KGELPPSCQRRAGTKRSSRSSHRSQPSSGDEDSDDASSHRLHQ KSPSQYSEEEEEEDGSEHSRSRSRSGRRHSSHRSSRSYSSSS DASSDQSCYSRQRGYSDDSYSDYSDRSRRHSKRSHDSDDSDYAS SKHRSKRHKYSSSDDDYSLSCQSRSRSRSHTRERSRSRSRS SSCSRSRKRRSRSTTAHSWQRSRSYSRDRSRSTRSPSQRSGR KRSWGHESPEERHSGRRDFIRSKIYRSQSPHYFRSGREGEGPGKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEDKNSVTAKLLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPPS LGNKPVLPLIGKLPATRKPNKKCEESGLERGEEQQSETEBGPP GSSDALFGQFF\SEETTGPLLDPPPESSKSGEVTADHPVAPLG PPAHFDCYLGDPTISHNYLPDPSDGNTLESLDSSSQPGPVESSL		ì		
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PPRRRRAQDDSQRRSLPAEEGSSGKKDEGGGGSSSQDHGGRKH KGELPPSSCQRRAGTKRSSRSSHRSQPSSGDEDSDDASSHRLHQ KSPSQYSEEEEEEDGSSEHSRSRSGRRHISHRSSRRSYSSSS DASSDQSCYSRQRSYSDDSYSDYSDRSRRHSKRSHDSDDSYAS SKHSKRHKYSSSDDDYSLSCSQSRSRSRSHTRERSRSRGRSRS SSCSRSKKRSRSTTAHSWQRSRSYSRDRSRTRSPSQRSGSR KRSWGHESPEERHSGRRDFIRSKIYRSQSPHYFRSGRGEGPGKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEDKNSVTAKLLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPPS LGNKPVLPLIGKLPATRKPNKKCEESGLERGEEQPETEBGPP GSSDALFGHQFF\SEETTGPLLDPPPESSKGEVTADHPVAPLG PPAHFDCYLGDPTISHNYLPDPSGNTLESLDSSSQPGPVESSL				
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KSPSQYSEEEEEDGGSEHSRSRSGRRHSSHRSSRRSYSSSS DASSDQSCYSRQREYSDDSYSDYSDRSRRHSKRSHDSDDSDYAS SKHRSKRKKYSSSDDDYSLSCSQSRSRSHTRERSRRGRSRS SSCSRSSKRSKRSTTAHSWQRSRSYSRDRSRSTRSPSQRSGSR KRSWGHESPEERHSGRRDFIRSKIYRSQSPHYFRSGREGPGKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEDKNSVTAKLLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPPS LGNKPVLPLIGHATRKPNKKCEESGLERGEBQEQSETEBGPP GSSDALFGUFF\SEETTGPLLDPPPESSKSGEVTADHPVAPLG PPAHFDCYLGDPTISHNYLPDPSDGNTLESLDSSSQPGPVESSL		İ	ł	
DASSDQSCYSRQRGYSDDSYSDRSRRHSKRSHDSDDSDYAS SKHRSKRHKYSSSDDDYSLSCSQSRSRSRSHTRERSRSRGRSRS SSCSRSRSKRRSRSTTAHSWQRSRSYSRDRSRSTRSPSQRSGSR KRSWGHESPEERHSGRRDFIRSKIYRSQSPHYFRSGRGEGPGKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEDKNSVTAKLLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPPS LGNRPVLPLIGKLPATRKPNKKCESGLSRGEGQEQSETEBGPP GSSDALFGHQFF\SEETTGPLLDPPPESKSGEVTADHPVAPLG PPAHFDCYLGDPTISHNYLPDPSDGNTLESLDSSSQPGPVESSL		ļ		
SKHRSKRHKYSSSDDDYSLSCSQSRSRSRSHTRERSRSRGRSRS SSCSRSRSKRRSRSTTAHSWQRSRSYSRDRSRSTRSPSQRSGSR KRSWGHESPEERIEGRRDFIRSKIYRSQSPHYFRSGRGEGPGKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEDKNSVTAKLLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPPS LGNKPVLPLIGKLPATRKPNKKCEESGLERGEBQEQSETEBGPP GSSDALFGHQFF\SEETTGPLLDPPEESKSGEVTADHPVAPLG PPAHPDCYLGDPTISHNYLPDPSDGNTLESLDSSSQPGPVESSL		ł	ı	
SSCSRSRSKRRSRSTTAHSWQRSRSYSRDRSRSTRSPSQRSGSR KRSWGHESPEERHSGRRDFIRSKIYRSQSPHYFRSGRGEGPGKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEDKNSVTAKLLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPPS LGNKPVLPLIGKLPATRKPNKKCEESGLERGEBQEGSETEBGPP GSSDALFGHQFF\SEETTGPLLDPPPESSKSGBVTADHPVAPLG PPAHFDCYLGDPTISHNYLPDPSDGNTLESLDSSSQPGPVESSL			ļ	
KRSWGHESPEERHSGRRDFIRSKIYRSQSPHYFRSGRGEGPGKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEDKNSVTAKLLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPPS LGNKPVLPLIGKLPATRKPNKKCEESGLERGEEQEQSETEEGPP GSSDALFGHQFF\SEETTGPLLDPPPESSKSGEVTADHPVAPLG PPAHPDCYLGDPTISHNYLPDPSDGNTLESLDSSSQPGPVESSL	1	}	ľ	
DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEDKNSVTAKLLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPPS LGNKPVLPLIGKLPATRKPNKKCEESGLERGEEQEQSETEEGPP GSSDALFGHQFP\SEETTGPLLDPPPEESKSGEVTADHPVAPLG PPAHPDCYLGDPTISHNYLPDPSDGNTLESLDSSSQPGPVESSL		1		
EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPPS LGNKPVLPLIGKLPATRKPNKKCEESGLERGEEQEGETEBGPP GSSDALFGHQFP\SEETTGPLLDPPPEESKSGEVTADHPVAPLG PPAHPDCYLGDPTISHNYLPDPSDGNTLESLDSSSQPGPVESSL				·-
LGNRPVLPLIGKLPATRKPNKKCEESGLERGEBQEQSETEBGPP GSSDALFGHQFP\SEETTGPLLDPPPEESKSGEVTADHPVAPLG PPAHFDCYLGDPTISHNYLPDPSDGNTLESLDSSSQPGPVBSSL	l I			
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	1		ĺ	
LPIAPDLEHFPSYAPPSGDPSIESTDGAEDA\SLAPLESOPITF	ŀ	İ		
				LPIAPDLEHFPSYAPPSGDPSIESTDGAEDA\SLAPLESQPITF

SEQ Predicted beginning beginning nucleotide location nucleotide location corresponding to first amino acid residue of amino acid sequence	E= e, top TPAL PHPQ IIPA
NO: nucleotide location corresponding to first amino acid residue of amino acid sequence Codon, /=possible nucleotide deletion, sequence PLAQVHHIPQPHLTPISLSHLTHSI IPGHPATFLASHPIH SAIHPGPFTFHPVPHAALYPTLLAPRPAAAAATALHLHPL FSCQDLQHPPSKIGT SPLYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTE	top TPAL PHPQ IIPA
location corresponding to first amino acid residue of amino acid sequence  TPEMEKYSKLQQAAQQHIQQOLLAKQVKAFFASAALAPA QPIHIQQPATASATSITTVQHAILQHHAAAAAAAIGIHPH PLAQVHHIPQPHLTPISLSHLITHSI PCHPATFLASHPIH SAIHPGPFTFPVPHAALYPTLLAPRPAAAAATALHLHPL FSGQDLQHPPSHGT  S971  53  2149  H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=S Codon, /=possible nucleotide deletion, QPIHIQQPATASATSITTVQHAILQHHAAAAAAAIGIHPH PLAQVHHIPQPHLTPISLSHLITHSI PCHPATFLASHPIH SAIHPGPFTFPVPHAALYPTLLAPRPAAAAATALHLHPL FSGQDLQHPPSHGT SPLYFVGVOMDNPIGNWDGRFDGVQLCSFACVESTILLHI PESVTQERRPPKLAFMSRGVGDKGSSSHNKPKATGSTSDP RSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTE	TPAL PHPQ IIPA
corresponding to first amino acid residue of amino acid sequence  Description acid sequence  Codon, /=possible nucleotide deletion, permittion acid sequence  Tebus Market Amino acid sequence  Tebus Market Amino acid sequence  Codon, /=possible nucleotide deletion, permittion  Tebus Market Amino acid sequence  Tebus Market Amino acid sequence  Tebus Market Amino acid sequence  Tebus Market Amino acid sequence  Tebus Market Amino acid sequence  Tebus Market Amino acid sequence  Tebus Market Amino acid sequence  Tebus Market Amino acid sequence  Tebus Market Amino acid sequence  Tebus Market Amino acid sequence  Tebus Market Amino acid sequence  Tebus Market Amino acid sequence  Tebus Market Amino, N=Asparagine, mean	TPAL PHPQ IIPA
to first amino acid residue of amino acid residue of amino acid sequence  Teproline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=S Codon, /=possible nucleotide deletion, \text{\codon} = possible nucleotide insertion)  TepemekysklQQAAQQHIQQOLLAKQVKAFFASAALAPA QPIHIQQPATASATSITTVQHAILQHHAAAAAAAIGIHPH PLAQVHHIPQPHLTPISLSHLTHSIIPGHPATFLASHPIH SAIHPGPFFFHPVPHAALYPTLLAPRPAAAAATALHLHPL FSGQDLQHPPSHGT  S971  53  2149  SPLYFVGVDMDNPIGNWDGRFDGVQLCSFACVESTILLHI PESVTQERRPPKLAFMSRGVGDKGSSSHNKPKATGSTSDP RSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTE	TPAL PHPQ IIPA
amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=S (Codon, /=possible nucleotide deletion, \text{ =possible nucleotide insertion)}  TPEEMEKYSKLQQAAQQHIQQOLLAKQVKAFPASAALAPA QPIHIQQPATASATSITTVQHAILQHKAAAAAAATGIHPH PLAQVHHIPQPHLTPISLSHLTHSIIPGHPATPLASHPIH SAIHPGPFTFHPVPHAALYPTLLAPRPAAAAATALHLHPL FSCQDLQHPPSHGT  SPLYFVGVDMDNPIGNWDGRFDGVQLCSFACVESTILLHT PESVTQERRPPKLAFMSRGVGDKGSSSHNKPKATGSTSDP RSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTE	TPAL PHPQ IIPA
residue of amino acid sequence Codon, /=possible nucleotide deletion, (=possible nucleotide insertion)  TPEEMEKYSKLQQAAQQHIQQOLLAKQVKAFPASAALAPA QPIHIQQPATASATSITTVQHAILQHHAAAAAAATGIHPH PLAQVHHIPQPHLTPISSHLTHSIIPGHPATFLASHPIH SAIHPGPFTFHPVPHAALYPTLLAPRPAAAAATALHLHPL FSGQDLQHPPSHGT  5971 53 2149 SFLYFVGVDMDNPIGNWDGRFDGVQLCSFACVESTILLHI PESVTQERRPPKLAFMSRGVGDKGSSSHNKPKATGSTSDP RSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTE	TPAL PHPQ IIPA
amino acid sequence Codon, /=possible nucleotide deletion,   -possible nucleotide insertion    TPEEMEKYSKLQQAAQQHIQQQLLAKQVKAFFASAALAFA     OPIHIQQPATASATSITTVQHAILQHHAAAAAAAIGIHPH     PLAQVHHIPQPHLTPISLSHLTHSI I PCHPATFLASHPIH     SAIHPGPFTFHPVPHAALYPTLLAPRPAAAAATALHLHPL     FSGQDLQHPPSHGT     53   2149   SFLYFVGVDMDNPIGNWDGRFDGVQLCSFACVESTILLHI     PESVTQERRPPKLAFMSRGVGDKGSSSHNKPKATGSTSDP     RSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTE	TPAL PHPQ IIPA
sequence \=possible nucleotide insertion)  TPEEMEKYSKLQQAAQQHIQQQLLAKQVKAFFASAALAFA QFIHIQQPATASATSITTVQHAILQHHAAAAAAAIGIHPH PLAQVHHIPQPHLTPISLSHLTHSIIPGHPATFLASHPIH SAIHPGPPTFHPVPHALYPTLLAFRPAAAATALHLHPL FSGQDLQHPPSHGT  S971 53 2149 SFLYFVGVDMDNPIGNWDGRFDGVQLCSFACVESTILLHI PESVTQERRPPKLAFMSRGVGDKGSSSHNKPKATGSTSDP RSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTE	PHPQ IIPA
TPEEMEKYSKLQQAAQQHIQQOLLAKQVKAFPASAALAPA QPIHIQQPATASATSITTVQHAILQHHAAAAAAAIGIHPH PLAQVHHIPQPHLTPISLSHLTHSIIPGHPATFLASHPIH SAIHPGPPTHPVPHAALYPTLLAPRPAAAAATALHLHPL FSGQDLQHPPSHGT 53 2149 SPLYFVQYDMDNPIGNWDGRFDGVQLCSFACVESTILLHI PESVTQERRPPKLAFMSRGVGDKGSSHNKPKATGSTSDP RSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTE	PHPQ IIPA
QPIHIQQPATASATSITTVQHAILQHHAAAAAAIGIHPH PLAQVHHIPQPHLTPISLSHLTHSIIPGHPATFLASHPIH SAIHPGPFTFHPVPHAALYPTLLAPRPAAAAATALHLHPL FSGQDLQHPPSHGT S971 53 2149 SPLYFVGYDMDNPIGNWDGRFDGVQLCSFACVESTILLHI PESVTQERRPPKLAFMSRGVGDKGSSHNKPKATGSTSDP RSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTE	PHPQ IIPA
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RSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTE	
FDROSPFEQFFFVNOLITERREADEPSETAMPN INGSIG	
SLSAQSVMEELNTAPVQESPPLAMPPGNSHGLEVGSLAEV	
PFYGVIRWIGQPPGLNEVLAGLELEDECAG\CTDGTF/RE	
FTCALKKALFVKLKSCRPDSRFASLQPVSNQIERCNSLAI LSEVVEENTPTQKWEKEGLEIMIG\KKKGIQGHYNSCYLD	
CLFAFSSVLDTVLLRPKEKNDVEYYSETQELLRTEIVNPL	
YVCATKIMKLRKILEKVEAASGFTSEEKDPEEFLNILFHH	
EPLLXIRSAGQKVQDCYFYQIFMEKNEKVGVPTIOOLLEW	
SNLKFAEAPSCLIIQMPRFGKDFKLFKKIFPSLELNITDLI	
PRQCRICGGLAMYECRECYDDPDISAGKIKQFCKTCNTQVI	
KRLNHKYNPVSLPKDLPDWDWRHGCIPCQNMELFAVLCIE	
VAFVKYGKDDSAWLFFDSMADRDGGQNGFNIPQVTPCPEV(	
KMSLEDLHSLDSRRIQGCARRLLCDAIYVPCTQSPTMSLYI	
5972 440 1761 ILLAGSPSPRDQCSQRQSSGGDKELVTRGCTFSTAVVSPS	
EPFREELAYDRMPTLERGRODPASYAPDAKPSDLQLSKRLi	
SHKTWVFSVLMGSCLLVTSGFSLYLGNVFPAEMDYLRCAAC	
PSAIVSFTVSRNANVIPNFQILFVSTFAVTTTCLIWFGC	
NPSAININFNLILLLLELLMAATVIIAARSSEEDCKKKK	
DSANILDEVPFPARVLKSYSVVEVIAGISAVLGGIIALNVI	
SGPHLSVTFFWILVACFPSAIASHVAAECPNKCLVEVLIA	
TSPLLFTASGYLSFSIMRIVEMFKDY2PAIKPSYDVLLLLI	
LLLQA/GPQHGHRHPVRALQGQCKAAGCILGHPERPAGAPC	
GQEPPEGVRQGESLESRRGANGPVTPRRGNRVAAPSLAPGN	
NP	
5973 65 -2007 NGDGKDLFGHIWAWRSNGIISNFRRSPHAGMAEDEPDAKSI	KTG
GRAPPGGAEAGEPTTLLQRLRGTISKAVQNKVEGILQDVQR	
NDKLYLYLQLPSGPTTGDKSSEPSTLSNEEYMYAYRWIRNE	
HTDTCLPKQSVYDAYRKYCESLACCRPLSTANFGKIIREI	PDI
KARRLGGRGQ9KYCYSGIRRKTLVSMPPLPGLDLKGSESPE	MGP
EVTPAPRDELVEAACALTCDWAERILKRSFSSIVEVARFLI	QQH
LISARSAHAHVLKAMGLAEEDEHAPRERSSKPKNGLENPEG	GAH
KKPERLAQPPKDLEARTGAGPLARGERKKSVVESSAPGANN	
NALVARLPLILLPRAPRSLIPPI PVSPPILAPRLSSGALKVA	
LSSRAGAPPAAVPIINMILPTVPALPGPGPGPGRAPPGGLT	
GTENREVGIGGDQGPHDKGVKRTAEVPVSEASGQAPPAKAA	
IEDTASDAKRKRGRPLKKSGGSGERNSTPLKSAAAMESAQS	
PWETWGSGGEGNSAGGAERPGPMGEAEKGAVLAQG\QGDGT	
GGRGPGSQHTKEAEDKIPLVPSKVSVIKGSRSQKEAFPLAK	GEV
DTAPOGNKDLKEHVLQSSLSQEHKDPKATPP	{
5974 4293 2200 LGLQMHTTSGRIHQAMVTSLNEDNESVTVEWIENGDTKGK\	
LESIFSLNP\DL\VPDGEIEPSP\ETPPPPASSAKVNKIVK	
TV\ASIKNDPPS\RDNRVVGSARARPSQFPEQFSSAQQNGS	
DISPVQAAKKEFGPPSRRKSNCVKEVEKLQEKREKRRLQQQ	
EKRAQDVDATNPNYEIMCMIRDFRGSLDYRPLTTADPIDEH	
VCVRKRPLNKKETQMKDLDVITIPSKDVVMVHEPKQKVDLT	
ENGTFRFDYAFDDSAPNEMUYRFTARPLVETIFERGMATCF	4
QTGSGKTHTMGGDFSGKNQDCSKGIYALAARDVFLMLKKPN	
LELQVYATFFEIYSGKVFDLLNRKTKLRVLEDGKQQVQVVG	
REVKCVEDVLKLIDIGNSCRTSGQTSANAHSSRSHAVFQII	,
KGKLHGKFSLIDLAGNERGADTSSADRQTRLEGAEINKSLL	
	SPG
ECIRALGRNKPHTPFRASKLTQVLRDSFIGENSRTCMIATI	, [
ECIRALGRNKPHTPFRASKLTQVLRDSFIGENSRTCMIATI MASCENTLNTLRYANRVKELTVDPTAAGDVRPIMHHPPNQI LETQWGVGSSPQRDDLKLLCEQNEEEVSPQLFTFHEAVSQM	

CTO.	Predicted	Predicted end	1 x-2
SEQ			Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alamine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
		1	
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	ł -	\=possible nucleotide insertion)
			EEQVVEDHRAVFQESIRWLEDEKALLEMTEEVDYDVDSYATQLE
	1	ŀ	
			AILEQKIDILTELRDKVKSFRAALQEEEQASKQINPKRPRAL
5975	4293	2200	LGLQMHTTSGRIHQAMVTSLNEDNESVTVEWIENGDTKGK\EID
J	i		LESIFSLNP\DL\VPDGEIEPSP\ETPPPPASSAKVNKIVKNRR
ı			TV\ASIKNDPPS\RDNRVVGSARARPSQFPEQFSSAQQNGSV\S
Į.		1	DISPVQAAKKEFGPPSRRKSNCVKEVBKLQEKREKRRLOQOELR
}		ł	EKRAODVDATNPNYEIMCMIRDFRGSLDYRPLTTADPIDEHRIC
ł	İ		VCVRKRPLNKKETOMKDLDVITIPSKDVVMVHEPKOKVDLTRYL
l	Į.		-
ł	ł	į.	ENQTFRFDYAFDDSAPNEMVYRFTARPLVETIFERGMATCFAYG
	1		QTGSGKTHTMGGDFSGKNQDCSKGIYALAARDVFLMLKKPNYKK
ļ	[		LELQVYATFFEIYSGKVFDLLNRKTKLRVLEDGKQQVQVVGLQE
1	1		REVKCVEDVLKLIDIGNSCRTSGQTSANAHSSRSHAVFQIILRR
1	1	İ	KGKLHGKFSLIDLAGNERGADTSSADROTRLEGAEINKSLLALK
	Į.		ECIRALGRNKPHTPFRASKLTQVLRDSFIGENSRTCMIATISPG
1	1	İ	1
1	1		MASCENTINTLRYANRVKELTVDPTAAGDVRPIMHHPPNQI\DD
1	1	]	LETQWGVGSSPQRDDLKLLCEQNEEEVSPQLFTFHEAVSQMVEM
1	1	1	EEQVVEDHRAVFQESIRWLEDEKALLEMTEEVDYDVDSYATQLE
L			AILEQKIDILTELRDKVKSFRAALQEEEQASKQINFKRPRAL
5976	20	2949	VHHLHLTRVSVVVNLDIILRIAQQMGIKTLNLVLG\LKRA\LBF
İ	[	ĺ	PEVSWMEVKDPNMKGAMLTNTGKYAIPTIDA\EAYAIGKKEKPP
			FLPEEPSSSSEEDDPIPDELLCLICKDIMTDAVVIPCCGNSYCD
İ		1	BCIRTALLESDEHTCPTCHQNDVSPDALIANKFLRQAVNNFKNE
	l		1
i	i	l	TGYTKRLRKQLPSPPPPIPPPRPLIQRNLQPLMRSPISRQQDPL
1	1	Ì	MIPVTSSSTHPAPSISSLTSNQSSLAPPVSGNPSSAPAPVPDIT
ŀ	1	ŀ	ATVSISVHSEKSDGPFRDSDNKILPAAALASEHSKGTSSIAITA
}	1	ł ·	LMEEKGYQVPVLGTPSLLGQSLLHGQLIPTTGPVRINTARPGGG
1		!	RPGWEHSNKLGYLVSPPQQIRRGERSCYRSINRGRHHSERSQRT
		1	CGPSLPATPVFVPVPPPPLYPPPPHTLPLPPGVPPPQFSPQFPP
l	i	İ	GQP\PPAGYSVPPPGFPPAPANLSTPWVSSGVQTAHSNTIPTTQ
İ	l .	i	
}	I	ļ	APPLSREEFYREQRRLKEEEKKKSKLDEFTNDFAKELMEYKKIQ
ł	1	Ì	KERRRSFSRSKSPYSGSSYSRSSYTYSKSRSGSTRSRSYSRSFS
		į	RSHSRSYSRSPPYPRRGRGKSRNYRSRSRSHGYHRSRSRSPPYR
	1	ì	RYHSRSRSPQAFRGQSPNKRNVPQGETEREYFNRYREVPPPYDM
	1		KAYYGRSVDFRDPFEKERYREWERKYREWYEKYYKGYAAGAQPR
	İ		PSANRENFSPERFLPLNIRNSPFTRGRREDYVGGQSHRSRNIGS
[	1		NYPEKLSARDGHNOKDNTKSKEKESENAPGDGKGNKHKKHRKRR
1	1		KGEBSEGFLNPELLETSRKSREPTGVEENKTDSLFVLPSRDDAT
1		}	
I			PVRDEPMDAESITFKSVSEKDKRERDKPKAKGDKTKRKNDGSAV
l			SKKENIVKPAKGPQEKVDG\DVRDLLDLNL\QLKKPKEETPKDL
Į.			TILNHHLPLRRMKKSL\EPP\EKLTLNQQK\TPRNKTSQRGKSE
L	<u></u>		EGLFQRCQIRKANN
5977	1363	1336	FLEDRGQVLSHFQCLSLHSINHTLHPGAGVAAGPATGW/REYLT
			PVLKESKFKETGVITPERFVAAGDHLVHHCPTWOWATGEELKVK
1			AYLPTGKQFLVTKNVPCYKRCKQMEYSDELEAIIEEDDGDGGWV
I	1		DTYHNTGITGITEAVKEITLENKDNIRLQDCSALCEEEEDEDEG
Į.			
l			EAADMEEYEESGLLETDEATLDTRKIVEACKAKTDAGGEDAILQ
i			TRTYDLYITYDKYYQTPRLWLFGYDEQRQPLTVEHMYEDISQDH
1			VKKTVTIENHPHLPPPPMCSVHPCRHAEVMKKIIETVAEGGGEL
		1	GVHMYLLIFLKFVQAVIPTIEYDYTRHFTM
5978	160	3213	RDGARRWGGCQSPLTWAPGFYRRFDLATSGRRLRGQTAEPAGRQ
1			RPRREPEAMDEQSVESIAEVFRCFICMEKLRDARLCPHCSKLCC
1			FSCIRRWLTEQRAQCPHCRAPLQLRELVNCRWAEEVTQQLDTLQ
i			
1	1		LCSLTKHEENEKDKCENHHEKLSVFCWTCKKCICHQCALWGGMH
I			GGHTFKPLAEIYBQHVTKVNEEVAKLRRRLMELISLVQEVERNV
I			EAVRNAKDERVREIRNAVEMMIARLDTQLKNKLITLMGQKTSLT
ł			QETELLES LOEVEHOLRS CSKSELISKS SEILMMFQQVHRKPM
1			ASFVTTPVPPDFTSELVPSYDSATFVLENFSTLRQRADPVYSPP
I			LOVSGLCWRLKVYPDGNGVVRGYYLSVFLELSAGLPETSKYEYR
[			<del>"</del>
Į.			VEMVHQSCNDPTKNIIREFASDFEVGECWGYNRFFRLDLLANEG
1			YLNĘQNDTVILRFQVRSPTFFQKSRDQHWYITQLEAAQTSYIQQ
1			INNLKERLTIELSRTQKSRDLSPPDNHLSPQNDDALETRAKKSA

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			CSDMLLER\GPYSAS\VREAKEDEEDEEKIQNEDYHHELSDGDL
			DLDLVYEDEVNQLDGSSSSASSTATSNTEENDIDEETMSGENDV
1			EYNNMELEEGELMEDAAAAGPAGSSHGYVGSSSRISRRTHLCSA
	}	İ	ATSSLLDIDPLILIHLLDLKDRSSIENLWGLQPRPPASLLQPTA
	1		SYSRKDKDQRKQQAMWRVPSDLKMLKRLKTQMAEVRCMKTDVKN
1		1	TLSEIKSSSAASGDMQTSLFSADQAALAACGTENSGRLQDLGME
i	Ì		LLAKSSVANCYIRNSTNKKSNSPKPARSSVAGSLSLRRAVDPGE
			NSRSKGDCQTLSEGSPGSSQSGSRHSSPRALIHGSIGDILPKTE
İ	ł		DRQCKALDSDAVVVAVFSGLPAVEKRRKMVTLGANAKGGHLEGL
			QMTDLENNSETGELQPVLPEGASAAPEEGMSSDSDIECDTENEE
1	1		QEEHTSVGGFHDSFMVMTQPPDEDTHSSFPDGEQIGPEDLSFNT
	·		DENSGR
5979	212	3665	<u></u>
1	"""	3003	LPDMTMYLWLKLLAFGFAFLDTEVFVTGQSPTPSPTDAYLNASE TTTLSPSGSAVISTTTIATTPSKPTCDEKYANITVDYLYNKETK
	j		LFTAKLNVNENVECGNNTCTNNEVHNLTECKNASVSISHNSCTA PDKTLILDVPPGVEKVPVHCCS\QVEQPDSTIWLKWKNIETSTC
	i		
		,	DTQNITYRFQCGNMIFDNKEIKLENLEPEHEYKCDSEILYNSHK
1	}		FTNASKIIKTDFGSPGEPQIIFCRSEAAHQGVITWNPPQRSFHN
		•	FTLCYIKETEKDCLNLDKNLIKYDLQNLKPYTKYVLSLHAYIIA
			KVQRNGSAAMCHFTTKSAPPSQVWNMTVSMTSDNSMHVKCRPPR
1			DRNGPHERYHLEVEAGNTLVRNESHKNCDFRVKDLQYSTDYTFK
1			AYFHNGDYPGEPFILHHSTSYNSKALIAFLAFLIIVTSIALLVV
1			LYKIYDLHKKRSCNLDEQQELVERDDEKQLMNVEPIHADILLET
}			YKRKIADEGRLFLAEFQSIPRVFSKFPIKEARKPFNQNKNRYVD
l .			ILPYDYNRVELSEINGDAGSNYINASYIDGFKEPRKYIAAQGPR
1			DETVDDFWRMIWEQKATVIVMVTRCEEGNRNKCAEYWPSMEEGT
1			RAFGECCCKDLTKHKRCP\DYIIQKLNIVNKKEKATGREVTHIQ
ļ			FTSWPDHGVPEDPHLLLKLRRRVNAFSNFFSGPIVVHCSAGVGR
			TGTYIGIDAMLEGLEAENKVDVYGYVVKLRRQRCLMVQVEAQYI
1			LIHQALVEYNQFGETEVNLSELHPYLHNMKKRDPPSEPSPLEAE
,			FQRLPSYRSWRTQHIGNQE\ENKSKNRNSNVIPYDYNRVPLKHE
ł			LEMSKESEHDSDESSDDDSDSEEPSKYINASFIMSYWKP\EVMI
		•	AAQGPLKETIGDFWQMIFQRKVKVIVMLTELKHGDQEICAQYWG
			EGKQTYGDIEVDLKDTDKSSTYTLRVFELRHSKRKDSRTVYQYQ
•			YTNWSVEQLPAEPKELISMIQVVKQKLPQKNSSEGNKHHKSTPL
1 1	' l		LIHCRDGSQQTGIFCALLNLLESAETEEVVDIFQVVKALRKARP
1			GMVSTFEQYQFLYDVIASTYPAQNGQVKKNNHQEDKIEFDNEVD
			KVKQDANCVNPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNGP
5980	3	2363	ASPALNOGS
3,00	٠	<b>∠</b> 363	DAWGCKLRRLRFTYGTQTRVSLALPGQYELVHTLVAHQGNWETI
1			PEEDLEVQENNEDAAHDLTELEVTMHHALLQEVDVVVAPCQGLR
[			PTVDVLGDLVNDFLPVITYALHKDELSERDEQELQEIRKYFSFP
Į .			VFFFKVPKLGSEIIDSSTRRMESERSPLYRQLIDLGYLSSSHWN
1			CGAPGQDTKAQSMLVEQSEKLRHLSTFSHQVLQTRLVDAAKALN
]		i	LVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKENELYESLMN
1			IANRKQEEMKDMIVETLNTMKEELLDDATNMEFKDVIVPENGEP
1	j	İ	VGTREIKCCIRQIQELIISRLNQAVANKLISSVDYLRESFVGTL
	İ		ERCLQSLEKSQDVSVHITSNYLKQILNAAYHVEVTFHSGSSVTR
į l			MLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAK
}	j	•	SICSQFRTRLNSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVRK
, ,	1		DHAPRLARLSLESRSLQDVLLHRKPKLGQELGRGQYGVVYLCDN
1			WGGHFPCALKSVVPPDEKHWNDLALEFHYMRSLPKHERLVDLHG
j 1			SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIAL
} !			DVVEGIRFLHSQGLVHRDIKLKNVLLDKQNRAKITDLGFCKPEA
}	1		MMSGSIVGTPIHMAPELFTGKYDNSVDVYAFGILFWYICSGSVK
	1		LPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACWDG
	· · · · · · · · · · · · · · · · · · ·		DPLKRPLLGIVQPMLQGIMNRLCKS\NSEQPNRGLDDST
5981	1	2519	GRKHSAAMERPWGAADGLSRWPHGLGLLLLLQLLPPSTLSQDRL
		1	DAPPPPAAPLPRWSGPIGVSWGLRAAAA\GGAFPRGGRWRRSAP
]	ļ		G\EDEECGRVRDFVAKLANNTHQHVFDDLRGSVSLSWVGDSTGV
<u> </u>			ILVLTTFHVPLVIMTFGQSKLYRSEDYGKNFKDITOLINNTFIR

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
{	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\=possible nucleotide insertion)
			TEFGMAIGPENSGKVVLTAEVSGGSRGGRIFRSSDFAKNFVQTD
ì			LPFHPLTQMMYSPQNSDYLLALSTENGLWVSKNFGGKWEEIHKA
ľ			VCLAKWGSDNTIFFTTYANGSCKADLGALELWRTSDLGKSFKTI
ļ			GVKIYSFGLGGRFLFASVMADKDTTRRIHVSTDQGDTWSMAQLP
1			SVGQEQFYSILAANDDMVFMHVDEPGDTGFGTIFTSDDRGIVYS
i			KSLDRHLYTTTGGETDFTNVTSLRGVYITSVLSEDNSIQTMITF DQGGRWTHLRKPENSECDATAKNKNECSLHIHASYSISQKLNVP
İ	]		MAPLSEPNAVGIVIAHGSVGDAISVMVPDVYISDDGGYSWTKML
1			EGPHYYTILDSGGIIVAIEHSSRPINVIKFSTDEGQCWQTYTFT
1			RDPIYPTGLASEPGARSMNISIWGFTESFLTSQWVSYTIDFKDI
1	Ì		LERNCEEKDYTIWLAHSTDPEDYEDGCILGYKEQFLRLRKSSVC
1			QNGRDYVVTKQPSICLCSLEDFLCDFGYYRPENDSKCVEQPELK
			GHDLEFCLYGREEHLTTNGYRKIPGDKCQGGVNPVREVKDLKKK
1			CTSNFLSPEKQNSKSNSVPIILAIVGLMLVTVVAGVLIVKKYVC
			GGRFLVHLYSVLQQH\AEA\NGVDGVDALDTASHTNKSGYHDDS
5982			DEDLLE
3302	56	2316	ATR PPRGSSWCRQFSRTASAAPGRSNMLRIPVRKALVGLSKSPK
1			GCVRTTATAASNLIEVFVDGQSVMVBPGTTVLQACEKVGMQIPR FCYHERLSVAGNCRMCLVEIEKAPKVVAACAMPVMKGWNILTNS
1			EKSKKAREGVMEFLLANHPLDCPICDQGGECDLQDQSMMFGNDR
			SRFLEGKRAVEDKNIGPLVKTIMTRCIQCTRCIRFASEIAGVDD
j			LGTTGRGNDMQVGTYIEKMFMSELSGNIIDICPVGALTSKPYAF
			TARPWETRKTESIDVMDAVGSNIVVSTRTGEVMRILPRMHEDIN
1	i		EEWISDKTRFAYDGLKRQRLTEPMVRNEKGLLTYTSWEDALSRV
1			AGMLQSFQGKDVAAIAGGLVDAEALVALKDLLNRVDSDTLCTEE
			VFPTAGAGTDLRSNYLLNTTIAGVEEADVVLLVGTNPRFEAPLF
			NARIRKSWLHNDLKVALIGSPVDLTYTYDHLGDSPKILQDIASG
1			SHPFSQVLKEAKKPMVVLGSSALQRNDGAAILAAVSSIAQKIRM TSGVTGDWKVMNILHRIASQVAALDLGYKPGVEAIRKNPPKVLF
1			LLGADGGCITRQDLPKDCFIIYQGHHGDVGAPIADVILPGAAYT
	1		EKSATYVNTEGRAQQTKVAVTPPGLAREDWKIIRALSEIAGMTL
] ]			PYDTL\DQVRNRLEEVSPNLVRYDDIEG\ANYFQQANELSKLVN
1			QQLLADPLVPPQLTMKDFYMTDSISRASQTMAKCVKAVTEGAQA
5983			VEEPSIC
3963	248	1763	EARGDGGRRHRASGRRAGRGEP\AGLKSQGQRAVPKRAVARGG
]			RQ\YSAAIALLEPAGSEIADDLSILYSNRAACYLKEGNCSGCIQ
			DCNRALELHPFSMKPLLRRAMAYETLEQYGKAYVDYKTVLQIDC GLQLANDSVNRLSRILMELDGPNWREKLSLIPAVPASVPLOAWH
[ [			PAKEMISKQAGDSSSHRQQGITDEKTFKALKEEGNQCVNDKNYK
1			DALSKYSECLKINNKECAIYTNRALCYLKLCQFEEAKQDCDQAL
1 1	İ		QLADGNVKAFYRRALAHKGLKNYQKSLIDLNKVILLDPSIIEAK
	İ	Ī	MELEEVTRLLNLKDKTAPFNKEKERRKIEIQEVNEGKEEPGRPA
] [	į	İ	GEVSTGCLASEKGGKSSRSPEDPEKLPIAKPNNAYEFGQIINAL
	Ì	ļ	STRKDKEACAHLLAITAPKDLPMFLSNKLEGDTFLLLIQSLKNN
	Į.		LIEKDPSLVYQHLLYLSKAERFKMMLTLISKGQKELIEQLFEDL
5984	755	1193	SDTPNNHFTLEDIQALKRQYEL SSVCMACTYVSNLGKKQRSVSFLASGLMRVSTGPELRLHHSFVL
'			TGDVGRRICRLLVGLFTKGDTSSKRVHPFSPGPCFLLCDLARVG
	1		SSPKINVSPFYQN\QTSTQRSCTVFVWQRCSLVGPFQVTVFTMY
			FHHSLRSISRFSSG
5985	22	1408	RRVARPGTAEPAKARRTVRRGRARRDLAGAERKAGVSERGDSGR
	ļ		RRPNPSIPSAAAGMSHIQIPPGLTELLQGYTVEVLRQQPPDLVE
			FAVEYFTRLREARAPASVLPAATPRQSLGHPPPEPGPDRVADAK
	ŀ	ł	GDSESEEDEDLEVPVPSRFNRRVSVCAETYNPDEEEEDTDPRVI
( )		l	HPKTDEQRCRLQEACKDILLFKNLDQEQLSQVLDAMFERIVKAD
	1	1	EHVIDQGDDGDNFYVIERGTYDILVTKDNQTRSVGQYDNRGSFG
		1	ELALMYNTPRAATIVATSEGSLWGLDRVTFRRIIVKNNAKKRKM
			FESFIESVPLLKSLEVSERMKIVDVIGEKIYKR/DGERIITQGE K\ADSFYIIESGEVSILIRSRTKSNKDGGNQEVEIARCHKGQYF
		į	GELALVTNKPRAASAYAVGDVKCLVMDVQAFERLLGPCMDIMKR
		ł	NISHYEEQLVKMFGSSVDLGNLGO

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
5986	1806	484	\=possible nucleotide insertion)
	1	102	DAWKSTSLTFHWKLWGRHRGRRRGLAHPKNHLSPQQGGATPQVP SPCCRFDSPRGPPPPRLGLLGALMAEDGVRGSPPVPSGPPMEED
	1	ł	GLRWTPKSPLDPDSGLLSCTLPNGFGGQSGPEGERSLAPPDASI
1			LISNVCSIGDHVAQELFQGSDLGMAEEAERPGEK\AGOHSPLRE
1	1		EHVTCVQSILDEFLQT\YGSLIPLSTDEVVEKLEDIFQQEFSTP
			SRKGLVLQLIQSYQRMPGNAMVRGFRVAYKRHVLTMDDLGTLYG
1			QNWLNDQVMNMYGDLVMDTVPEK\VHFPNSFFY\DKLRTKGYDG
J	1		VKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSQ
1			RTLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMNVARQNN
	İ		DSDCGAFVLQYCKHLALSQPFSFTQQDMPKLRRQIYKELCHCKL
			TV
5987	1806	484	DAWKSTSLTFHWKLWGRHRGRRRGLAHPKNHLSPQQGGATPQVP
1			SPCCRFDSPRGPPPPRLGLLGALMAEDGVRGSPPVPSGPPMEED
1	ţ		GLRWTPKSPLDPDSGLLSCTLPNGFGGQSGPEGERSLAPPDASI
1			LISNVCSIGDHVAQELFQGSDLGMAEEAERPGEK\AGQHSPLRE
			EHVTCVQSILDEFLQT\YGSLIPLSTDEVVEKLEDIFQQEFSTP
			SRKGLVLQLIQSYQRMPGNAMVRGFRVAYKRHVLTMDDLGTLYG CNWLNDQVMNMYGDLVMDTVPEK\VHFFNSFFY\DKLRTKGYDG
			VKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSO
			RTLNERCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMNVARQNN
			DSDCGAFVLQYCKHLALSQPFSFTQQDMPKLRRQIYKELCHCKL
ļ	1		TV
5988	1292	410	FKKYPLSFLGLLESSHSRDRIHNLVLMFLLATHNLVWWFTCRFO
			RLDCIYLNAGIMPNPQLNIKALLFGLFS\AEGLLTQGDKITADG
			LQEVFETDVFGHFILIRELEPLLCHSDNPSQLIWTSSRNARKSN
1	•		FSLEDFQHSKGKEPYSSSKYATDLLSVALNRNFNQQGLYSNVAC
1			PGTALTNLTYGILPPFIWTLLMPAILLLRFFANAFTLTPYNGTE
1 1		•	ALVWLFHQKPESLNPLIKYLSATTGFGRNYIMTQKMDLDEDTAE
5989	194	2610	KFYQKLLELEKHIRVTIQKTDNQARLSGSCL
3363	134	2610	AMDFPQHSQHVLEQLNQQRQLGLLCDCTFVVDGVHFKAHKAVLA ACSEYFKMLFVDQKDVVHLDISNAAGLGQVLEFMYTAKLSLSPE
l i			NVDDVL\AVATFLQMQDIITACHALKSLAEPATSPGGNARALAT
1			EGGDKRAKEEKVATSTLSRLEQAGRSTPIGPSRDLKEERGGQAQ
1			SAASGAEQTEKADAPREPPPVELKPDPTSGMAAAEAEAALSESS
			EQEMEVEPARKGEEEQKEQEEQEEGAGPAEVKEEGSQLENGEA
1			PEENENEESAGTDSGQELGSEARGLRSGTYGDRTESKAYGSVIH
	<b>†</b>		KCEDCGKEFTHTGNFKRHIRIHTGEKPFSCRECSKAFSDPAACK
1			AHEKTHSPLKPYGCEECGKSYRLISLLNLRKKRHSGEARYRCED
] [		į	CGKLFTTSGNLKRHQLVHSGEKPYQCDYCGRSFSDPTSKMRHLE
			THOTOKEHKCPHCDKKFNQVGNLKAHLKIHIADGPLKCRECGKQ
			FTTSGNLKRHLRIHSGEKPYVCIHCQRQFADPGALQRHVRIHTG
1 . 1	1	Í	EXPCQCVMCGKAFTQASSLIAHVRQHTGEKPYVCERCGKRFVQS
			SQLANHIRHHDNIRPHKCSVCSKAFVNVGDLSKHIIIHTGEKPY LCDKCGRGFNRVDNLRSHVKTVHQGKAGIKILEPEEGSEVSVVT
			VDDMVTLATEALAATAVTQLTVVPVGAAVTADETEVLKAEISKA
]			VKQVQEEDPNTHILYACDSCGDKFLDANSLAQHVRIHTAQALVM
			FQTDADFYQQYGFGGTWPAGQVLQAGELVFRPRDGAEGOPALAE
<u> </u>	ł		TSPTAPECPPPAE
5990	2	4700	FGPGPDSGGGARGSGWGSRSQAPYGTLGAVSGGEQVLLHEEAGD
	1		SGFVSLSRLGPSLRDKDLEMEELMLQDETLLGTMQSYMDASLIS
<u> </u>			LIEDFGSLGEVEMSLPDPSWDFSPPSFLETSSPKLPSWRPPRSR
[ ]	ł		PRWGQSPPPQQRSDGEEEEEVASFSGQILAGELDNCVSSIPDFP
]	į		MHLACPEBEDKATAAEMAVPAAGDESISSLSELVRAMHPYCLPN
] ]	j		LTHLASLEDELQEQPDDLTLPEGCVVLEIVGQAATAGDDLEIPV
] ]	ļ		VVRQVSPGPRPVLLDDSLETSSALQLLMPTLESETEAAVPKVTL
			CSEKEGLSLNSEEKLDSACLLKPREVVEPVVPKEPQNPPANAAP
	}	ļ	GSQRARKGRKKKSKEQPAACVEGYARRLRSSSRGQSTVGTEVTS
		i	QVDNLQKQPQEELQKESGPLQGKGKPRAWARAWAAALENSSPKN
		Ì	LERSAGQSSPAKEGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS
ı		Į.	PMPVDSVEADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA EPVLINPVLADSAAVDPAVVPISDNLPPVDAVPSGPAPVDLALV
į.	1		

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
İ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ı	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
			DPVPNDLTPVDPVLVKSRPTDPRRGAVSSALGGSAPQLLVESES
ľ	1		LDPPKTIIPEVKEVVDSLKIESGTSATTHEARPRPLSLSEYRRR
			ROQROAETEERSPOPPTGKWPSLPETPTGLADIPCLVIPPAPAK
			KTALQRSPETPLEICLVPVGPSPASPSPEPPVSKPVASSPTEQV
1			PSQEMPLLARPSPPVQSVSPAVPTPPSMSAALPFPAGGLGMPPS
1	İ		LPPP?LQPPSLPLSMGPVLPDPFTHYAPLPSWPCYPHVSPSGYP
	ł		CLPPPPTVPLVSGTPGAYAVPPTCSVPWAPPPAPVSPYSSTCTY
i			GPLGWGPGPQHAPFWSTVPPPPLPPASIGRAVPQPKMESRGTPA
1	ŀ		GPPENVLPLSMAPPLSLGLPGHGAPQTEPTKVEVKPVPASPHPK
į.	į i		HKVSALVQSPQMKALACVSAEGVTVEEPASERLKPETQETRPRB
1			KPPLPATKAVPTPRQSTVPKLPAVHPARLRKLSFLPTPRTQGSE
1			DVVQAFISEIGIEASDLSSLLEQFEKSEAKKECPPPAPADSLAV
1	1		GNSGGVDIPQEKRPLDRLQAPELANVAGLTPPATPPHQLWKPLA
1			AVSLLAKAKSPKSTAQEGTLKPEGVTEAKHPAAVRLQEGVHGPS
1	]		RVHVGSGDHDYC\VRSRTPPKK\MPALLIPEVGSRWNVKRHQDI
]-			TIKPVLSLGPAAPPPPCIAASREPLDHRTSSEQADPSAPCLAPS
			SLLSPEASPCRNDMNTRTPPEPSAKQRSMRCYRKACRSASPSSQ
1			GWQGRRGRNSRSVSSGSNRTSEASSSSSSSSSSSSRSRSRSLSPP
1.		•	HKRWRRSSCSSSGRSRRCSSSSSSSSSSSSSSSSSSSRSRSRS
l			PSPRRRSDRRRRYSSYRSHDHYQRQRVLQKERAIEERRVVFIGK
			IPGRMTRSELKQRFSVFGEIEECTIHFRVQGDNYGFVTYRYAEE
]			AFAAIESGHKLRQADEQPFDLCFGGRRQFCKRSYSDLDSNREDF
			DPAPVKSKFDSLDFDTLLKQAQKNLRR
5991	334	1379	RLSSHFSQCSPSIYC\TKFDKQGNVTSFERKKTELYQELGLQAR
			DLRFQHVMSITVRNNRIIMRMEYLKAVITPECLLILDYRNLNLK
1			QWLFRELPSQLSGEGQLVTYPLPFEFRAIEALLQYWINTLQGKL
			SILQPLILETLDALGDPKHSSVDRSKLHILLQNGKSLSELETDI
<b>,</b>			. KIFKESILEILDEEELLEBLCVSKWSDPQVFEKSSAGIDHAEEM
[		•	ELLLENYYRLADDLSNAARELRVLIDDSQSIIFINLDSHRNVMM
i I			RLNLQLTMGTFSLSLFGLMGVAFGMNLESSLEEDHRIFWLITGI
5992			MFMGSGLIWRRLLSFLGR/LARSSIASYGMKDMVHGGIVEGL
5992	2	609	AGPDFRLVCGVSGSGFPGGRQGQATEWRPLRPWNGAMEKLRRVL
1 1	· .		SGQDDEEQGLTAQDSQINL/SEVLDASSLSFNTRLKWFAICFVC
)	İ		GVFFSILGTGLLWLPGGIKLFAVFYTLGNLAALASTCFLMGPVK
1 .			QLKKMFEATRLLATIVMLLCFIFTLCAALWWHKKGLAVLFCILQ
5993	1650		FLSMTWYSLSYIPYARDAVIKCCSSLLS
3333	1030	594	AEGLGSWAVWAGLGWAGRHMEAGGATGALGVGCKLPSAFCFPGS
ļ <u>1</u>	į		SVAMDMFQKVEKIGEGTYGVVYKAKNRETGQLVALKKIRLDLEM
, ,	1		EGVPSTAIREISLLKELKHPNIVRLLDVVHNERKLYLVFEFLSQ
	į		DLKKYMDSTPGSELPLHLIKSYLFQLLQGVSFCHSHRVIHRDLK
1	İ	İ	PQNLLINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYRAPEI LLATRFYTTAVDIWSIGCIFAEMVTRKALFPGDS\EIDQ\LFRI
] [		i	FRMLGTPSEDTWPGVTQLPDYKGSFPKWTRKGLEEIVPNLEPEG
	Į		
			RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQYVLQRF RH
5994	394	1934	AGEVQLHVWIRGMRIQPQ/KAAAIIDLDPDFEPQSRPRSCTWPL
		1734	PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG
1 1		]	PQPGILGAVTGPRKGGSRRNAWGNQSYAELISQAIESAPEKRLT
[ ]	ļ	j	LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKV
ļ l		ļ	HNEATGKSSWWMLNPEGGKSGKAPRRAASMDSSSKLLRGRSKA
1 1	.	ļ	PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWTT
		ĺ	FRPRSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPPT
		1	LNEGLELLDGLNLTSSHSLLSRSGLSGFSLOHPGVTGPLHTYSS
		1	SLFSPAEGPLSAGEGCFSSSQALEALLTSDTPPPPPADVLMTQVD
		1	PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPTL
	ļ	i	SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY
l			MENLECDMDNIISDLMDEGEGLDFNFEPDP
5995	2	2437	RPPGPGPASGAWLCTRARGSAAFVPPLPRPPSRGARRRRLPGR
[	}		GVAALRRGPGSAPGLPRGRAERSAAGSGRGPSREERGAAAAAA
	1		AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPLNSESSNQSL
			CSVGSLSDKEVETPEKKQNDQRNRKRKAEPYETSQGKGTPRGHK